Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
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young liver	GIBCO	ALV001	5-8 11 20-21 46 50-51 58 65-66
,om.9 11.02			75 79 82 93 97 102-103 108 110
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			493 510-512 516 520 522 526 536
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		ĺ	1283 1295 1317-1320 1332 1339
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adult liver	Invitrogen	ALV002	75 77 86 89 102 108 117 119 175-
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Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
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adult liver	Clontech	ALV003	29 676 997 1063 1119 1536 1766
adult ovary	Invitrogen	ADV003	1 4-18 20-23 29 35-40 42-48 50-
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Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
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adult placenta	Clontech	APLC01	5-8 44-45 90-91 107-108 159 178
			311 351 414 476 503 545 574 624
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			947 955-956 962 990 992 1002
1			1045 1202 1320 1369 1628 1686 1713-1714 1743-1744
placenta	Invitrogen	APL002	14-16 26 29 43 60-61 79-80 103
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l			1664 1673 1675 1722 1727 1730
adult spleen	GIBCO	ASP001	1746 1776 3 5-8 12 15-16 19-21 24 29 34-36
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Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
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		Į	738 744 746 773 780 784 788-789
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ł		}	913 916 919 921 926 929 937 950
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Ì	ļ		1496-1497 1501 1505 1509-1513
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Genomic DNA	Research	BAC001	686 1352 1412
from BAC 63I18	Genetics		j
	(CITB BAC Library)	[
Genomic DNA	Research	BAC002	1411-1412
from BAC 39316	Genetics		
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	Library)	<u> </u>	

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
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addit bradder	invitiogen	BUDGOT	80 93 100 120-121 169 201 237 251-252 272 278 311 348 363 382
			413 415 424 430 443 483 502 542- 543 562 564 607 616-617 626 635 652 667 671 710 727 755-756 762
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	<u> </u>	- FWD001	1732 1739 1741 1760-1761 1779
bone marrow	Clontech	BMD001	3-8 11 13 18 29-31 33 35-36 40 43-45 47-48 50-51 57 60 65-66 75
			80 82 85 88-89 94 100 103 107 110 115 118-119 124-125 133-134
	1		136-137 139-141 146 150 152-153 155 161 163 168-170 172 178-180
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1		•	569-577 581 583-586 588 593 601 603-604 608-609 613-619 621-622
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!			796 798 802 810-812 823-824 826 830 832-833 837-838 843-844 848-
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Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
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•	İ	•	1626-1628 1630-1632 1634 1636
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bone marrow	Clontech	BMD002	11 15-16 19 30-31 35-36 68-69 75
			83-84 93 99 103 108-109 118 137 139 169-170 174 177 180 190 193
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bone marrow	Clontech	BMD004	73-74 503 922 1036 1711
bone marrow	Clontech	BMD007	95-96 866 1320 1475
adult colon	Invitrogen	CLNOOL	17 56-58 103 110 117 144 150 171
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Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
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l			1765
Mixture of 16	Various	CTL016	401 1490 1686
tissues -	Vendors		
mRNAs			
Mixture of 16	Various	CTL021	312 782 1132-1133 1403 1712 1715
tissues -	Vendors		
mRNAs			
adult cervix	BioChain	CVX001	1 4-8 11 13 18-21 25-26 30-31 33
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Į.	ļ		1383-1384 1386 1394 1397 1405-
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^{*} The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphablastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

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fetal brain	Clontech	FBR001	62-63 89 112 126 194 322 336-338
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fetal brain	Clontech	FBR006	80 87 92 101 103 108 114 136 139
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Tissue Origin	DNA Course	Uses =	T CDO TO HOS
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fetal brain	Invitrogen	FBT002	15-18 20-21 24-25 29 34 43 61-63
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lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325-
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lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906-
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050
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1	Y41736	Homo sapiens	Human PRO1114 protein sequence.	1398	100
2	Y66656	Homo sapiens	Membrane-bound protein PRO943.	2389	99
3	AF113136	Homo sapiens	IL-1 receptor-associated- kinase-M; IRAK-M	3043	100
4	AF017806	Mus musculus	Zn-15 transcription factor	6351	77
5	X02761	Homo sapiens	fibronectin precursor	10535	98
6	X02761	Homo sapiens	fibronectin precursor	8990	89
В	X02761	Homo sapiens	fibronectin precursor	12564	99
9	AJ011679	Homo sapiens	Rab6 GTPase activating protein, GAPCenA	5251	99
10	W88501	Homo sapiens	Human stomach carcinoma clone HP10415-encoded protein.	2381	100
11	AF117754	Homo sapiens	thyroid hormone receptor- associated protein complex component TRAP240	11336	98
12	297630	Homo sapiens	dJ466N1.4 (novel protein similar to ANK3 (ankyrin 3, node of Ranvier (ankyrin G)))	896	100
13	Y58620	Homo sapiens	Protein regulating gene expression PRGE-13.	1894	98
14	AF213457	Homo sapiens	triggering receptor expressed on myeloid cells 2	1238	100
16	AF233453	Homo sapiens	RACK-like protein PRKCBP1	3124	99
17	AF201303	Homo sapiens	dhfr oribeta-binding protein	3130	98
18	AF064205	Homo sapiens	dynactin 1 p150 isoform	6377	100
19	U00059	Saccharomyce s cerevisiae	Yhr121wp	174	26
20	AB032903	Homo sapiens	guanosine monophosphate reductase isolog	1801	99
21	AB032903	Homo sapiens	guanosine monophosphate reductase isolog	1485	99
22	AF140507	Homo sapiens	Ca2+/calmodulin-dependent protein kinase kinase beta	3083	99
23	AF140507	Homo sapiens	Ca2+/calmodulin-dependent protein kinase kinase beta	2300	99
24	AJ289131	Homo sapiens	chondroitin 4-0- sulfotransferase	2211	99
25	U33460	Homo sapiens	DNA-directed RNA polymerase I, largest subunit	8777	98
26	Y44488	Homo sapiens	ACRP30R2 variant protein.	1387	100
27	U43701	Homo sapiens	ribosomal protein L23a	791	100
28	U02032	Homo sapiens	ribosomal protein L23a	767	97
29	Y41324	Homo sapiens	Human secreted protein encoded by gene 17 clone HNFIY77.	1083	99
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30	W71749	Homo sapiens	Human ubiquitin conjugation	715	90
31	W71749	Homo sapiens Homo sapiens	system protein 2. Human ubiquitin conjugation	715 631	82
			system protein 2. Human ubiquitin conjugation system protein 2. long-chain 2-hydroxy acid		[
31	W71749	Homo sapiens	system protein 2. Human ubiquitin conjugation system protein 2. long-chain 2-hydroxy acid oxidase HAOX2 3-hydroxyanthranilic acid	631	82
31	W71749 AF231917 Z29481	Homo sapiens Homo sapiens Homo sapiens	system protein 2. Human ubiquitin conjugation system protein 2. long-chain 2-hydroxy acid oxidase HAOX2 3-hydroxyanthranilic acid dioxygenase	1811 1507	100
31 32 33	W71749 AF231917	Homo sapiens	system protein 2. Human ubiquitin conjugation system protein 2. long-chain 2-hydroxy acid oxidase HAOX2 3-hydroxyanthranilic acid dioxygenase Sck precursor polypeptide (AA -34	631	100
31 32 33	W71749 AF231917 Z29481 AB001451	Homo sapiens Homo sapiens Homo sapiens	system protein 2. Human ubiquitin conjugation system protein 2. long-chain 2-hydroxy acid oxidase HAOX2 3-hydroxyanthranilic acid dioxygenase Sck precursor polypeptide (AA -34 to 287) precursor polypeptide (AA -34	1811 1507 2869	82 100 99
31 32 33 34 35	W71749 AF231917 Z29481 AB001451 Y00644	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	system protein 2. Human ubiquitin conjugation system protein 2. long-chain 2-hydroxy acid oxidase HAOX2 3-hydroxyanthranilic acid dioxygenase Sck precursor polypeptide (AA -34 to 287)	631 1811 1507 2869 1667	82 100 99 100 99

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
39	Y78795	Homo sapiens	Human antizuai-2 (AZ-2) amino acid sequence.	3556	77
40	U93121	Homo sapiens	M-phase phosphoprotein-1	3747	100
41	Y42750	Homo sapiens	Human calcium binding protein 1 (CaBP-1).	795	100
42	AF282626	Homo sapiens	latexin	1189	100
43	G02150	Homo sapiens	Human secreted protein, SEQ ID NO: 6231.	384	94
44	U19617	Mus musculus	Elf-1	2724	88
45	U19617	Mus musculus	Elf-1	2062	86
46	AF100758	Homo sapiens	osteoinductive factor OIF	1538	100
47	Y87591	Homo sapiens	Human SPROUTY-1 protein, SEQ ID NO:24.	1737	99
49	X04145	Homo sapiens	T3 gamma precursor (aa -22 to 160)	942	99
51	X63547	Homo sapiens	oncogene	5845	99
52	M94043	Rattus	rab-related GTP-binding	1089	96
	121762	norvegicus	protein uridine kinase	917	71
53	L31783 X83973	Mus musculus Homo sapiens	transcription factor	4486	98
54 55	X83973 AF224741	Homo sapiens	chloride channel protein 7	4128	99
56	W74805	Homo sapiens	Human secreted protein	1491	100
56	1 414003	nomo saprema	encoded by gene 77 clone HOEAS24.		
57	250907	Homo sapiens	Human TBC-1 cDNA from second transcript.	4824	100
58	D79994	Homo sapiens	similar to ankyrin of Chromatium vinosum.	6089	99
59	D79994	Homo sapiens	similar to ankyrin of Chromatium vinosum.	4014	91
60	Y59738	Homo sapiens	Human normal ovarian tissue derived protein 15.	601	100
61	AB031069	Homo sapiens	protein containing CXXC domain 1	1390	100
62	X66660	Homo sapiens	Membrane-bound protein PRO783.	2492	99
63	Y66660	Homo sapiens	Membrane-bound protein PRO783.	1709	99
64	S70011	Rattus sp.	tricarboxylate carrier	895	55
65	AF139518	Rattus norvegicus	A-kinase anchor protein	178	24
66	W29666	Homo sapiens	Homo sapiens DH1308_1 clone secreted protein.	157	30
67	AJ245738	Homo sapiens	claudin-15	1206	100
68	AF099138	Rattus norvegicus	GLUT4 vesicle protein	4183	87
69	AF099138	Rattus norvegicus	GLUT4 vesicle protein	4906	86
70	Z82059	Caenorhabdit is elegans	Similarity to Drosophila ring canal protein comes from this gene	1285	44
71	AF224278	Homo sapiens	PMEPAl protein	1282	100
72	AF126426	Homo sapiens	neurotrimin	1809	100
73	Y41652	Homo sapiens	Human MEK2 protein sequence.	2065	99
74	Y41652	Homo sapiens	Human MEK2 protein sequence.	1207	100
75	AF188622	Mus musculus	selectively expressed in embryonic epithelia protein-1	1485	74
76	AE000406	Escherichia coli	putative DNA topoisomerase	950	100
77	X99302	Homo sapiens	Pop1	655	100
78	AL136538	Schizosaccha romyces pombe	similarity to S. cerevisiae kti12 protein	210	31
	•	I houme	1		1

TABLE 2

SEQ	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	identity
NO:				SCORE	
80	AL096768	Homo sapiens	dJ858B16.2 (phosphatidylserine	2033	100
	1		decarboxylase (PSSC, EC	1	
			4.1.1.65))	}	ļ
81	AL096768	Homo sapiens	dJ858B16.2	1220	96
			(phosphatidylserine	1	
	Į.		decarboxylase (PSSC, EC 4.1.1.65))		
82	X57351	Homo sapiens	1-8D	677	98
83	AC005594	Homo sapiens	R26984 1	2700	98
84	X73113	Homo sapiens	fast MyBP-C	5959	99
85	AF097330	Homo sapiens	H1 chloride channel; p64H1;	1305	99
		ļ	CLIC4		
86	AB018423 AF272151	Mus musculus	SH2 domain-containing protein	3084	78
88	AF196329	Homo sapiens	adaptor protein CIKS triggering receptor expressed	1214	99
80	AF 1 3 6 3 2 3	sapiens	on monocytes 1	1214	100
89	AB016879	Arabidopsis	contains similarity to pre-	634	36
		thaliana	mRNA splicing	1	•
	<u></u>	<u> </u>	factor~gene_id:MRB17.2		
90	AJ133721	Mus musculus	homeodomain protein	654	57
91	AJ242864 A61971	Mus musculus unidentified	phtf protein	619 11676	61
93	Y99365	Homo sapiens	Human PRO1250 (UNQ633) amino	3890	100
73	133303	nomo sapiens	acid sequence SEQ ID NO:86.	3690	100
94	Y87231	Homo sapiens	Human signal peptide	1031	100
			containing protein HSPP-8		
			SEQ ID NO:8.		
95	AF227741	Rattus	protein kinase WNK1	2428	95
96	AF227741	norvegicus Rattus	protein kinase WNK1	1961	94
70	AL 22//11	norvegicus	procein kinase maki	1361	1 34
97	Y92513	Homo sapiens	Human OXRE-10.	1626	100
98	AL021366	Homo sapiens	cICK0721Q.3 (Kinesin related	3423	100
	<u> </u>		protein)		
99	AC005783	Homo sapiens	R33083_1	1974	99
100	Y95293	Homo sapiens	Human GEF containing NEK-like kinase substrate sGNK.	4092	99
101	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein	1509	100
202	1.12110301	nomo bapreno	(translation of the cDNA	1305	100
			DKFZp566A0946, Em:AL050069))		J
102	AJ006267	Homo sapiens	ClpX-like protein	3233	100
103	AF100753	Homo sapiens	ancient ubiquitous 46 kDa	2042	96
104	1,500		protein AUP1	122	
104	AB015982 AF151074	Homo sapiens	serine/threonine kinase	4718 831	100
106	M35522	Canis	GTP-binding protein (rab7)	354	50
	1.2322	familiaris	January Process (1997)	33.	30
107	R99800	Homo sapiens	NTII-1 nerve protein,	2337	93
			facilitates regeneration of	}	1
		<u> </u>	nerve cells.		
108	AF125533	Homo sapiens	NADH-cytochrome b5 reductase	1290	93
109	AC005614	Homo sapiens	isoform F23269 2	3369	99
110	AF064729	Homo sapiens	RAN binding protein 16	3285	100
111	X52425	Homo sapiens	interleukin 4 receptor	4496	100
112	Y41686	Homo	Human PRO274 protein	2285	100
		sapiens	sequence.		
113	W15506	Homo sapiens	Mitogen activating protein	1991	100
			kinase ERK1.		
114	Y71071	Homo sapiens	Human membrane transport	1190	99
115	AL049548	Homo sapiens	protein, MTRP-16. dJ398G3.1 (ortholog of rat	3497	99
**7	AUUTSSTO	TOWN BADIENS	CPG2)	343/	99
116	AF189817	Mus musculus	evectin-2	1124	90
117	W30891	Homo	Human cytostatin III protein.	715	99

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
		sapiens			
118	AF116618	Homo sapiens	PRO1038	1469	100
119	Y08915	Homo sapiens	alpha 4 protein	1748	100
120	AF098070	Drosophila melanogaster	Lis1 homolog	192	39
121	AF052432	Homo sapiens	katanin p80 subunit	181	37
122	Y70743	Homo sapiens	PSEQ-1 protein encoded by NSEQ gene associated with matrix remodelling.	2637	98
123	AF083246	Homo sapiens	HSPC028	2132	100
124	Y27096	Homo sapiens	Human viral receptor protein (ACVRP).	833	99
125	M63109	Leishmania major	glycoprotein 96-92	172	27
126	U75467	Drosophila melanogaster	Atu	935	36
127	268220	Caenorhabdit is elegans	Similarity to Human ADP/ATP carrier protein	438	43
128	AF095927	Rattus norvegicus	protein phosphatase 2C	1927	94
129	W92958	Homo sapiens	Human zsig44 protein.	463	100
130	AF115391	Lactobacillu s sakei	ribokinase RbsK	508	37
131	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	1250	100
132	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	916	87
133	W52811	Homo sapiens	Human DBI/ACBP -like protein (DBIH).	705	97
134	Y84444	Homo sapiens	Amino acid sequence of a human RNA-associated protein.	3230	100
135	M69181	Homo sapiens	non-muscle myosin B	189	20
136	W74882	Homo sapiens	Human secreted protein encoded by gene 154 clone HE6FL83.	480	100
137	W78200	Homo sapiens	Human secreted protein encoded by gene 75 clone HHGAU81.	855	99
138	AL033520	Homo sapiens	dJ349A12.1 (similar to KIAA0701 protein)	424	39
139	AF020261	Santalum	proline rich protein	119	30
140	X70394	Homo sapiens	zinc finger protein	1634	100
141	Y06439	Homo sapiens	Human protease HUPM-8.	936	100
142	Z68493	Caenorhabdit is elegans	predicted using Genefinder	365	42
143	AB018107	Arabidopsis thaliana	ADP-ribosylation factor-like protein	596	65
144	AF161483	Homo sapiens	HSPC134	580	51
145	Y84902	Homo sapiens		480	100
146	AB004906	Ipomoea purpurea	transposase	146	20
147	AC007357	Arabidopsis thaliana	F3F19.18	647	31
148	W75155	Homo sapiens	encoded by gene 41 clone HNTME13.	1494	98
149	AP056490	Homo sapiens	phosphodiesterase 8A	3710	99
150	Y58171	Homo sapiens	Human hydrolase homologue HHH-7.	785	99
151	U10397	Saccharomyce s cerevisiae	Yhr148wp	515	53
152	X73478	Homo sapiens	1	1719	99

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:				SCORE	
	 		similar to arginyl-tRNA)		
154	AF169802	Homo sapiens	cytochrome b5 reductase b5R.2	1455	99
155	X94703	Homo sapiens	rab28	1126	99
156	Y25716	Homo sapiens	Human secreted protein encoded from gene 6.	1471	100
158	W77404	Homo sapiens	Secreted salivary polypeptide zsiq32.	937	100
159	Y17248	Homo sapiens	Human protein kinase inhibitor-2 (PKI-2).	383	100
160	J04970	Homo sapiens	carboxypeptidase M precursor	2395	100
161	W54040	Homo sapiens	Human interferon-inducible protein, HIFI.	484	98
162	AL022724	Homo sapiens	dJ413H6.1.1 (hamster Androgen-dependent Expressed Protein LIKE PUTATIVE protein) (isoform 1)	1357	100
163	AF125535	Homo sapiens	pp21 homolog	193	45
164	G03632	Homo sapiens	Human secreted protein, SEQ ID NO: 7713.	463	97
165	AJ250839	Homo sapiens	serine/threonine protein kinase	1442	71
166	L09649	Zymomonas mobilis	zm2	173	37
167	¥73337	Homo sapiens	HTRM clone 1944530 protein sequence.	1204	100
168	W88645	Homo sapiens	Secreted protein encoded by gene 112 clone HUKFC71.	1084	100
169	AF214731	Homo sapiens	ATP-dependent RNA helicase	4402	100
170	AE000871	Methanobacte rium thermoautotr ophicum	conserved protein	166	27
171	Y27684	Homo sapiens	Human secreted protein encoded by gene No. 118.	821	100
172	AF226044	Homo sapiens	HSNFRK	2904	100
173	AJ245946	Homo sapiens	neuroglobin	779	100
174	D43949	Homo sapiens	This gene is novel.	3202	100
175 176	¥07923 ₩90338	Homo sapiens	GTP-binding protein Human DP1 homologue protein.	966	100
177	Y41675	sapiens Homo sapiens	Human channel-related molecule HCRM-3.	1122	100
178	Y41674	Homo sapiens	Human channel-related molecule HCRM-2.	936	99
179	AF220492	Homo sapiens	krueppel-like zinc finger protein HZF2	4100	99
180	X03084	Homo sapiens	Clq B-chain precursor	1240	100
181	U57344	Mus musculus	Meis3	1813	89
183	U57344	Mus musculus	Meis3	1743	86
184	U57344	Mus musculus	Meis3	1070	86
185	AF033120	Homo sapiens	p53 regulated PA26-T2 nuclear protein	1389	58
186	AF200357	Mus musculus	pantothenate kinase 1 beta	1605	82
187	W75058	Homo sapiens	Human secreted protein encoded by gene 2 clone HLDBG33.	1188	99
188	AJ292529	Homo sapiens	suppressor of sterile four 1	2424	100
190	X54134	Homo sapiens	protein-tyrosine phosphatase	3705	100
191	Y22203	Homo sapiens	Human calcium-binding phosphoprotein, CBPP-1, protein sequence.	1083	99
192	W63692	Homo sapiens	Human secreted protein 12.	1975	100
193	W87772	Homo sapiens	Human serum glucocorticoid- regulated kinase (H-SGK2) polypeptide.	2605	99

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	*
ID NO:	NUMBER			WATERMAN SCORE	IDENTITY
		Mus musculus	bromodomain-containing protein BP75	693	54
195	Y00752	Rattus norvegicus	serine dehydratase (AA 1 - 327)	994	61
196	W95349	Homo sapiens	Human foetal brain secreted protein fh170_7.	2596	100
197	AB028859	Homo sapiens	hDj9	1890	100
198	W95633	Homo sapiens	Homo sapiens secreted protein gene clone hm236_1.	1614	100
199	Y44277	Homo sapiens	Human nucleic acid methylase- 2.	2096	99
200	AB030039	Homo sapiens	hPACPL1	2258	100
201	X54162	Homo sapiens	64 Kd autoantigen	2918	99
202	G02061	Homo sapiens	Human secreted protein, SEQ ID NO: 6142.	558	99
203	X13885	Nicotiana tabacum	extensin (AA 1-620)	185	33
204	J04204	Bos taurus	32 kd accessory protein	1837	100
205	J04204	Bos taurus	32 kd accessory protein	1101	100
207	Y87283	Homo sapiens	Human signal peptide containing protein HSPP-60 SEQ ID NO:60.	1318	100
208	Y02860	Homo sapiens	Fragment of human secreted protein encoded by gene 65.	936	98
209	AL121889	Homo sapiens	dJ1076E17.1 (KIAA0823 protein (continues in AL023803))	694	54
210	AF226732	Homo sapiens	NPD007	1345	76
211	X66295	Mus musculus	Clq C chain	970	73
212	Z29328	Homo sapiens	Ubiquitin-conjugating enzyme UbcH2	966	100
213	229328	Homo sapiens	Ubiquitin-conjugating enzyme UbcH2	542	98
214	AJ002030	Homo sapiens	progresterone binding protein	1163	100
215	X70649	Homo sapiens	member of DEAD box protein family	3933	100
216	AF250558	Homo sapiens	claudin-2	1169	99
217	AL021453	Homo sapiens	dJ821D11.1 (PUTATIVE protein)	259	100
218	Y08565	Homo sapiens	UDP-GalNAc:polypeptide N- acetylgalactosaminyltransfera se	3331	99
219	Y94452	Homo sapiens	Human inflammation associated protein	2067	100
220	AL035521	Arabidopsis thaliana	putative protein	315	42
221	AL031786	Schizosaccha romyces pombe	putative proline-trna synthetase	811	41
222	AL109736	Schizosaccha romyces pombe	WD repeat protein	626	40
223	X52493	Glycine max	DNA-directed RNA polymerase	136	23
224	AL035659	Homo sapiens	dJ979N1.1 (dJ979N1.1)	5199	98
226	AB032401 AB032401	Mus musculus	mmDj4	1761	92
227	X83502	Mus musculus	mmDj4	1988	92
228		Saccharomyce s cerevisiae	J1007	112	26
	X83502	Saccharomyce s cerevisiae	J1007	79	25
229	AF143723	Homo sapiens	heat shock protein HSP60	2557	99
230	Y66677	Homo sapiens	Membrane-bound protein PRO828.	982	100
231	AB027466	Homo sapiens	spondin 2	1756	99
232	W95634	Homo sapiens	Homo sapiens secreted protein.	1391	100
233	W00365	Homo sapiens	Human cyclin Bl.	2218	99
234	Y53762	Homo sapiens	A GTP-binding polypeptide	1017	100

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	+
ID NO:	NUMBER			WATERMAN SCORE	IDENTITY
			designated RAQ.		
235	Z50749	Homo sapiens	yeast sds22 homolog	1800	100
236	Z50749	Homo sapiens	yeast sds22 homolog	1754	98
237	AB026491	Homo sapiens	PICK1	2137	100
238	AJ270205	Entodinium	putative	114	37
	ļ	caudatum	phosphatidylinositol-4-	}]
	1		phosphate 5-kinase contains transmembrane (TM)		ļ
239	AB030189	Mus musculus	region and ATP binding region	710	93
240	W56538	Homo sapiens	Human hedgehog interacting protein (HIP).	3785	99
241	W56538	Homo sapiens	Human hedgehog interacting protein (HIP).	3436	99
242	AF155107	Homo sapiens	NY-REN-37 antigen	996	99
243	AF155107	Homo sapiens	NY-REN-37 antigen	1005	100
244	AL031320	Homo sapiens	dJ20N2.1 (novel protein	763	99
		, nome daptions	similar to yeast and bacterial cytosine		
245	U37026	Rattus	deaminase) sodium channel beta 2 subunit	162	30
		norvegicus			
246	AL078599	Homo sapiens	dJ991C6.1 (novel protein	2391	98
			similar to C. elegans	i	1
			F55A12.9 (Tr:P91086))		1
247	U32274	Saccharomyce s cerevisiae	Ydr386wp; CAI: 0.12	191	37
248	Y41719	Homo sapiens	Human PRO864 protein sequence.	1879	100
249	AB029434	Homo sapiens	ghrelin precursor	611	100
250	X97831	Rattus norvegicus	carnitine/acylcarnitine carrier protein	246	38
251	W80993	Homo sapiens	Human RIP-interacting factor RIF.	1724	100
252	Y94873	Homo	Human protein clone HP02632.	1876	100
253	W59878	sapiens Homo sapiens	Amino acid sequence of the	765	100
254	AL354533	Leishmania	cDNA clone AIF-2 (HEBGM49). possible adenylate kinase	265	34
		major	, , , , , , , , , , , , , , , , , , , ,	1	
255	AF233322	Mus musculus	zinc transporter like 2	1916	95
256	Y78113	Homo sapiens	Human cytokine signal regulator CKSR-1 SEQ ID NO:1.	2247	99
257	AL035539	Arabidopsis	putative amino acid transport	390	27
258	W74787	thaliana Homo sapiens	protein Human secreted protein	1171	100
258	W/4/8/	Homo sapiens	encoded by gene 58 clone HHFHN61.	11/1	100
259	AL035689	Homo sapiens	dJ187J11.1 (novel protein	974	100
			similar to protein kinase C inhibitors)		
260	AE000909	Methanobacte	serine/threonine protein	363	30
		rium thermoautotr	kinase related protein		1
		ophicum]
261	AL050131	Homo sapiens	hypothetical protein	626	100
262	AF019661	Mus musculus	zeta proteasome chain; PSMA5	1214	100
263	AL035593	Homo sapiens	dJ310J6.1 (novel protein)	821	100
264	AL022318	Homo sapiens	bK150C2.3 (PUTATIVE novel	1072	100
			protein similar to APOBEC1)	·	
265	AF205940	Homo sapiens	endomucin	1289	100
266	AL023583	Homo sapiens	dJ500L14.1 (novel protein)	789	100
267	AL034548	Homo sapiens	dJ1103G7.3 (novel protein kinase domains containing	1888	99
	1	Į.	protein similar to		l .

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	-
ID NO:	NUMBER			WATERMAN SCORE	IDENTITY
268	AF161470	Homo sapiens	HSPC121	1884	98
269	AF161470	Homo sapiens	HSPC121	1232	96
270	X90763	Ното	HHa5 hair keratin type I	2190	99
2.0	1.50703	sapiens	intermediate filament	12130	33
271	AF207600	Homo sapiens	ethanolamine kinase	1952	100
272	M32334	Homo sapiens	intercellular adhesion	1436	100
	1.52551	lionio bapaono	molecule 2	1430	100
273	AF161483	Homo sapiens	HSPC134	663	61
274	Y53C52	Homo sapiens	Human secreted protein clone df202 3 protein sequence SEQ	587	100
		j	ID NO:110.		
276	Y77576	Homo sapiens	Human cytoskeletal protein (HCYT) (clone 2195418).	762	100
277	AF077042	Homo sapiens	30S ribosomal protein S7	1269	100
0.50	704000		homolog		
278	Y94907	Homo sapiens	Human secreted protein clone ca106_19x protein sequence SEQ ID NO:20.	1619	98
279	Y68788	Homo sapiens	Amino acid sequence of a	2801	-99
			human phosphorylation effector PHSP-20.		
280	275134	Canis	rod transducin	1816	100
		familiaris			İ
281	275134	Canis familiaris	rod transducin	1718	96
282	AF249873	Homo sapiens	muscle-specific protein	1395	100
283	AL050007	Homo sapiens	hypothetical protein	405	98
284	AF201931	Homo sapiens	DC1	1859	99
285	AF156102	Homo sapiens	ELL complex EAP30 subunit	1318	99
286	Y35897	Homo sapiens	Extended human secreted	1250	99
200	133037	nomo baptens	protein sequence, SEQ ID NO.	1230	
287	U88964	Homo sapiens	HEM45	923	100
288	AL050143	Homo sapiens	hypothetical protein	598	100
289	AJ011098	Homo sapiens	telethonin	574	100
290	Y66724	Homo	Membrane-bound protein	2321	100
		sapiens	PRO836.		
291	AF034801	Homo sapiens	liprin-alpha4	2565	98
292	AF034801	Homo sapiens	liprin-alpha4	2590	100
293	AL049851	Homo sapiens	dJ889J22B.1 (novel protein	1738	100
294	Y73348	Homo sapiens	(isoform 1)) HTRM clone 839651 protein	1245	99
			sequence.		l
295	L11672	Homo sapiens	zinc finger protein	1694	44
296	AL035423	Homo sapiens	dJ2013.1 (brain mitochondrial carrier protein-1 (BMCP1))	1024	79
297	AF198532	Homo sapiens	lymphoid enhancer binding factor-1	2173	100
298	AF161417	Homo sapiens	HSPC299	1147	85
299	AF159141	Homo sapiens	breast cancer metastasis- suppressor 1	1236	99
300	U26397	Rattus	inositol polyphosphate 4-	160	30
301	AF036145	norvegicus Homo sapiens	phosphatase meningioma-expressed antigen	3458	100
			5		L
302	Z82022	Homo sapiens	GlcNac-1-P transferase	2067	99
303	AF269232	Mus musculus	butyrophilin-like protein BUTR-1	271	50
304	AJ222644	Arabidopsis thaliana	asparaginyl-tRNA synthetase	659	50
305	AF054180	Homo	hematopoietic cell derived	351	79
200	3 70 70 0 70	sapiens	zinc finger protein		
306	AJ272079	Homo sapiens	APOBEC-1 stimulating protein	3056	100
308	Y44486	Homo sapiens	Human GPRW receptor polypeptide.	1721	100
309	AJ131891	Homo sapiens	DNA polymerase mu	2598	100

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	*
NO:	NUMBER	1		WATERMAN	IDENTITY
310	AF293335	Homo sapiens	p30 DBC	SCORE 1248	J
311	AF176525	Mus musculus	F-box protein FBL12	1501	92
312	X57802	Homo sapiens	immunoglobulin lambda light	959 .	81
3-1	X37002	HOMO Baptens	chain	759 .	1 **
313	Z36715	Homo sapiens	Net	2048	98
314	AF161532	Homo sapiens	HSPC047	727	100
315	AF208068	Homo sapiens	kelch-like protein KLHL3a	3046	100
316	Y66666	Homo	Membrane-bound protein	1166	100
		sapiens	PRO1013.	1100	100
317	Y29666	Homo sapiens	Human Ras protein RAPR-1.	1253	98
318	AJ387747	Homo sapiens	sialin	2614	99
319	AF161362	Homo sapiens	HSPC099	224	40
320	Y68773	Homo sapiens	Amino acid sequence of a	2243	99
			human phosphorylation		
			effector PHSP-5.		
321	AJ238379	Homo sapiens	putative TH1 protein	3013	100
322	AB040812	Homo sapiens	protein kinase PAK5	3792	99
323	Y95013	Homo sapiens	Human secreted protein	913	100
			vc48_1, SEQ ID NO:66.		
324	Y13381	Homo sapiens	Amino acid sequence of	1976	100
	1		protein PRO271.		l
325	Y94944	Homo sapiens	Human secreted protein clone	2305	98
l			bf157_16 protein sequence		ľ
	7/5/2014		SEQ ID NO:94.		
326	Y76884	Homo sapiens	Retinoblastoma binding	6728	99
327	AF198532	Homo sapiens	protein-7sequence. lymphoid enhancer binding	2173	100
321	AC130552	Homo saprens	factor-1	21/3	100
328	278013	Caenorhabdit	Similarity to Drosophila	569	33
""	2,0025	is elegans	Cadherin-related tumor	1 309	33
			suppressor		
329	AF212921	Mus musculus	MMTV receptor variant 1	484	94
330	Z75330	Homo	nuclear protein SA-1	6492	99
1		sapiens]	-		
		>R65207			
İ	}	R65207 02-			1
1	1	MAR-1995 27-			1
		AUG-1993		1	}
		Human stromalin-1.		1	
		[Homo			1
	1	sapiens			
331	At-008583	Homo sapiens	dJ327J16.3 (supported by	2133	99
		liomo baprono	GENSCAN, FGENES and GENEWISE)	1 2 2 3 3	"
332	Y36104	Homo sapiens	Extended human secreted	310	41
			protein sequence, SEQ ID NO.		
	j		489.		1
333	AJ271669	Homo sapiens	putative sialoglycoprotease	1747	100
334	AF156598	Mus musculus	p53-regulated DDA3	997	64
335	M99058	Eimeria	em100 gene is homologous the	154	26
		maxima	Bimeria tenella gene et100		
336	Y85564	Homo sapiens	Human homologue of UNC-53	3386	97
	110.55	ļ <u>.</u>	(Hs-UNC-53/1) sequence.	<u> </u>	
337	Y85564	Homo sapiens	Human homologue of UNC-53	2602	94
226	VOEEC4	11000 0==1=	(Hs-UNC-53/1) sequence.		
338	Y85564	Homo sapiens	Human homologue of UNC-53	3447	98
339	Z66561	Caenorhabdit	(Hs-UNC-53/1) sequence.	726	
و د د	200201	is elegans	Similarity to Human rabl3	716	34
1		To eredans	protein (PIR Acc. No. A49647).		İ
340	AB021643	Ното	gonadotropin inducible	2761	99
		sapiens	transcription repressor-3	2,01	33
341	G01946	Homo sapiens	Human secreted protein, SEQ	465	98
			ID NO: 6027.	100	
1 1 1 1	AF020591	Homo sapiens	zinc finger protein	1091	48
342	AF020551	l mone against	zinc ringer procern	1 1031	70 1
342	L29154	Homo sapiens	immunoglobulin heavy chain	439	84

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
ID	NUMBER			WATERMAN	IDENTITY
NO:				SCORE	
			VDJ region		
344	U10281	Sus scrofa	gastric mucin	279	24
345	AK000404	Homo sapiens	unnamed protein product	1177	99
346	L22557	Rattus norvegicus	calmodulin-binding protein	1949	84
347	L22557	Rattus norvegicus	calmodulin-binding protein	2363	91
348	AL049481	Arabidopsis thaliana	AIG1-like protein	316	30
350	AJ251516	Mus musculus	cysteine and histidine-rich protein	1460	99
351	AK024477	Homo sapiens	FLJ00070 protein	1773	100
352	U50133	Homo sapiens	ankyrin	502	33
353	AK000625	Homo sapiens	unnamed protein product	721	100
354	AF161420	Homo sapiens	HSPC302	2623	97
355	AJ010014	Homo sapiens	M96A protein	1269	47
356	AF151029	Homo sapiens	HSPC195	941	91
357	AL022327	Homo sapiens	dJ355C18.1 (KIAA0027)	1911	100
358	W78128	Homo sapiens	Human secreted protein encoded by gene 3 clone HOSBI96.	1117	100
359	X03414	Drosophila melanogaster	Kr polypeptide	316	45
360	AF151079	Homo sapiens	HSPC245	643	100
361	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	530	41
362	AF254741	Drosophila melanogaster	Centaurin Gamma 1A	681	46
363	AF213465	Homo sapiens	dual oxidase	2016	100
364	AF181562	Homo sapiens	proSAAS	1319	100
365	AF181562	Homo sapiens	proSAAS	1024	99
366	U73200	Mus musculus	pl16Rip	884	82
367	AF263744	Homo sapiens	erbb2-interacting protein ERBIN	4973	99
368	U37501	Mus musculus	laminin alpha 5 chain	5867	72
369	AF043695	Caenorhabdit is elegans	similar to the protein phosphates 2c family	549	36
370	Y73440	Homo sapiens	Human secreted protein clone yj23_1 protein sequence SEQ ID NO:102.	1484	99
371	AF272833	Homo sapiens	misato	2869	97
372	AF198454	Homo sapiens	epithelial protein lost in neoplasm beta	3927	100
373	Y73345	Homo sapiens	HTRM clone 438283 protein sequence.	273	80
374	AF169017	Homo sapiens	formiminotransferase cyclodeaminase	2717	98
375	A95106	unidentified	RED ALPHA	1202	99
376	W74828	Homo sapiens	Human secreted protein encoded by gene 100 clone HLQAB52.	1012	99
377	Y32131	Homo sapiens	Human LYST-2 protein.	3556	99
378	M14912	Homo sapiens	pol	132	86
379	AF090934	Homo sapiens	PR00518	382	100
380	X66363	Homo sapiens	serine/threonine protein kinase	2499	100
381	Y41699	Homo sapiens	Human PR0703 protein sequence.	2362	100
382	AF174498	Homo sapiens	GR AF-1 specific protein phosphatase	7008	98
383	U6460B	Caenorhabdit is elegans	coded for by C. elegans cDNA yk173c12.5	246	36
384	U50133	Homo sapiens	ankyrin	502	33
385	AJ238520	Homo sapiens	putative transcription	4123	97
	<u> </u>		factor-like nuclear regulator		

TABLE 2

SEQ	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:				SCORE	IDENTITI
387	AF208845	Homo sapiens	BM-003	1375	99
389	X57821	Homo sapiens	immunoglobulin lambda light chain	797	76
390	AF182404	Homo sapiens	mitochondrial uncoupling protein 1	1670	99
391	Y85564	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	3386	97
393	AF178432	Homo sapiens	SH3 protein	3700	100
394	AF229928	Drosophila melanogaster	cytoplasmic protein 89BC	1616	62
395	AF181721	Homo sapiens	RU2S	2254	100
396	Y69197	Homo sapiens	Amino acid sequence of a human betaIV-spectrin protein.	1626	98
397	U48238	Mus musculus	zinc finger protein neuro-d4	749	60
398 399	AL390137	Homo sapiens	hypothetical protein	263	51
	AF217525	Homo sapiens	Down syndrome cell adhesion molecule	5337	60
400	AL022599	Schizosaccha romyces pombe	WD repeat protein	447	27
401	AC004B59	Homo sapiens	similar to 2-oxoglutarate dehydrogenase; similar to Q02218 (PID:g1352618)	4176	78
402	AB010266	Mus musculus	tenascin-X	10246	62
403	AL133288	Homo sapiens	dJ671D7.1 (similar to D.melanogaster CG5986 protein)	761	100
404	268753	Caenorhabdit is elegans	ZC518.3b	888	48
405	Z78013	Caenorhabdit is elegans	Similarity to Drosophila Cadherin-related tumor suppressor	569	33
406	AB031230	Homo sapiens	protein containing CXXC domain 2	1196	97
407	AF155106	Homo sapiens	NY-REN-36 antigen	1168	100
408	Y57945	Homo sapiens	Human transmembrane protein HTMPN-69.	1538	99
409	Z18361	Ovis aries	trichohyalin	184	30
410	AF249744	Homo sapiens	RhoGEF	2733	100
411	AF176529	Mus musculus	F-box protein FBX13	2072	94
412	AF210842	Homo sapiens	HARP	4880	100
413	AL031658	Homo sapiens	dJ310013.7 (novel protein similar to H. roretzi HRPET- 3)	776	98
414	X57398	Homo sapiens	pm5 protein	6131	99
415	AB029826	Homo sapiens	3-methylcrotonyl-CoA carboxylase biotin-containing subunit	2961	99
416	U43503	Saccharomyce s cerevisiae	Lph1p	115	42
417	AL160493	Leishmania major	possible t26f17.21	239	35
418	Y08100	Homo sapiens	Human PRO331 protein.	330	29
419	U15131	Homo sapiens	p126	2228	54
420	AF117946	Homo sapiens	Link guanine nucleotide exchange factor II	2363	100
421	AF190635	Drosophila melanogaster	ankyrin 2	755	30
422	AF302150	Homo sapiens	phosphoinositol 3-phosphate- binding protein-2	1962	100
423	AL137530	Homo sapiens	hypothetical protein	433	94
424	X63753	Homo sapiens	son-a	7269	100
425	AB027249	Homo sapiens	MAPKK like protein kinase	1693	100
426	AF279144	Homo sapiens	tumor endothelial marker 7	1084	55

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	*
ID NO:	NUMBER			WATERMAN SCORE	IDENTITY
427	AF279144	Homo sapiens	tumor endothelial marker 7 precursor	1259	56
428	AE003683	Drosophila melanogaster	CG8312 gene product	149	29
429	Y07829	Homo sapiens	RING finger protein	2201	99
430	AF096897	Drosophila melanogaster	pushover	4442	47
431	U41387	Homo sapiens	Gu protein	4021	99
432	AF023674	Homo sapiens	nephrocystin	3783	100
433	AF146760	Homo sapiens	septin 2-like cell division control protein	2284	100
434	AB006697	Arabidopsis thaliana	cleft lip and palate associated transmembrane protein-like	886	42
437	Y94247	Homo sapiens	Human calcium binding protein hCBP.	1704	100
438	AB040672	Homo sapiens	UDP-GalNac: polypeptide N- acetylgalactosaminyltransfera se	1075	63
439	AF105228	Bos taurus	tuftelin .	285	33
440	R06463	Homo sapiens	Derived protein of clone ICA13 (ATCC 40553).	3073	99
441	X14971	Mus musculus	alpha-adaptin (A) (AA 1-977)	4897	98
442	X53773	Rattus norvegicus	alpha-c large chain (AA 1- 938)	3979	81
443	Y66689	Homo sapiens	Membrane-bound protein PRO1136.	3299	99
444	AC067754	Arabidopsis thaliana	unknown protein; 20348-23707	114	33
445	AF229032	Mus musculus	piL	2077	93
446	AF056035	Rattus norvegicus	s-nexilin	2662	85
447	AF132484	Mus musculus	unknown	478	51
448	W89024	Homo sapiens	Polypeptide fragment encoded by gene 156.	528	45
449	AF161445	Homo sapiens	HSPC327	1606	100
450	268753	Caenorhabdit is elegans	ZC518.3b	951	49
451	W39160	Homo sapiens	Human partial complement factor H protein fragment 3.	155	32
452	W85727	Homo sapiens	Novel protein (Clone BM46_10).	2799	99
453	Y53629	Homo sapiens	A bone marrow secreted protein designated BMS115.	2810	100
454	D87438	Homo sapiens	Similar to a C.elegans protein in cosmid C14H10	4069	100
455	AF240468	Homo sapiens	nicastrin	3687	100
456	Z15005	Homo sapiens	CENP-E	13305	99
457	M59216	Homo sapiens	gamma-aminobutyric acid receptor beta-1 subunit	2477	100
458	Y73467	Homo sapiens	Human secreted protein clone yd61_1 protein sequence SEQ ID NO:156.	966	100
459	W67824	Homo sapiens	Human secreted protein encoded by gene 18 clone HSLFM29.	535	100
460	AF163151	Homo sapiens	dentin sialophosphoprotein precursor	279	19
461	D87446	Homo sapiens	Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)	9196	99
462	G04044	Homo sapiens	Human secreted protein, SEQ ID NO: 8125.	486	93
463	AC002398	Homo sapiens	F25965_1	1018	100
464	AF064856	Rattus sp.	7acomp protein	1845	84
465	AF223408	Homo sapiens	B99	3686	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
466	AF223408	Homo sapiens	B99	2878	87
467	AF104415	Mus musculus	gene trap locus-13	6336	91
468	U53450	Rattus norvegicus	Jun dimerization protein 1 JDP-1	196	49
469	AL031297	Homo sapiens	dJ97P20.1 (novel gene)	3564	99
470	AF257077	Homo sapiens	eukaryotic translation initiation factor EIF2B subunit 3	1274	95
471	L28125	Podospora anserina	beta transducin-like protein	284	38
472	¥84903	Homo sapiens	A human proliferation and apoptosis related protein.	2337	100
473	AF144237	Homo sapiens	LOMP protein	252	44
474	Y71213	Homo sapiens	Human irritable bowel disease related polypeptide IMX39.	838	100 .
475	Y95006	Homo sapiens	Human secreted protein vel3_1, SEQ ID NO:52.	3411	100
476	D38549	Homo sapiens	hal025 is new	6533	99
477	AF241230	Homo sapiens	TAK1-binding protein 2	3656	100
478	AL031534	Schizosaccha romyces pombe	putative asparagine synthase	482	40
479	L28125	Podospora anserina	beta transducin-like protein	233	26
480	AF161544	Homo sapiens	HSPC059	434	77
481	AJ238248	Homo sapiens	centaurin beta2	3986	99
482	Z38061	Saccharomyce s cerevisiae	mal5, stal, len: 1367, CAI: 0.3, AMYH_YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3)	295	23
483	AF161381	Homo sapiens	HSPC263	1404	100
484	AF223468	Homo sapiens	AD021 protein	1314	100
486	X57527	Homo sapiens	alpha 1(VIII) collagen	4166	99
487	Y19062	Homo sapiens	39k3 protein	2475	100
488	Y73373	Homo sapiens	HTRM clone 921803 protein sequence.	555	56
489	AL021918	Homo sapiens	b3418.1 (Kruppel related Zinc Finger protein 184)	4184	100
490	X53773	Rattus norvegicus	alpha-c large chain (AA 1- 938)	4675	97
491	U52426	Homo sapiens	GOK	1459	59
492	AL359773	Leishmania major	possible threonine synthase	702	45
493	AF226614	Homo sapiens	ferroportin1	2929	100
494	Z93241	Homo sapiens	dJ222Ei3.1 (novel protein with some similarity to Drosophila KRAKEN)	513	96
495	AF036977	Homo sapiens	unknown	1812	100
496	U93564	Homo sapiens	p40	133	45
497	Y91405	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:126.	357	100
498	AF069781	Drosophila melanogaster	Bem46-like protein	653	43
499	Y16601	Homo sapiens	Human cell-cycle phosphoprotein CECYP-2.	1658	98
500	X70944	Homo sapiens	PTB-associated splicing factor	3883	100
501	AF027503	Mus musculus	putative membrane-associated guanylate kinase 1	205	36
502	AF282874	Homo sapiens	nectin 3; PRR3	2856	99
503	AJ249732	Homo sapiens	G8 protein	669	100
504	AF208861	Homo sapiens	BM-019	1629	100
505	L09708	Homo sapiens	complement component C2	4022	100
507	X66285	Mus musculus	HC1 ORF	115	43
508	D00189	Rattus	Na+,K+-ATPase alpha-subunit	5227	99
		norvegicus			

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	*
NO:	NUMBER			WATERMAN SCORE	IDENTITY
	Y94971	Homo sapiens	Human secreted protein clone fal71_1 protein sequence SEQ ID NO:148:	2176	100
510	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	781	77
511	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	1347	100
512	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	1520	99
513 514	X84908	Homo sapiens	phosphorylase kinase	5729	99
514	X52851 AF186084	Homo sapiens	peptidylprolyl isomerase	650	76
		Homo sapiens	epidermal growth factor repeat containing protein	3046	99
516	G03602	Homo sapiens	Human secreted protein, SEQ ID NO: 7683.	505	99
517	U04706	Bos taurus	50 kDa protein	1749	77
518	G00653	Homo sapiens	Human secreted protein, SEQ ID NO: 4734.	530	100
519	AF161475	Homo sapiens	HSPC126	1368	100
520	Y99366	Homo sapiens	Human PRO1475 (UNQ746) amino acid sequence SEQ ID NO:88.	3394	97
521	AF266852	Homo sapiens	PTPLA	1295	100
522	AE000995	Archaeoglobu	chromosome segregation	153	20
533	180500	s fulgidus	protein (smc1)		1
523	AF062249	Homo sapiens	immunoglobulin heavy chain variable region	605	97
524	AJ223830	Rattus norvegicus	ARE1	2950	98
525	W01535	Homo sapiens	Cellular homologue of the SV40 large T antigen.	1276	83
526	AF145658	Drosophila melanogaster	BcDNA.GH10229	320	33
527	AF112213	Homo sapiens	putative Rab5-interacting protein	524	79
528	D49387	Homo sapiens	NADP dependent leukotriene b4 12-hydroxydehydrogenase	1616	100
529	Y30819	Homo sapiens	Human secreted protein encoded from gene 9.	328	32
530	AL079335	Homo sapiens	dJ132F21.3 (72.1 KDa protein (DKF2P564A032, SBB188) similar to mouse IFN-gamma induce MG11.)	1059	99
531	Y91506	Homo sapiens	Human secreted protein sequence encoded by gene 56 SEQ ID NO:179.	1159	98
532	X76116	Caenorhabdit is elegans	carrier protein (c2)	576	50
533	X76116	Caenorhabdit is elegans	carrier protein (c2)	506	50
534	X12966	Homo sapiens	3-oxoacyl-CoA thiolase	1972	100
535	Y09267	Homo sapiens	flavin-containing	2486	100
536	Z11773	Homo sapiens	monooxygenase 2 SRE-ZBP	2203	
537	D84224	Homo sapiens	methionyl tRNA synthetase	2201 4741	99
538	D84224	Homo sapiens	methionyl tRNA synthetase	3887	99
539	D84224	Homo sapiens	methionyl tRNA synthetase	2933	96
540	D84224	Homo sapiens	methionyl tRNA synthetase	4529	99
541	J03244	Bos taurus	H+ ATPase 31kDa subunit (EC 3.6.1.3)	848	77
542	Y92514	Homo sapiens	Human OXRE-11.	2301	99
543	AF221712	Homo	Smad- and Olf-interacting	2151	61
544	NEODO O TO	sapiens	zinc finger protein		
J##	AE000919	Methanobacte rium thermoautotr ophicum	conserved protein	207	38
545	A06669	synthetic	preTGF-betal	2070	99
		construct			

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
546	Y02698	Homo sapiens	Human secreted protein encoded by gene 49 clone HTPCS60.	854	98
547	AF112205	Homo sapiens	WSB-1 protein	2275	100
548	X60271	Mus musculus	c-rel	2264	74
549	AC016827	Arabidopsis thaliana	putative GTPase	810	42
550	Y70400	Homo sapiens	Human cell-signalling protein-2.	429	68
551	AB048365	Homo sapiens	NEDD4-like ubiquitin ligase 1	8290	99
552	Y57880	Homo sapiens	Human transmembrane protein HTMPN-4.	1112	95
553	AF119855	Homo sapiens	PRO1847	265	67
554	M17236	Homo sapiens	MHC HLA-DQ alpha precursor	1332	100
555	AL078468	Arabidopsis thaliana	putative protein	540	40
556	AC006963	Homo sapiens	similar to Kelch proteins; similar to BAA77027 (PID:g4650844)	515	44
557	AK024487	Homo sapiens	FLJ00086 protein	1623	98
558	M12140	Homo sapiens	pol gene protein; Xxx	117	48
559	W74825	Homo sapiens	Human secreted protein encoded by gene 97 clone HAQBF73.	225	56
560	X56681	Homo sapiens	junD protein	373	88
561	AF003136	Caenorhabdit is elegans	contains weak similarity to an AMP-binding motif	2926	54
562	AL109839	Homo sapiens	dJ1069P2.3.1 (novel PABPC1 (poly(A)-binding protein)	877	100
563	AF181640	Drosophila melanogaster	BcDNA.GH09817	289	42
564	AF052723	Feline leukemia virus	gag-pol precursor polyprotein gPr80	1547	43
565	AF161472	Homo sapiens	HSPC123	439	44
566	Y28817	Homo sapiens	pt326_4 secreted protein.	3338	100
567	U09848	Homo sapiens	zinc finger protein	1738	100
569	AF155113	Homo sapiens	NY-REN-55 antigen	3603	93
570	AF155113	Homo sapiens	NY-REN-55 antigen	3951	99
571	AL032821	Homo sapiens	dJ55C23.1 (vanin 1)	1821	98
572	M69181	Homo sapiens	non-muscle myosin B	7350	99
573	M69181	Homo sapiens	non-muscle myosin B	7311	98
574	YS9678	Home sapiens	Secreted protein 108-008-5-0- E6-PL.	772	100
575	AL365234	Arabidopsis thaliana	putative protein	788	40
576	AL365234	Arabidopsis thaliana	putative protein	788	40
577	X06745	Homo sapiens	DNA polymerase alpha-subunit (AA 1 - 1462)	7619	99
578	AB041642	Homo sapiens	PAR-6	1342	100
579	D86984	Homo sapiens	similar to yeast adenylate cyclase (S56776)	2446	100
580	AF165124	Homo sapiens	gamma-aminobutyric acid A receptor gamma 2	2499	99
581	W88812	Homo sapiens	Polypeptide fragment encoded by gene 58.	2339	99
582	U82319	Homo sapiens	novel ORF	342	100
583	P92219	Homo sapiens (human)	CR1 protein.	11425	99
584	AJ223948	Homo sapiens	RNA helicase	6608	99
585	Y08612	Homo sapiens	88kDa nuclear pore complex protein	3874	99
586	Y42384	Homo sapiens	Amino acid sequence of 1v310 7.	1007	37
587	AF129756	Homo sapiens	BAT4	1873	98

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
588	AF131775	Homo sapiens	Unknown	1929	99
589	AJ250865	Homo sapiens	TESS 2	2348	100
591	298885	Homo sapiens	dJ522J7.2 (bromodomain- containing 1 (similar to peregrin, BR140))	4167	100
592	L76571	Homo sapiens	nuclear hormone receptor	1355	100
593	AF091622	Homo sapiens	PHD finger protein 3	9054	100
594	X56807	Homo sapiens	desmocollin type 2a	4443	100
595	AL137802	Homo sapiens	dJ798A10.1 (novel protein)	212	55
596	AL022329	Homo sapiens	bK407F11.2 (adrenergic, beta, receptor kinase 2)	3653	100
597	AF226048	Homo sapiens	GL003	2009	99
598	AJ278112	Homo sapiens] >Y49635 Y49635 21- OCT-1999 15- APR-1998 Human sdp3.5 protein. [Homo	putative cell cycle control protein	335	23
		sapiens]	
599	Y59741	Homo sapiens	Human normal ovarian tissue derived protein 18.	1574	99
600	L36531	Homo sapiens	integrin alpha 8 subunit	5386	99
601	Y38458	Homo sapiens	Human secreted protein encoded by gene No. 20.	895	100
602	AF218584	Homo sapiens	GGA1	3265	100
603	Y13115	Homo sapiens	serine/threonine protein kinase	5071	99
604	AL132776	Homo sapiens	dJ393D12.1 (KIAA0776)	2413	99
605	AL034452	Homo sapiens	dJ682J15.1 (novel Collagen triple helix repeat containing protein)	1979	100
606	Y14494	Homo sapiens	aralari	3465	99
607	AJ001981	Homo sapiens	OXA1L	2603	100
608	X86098	Homo sapiens	binds directly to adenovirus type 5 ElA protein	3069	100
610	AF163572	Homo sapiens	Forssman glycolipid synthetase	1865	99
611	AF161503	Homo sapiens	HSPC154	1261	97
612	L41834	Ensis minor	nuclear protein	345	30
613	Y91954	Homo sapiens	Human cytoskeleton associated protein 9 (CYSKP-9).	3668	100
614	AL022327	Homo sapiens	dJ355C18.1 (KIAA0027)	361	94
615 616	X85786 Y08319	Homo sapiens	binding regulatory factor kinesin-2	3203	100
617	D12644	Homo sapiens Mus musculus	KIRESIN-2 KIF2 protein	3487	99
618	U28789	Mus musculus	PACT	5936	89
619	Y35914	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 163.	1684	99
620	AB046382	Mus musculus	testis-abundant finger protein	199	23
621	Y00062	Homo sapiens	precursor polypeptide (AA -23 to 1120)	3440	99
622	AF068286	Homo sapiens	HDCMD38P	861	100
623	X98248	Homo sapiens	sortilin	4436	99
624	X61100	Homo sapiens	75 kDa subunit NADH dehydrogenase precursor	3734	99
625	S58544	Homo sapiens	75 kda infertility-related sperm protein	2125	99
626	AF151027	Homo sapiens	HSPC193	582	93
627	X14968	Homo sapiens	RII-alpha subunit (AA 1-404)	2079	100
628	Y50911	Homo sapiens	Human fetal brain cDNA clone vb7_1 derived protein	1983	100

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
629	Y50911	Homo sapiens	Human fetal brain cDNA clone vb7 1 derived protein	1694	100
630	AF098786	Homo sapiens	17 beta-hydroxysteroid dehydrogenase type VII	1754	100
631	AL034555	Homo sapiens	dJ134019.3 (zinc finger protein 151 (pHZ-67))	4273	100
632	W74826	Homo sapiens	Human secreted protein encoded by gene 98 clone HAOBIT4.	794	96
633	AF288288	Homo sapiens	HPT protein	2236	.100
634	AF041429	Homo sapiens	pRGR1	823	99
635	X66357	Homo sapiens	serine/threonine protein kinase	1589	100
636	Y11284	Homo sapiens	AFX1	2571	98
637	AB004884	Homo sapiens	PKU-alpha	3718	99
638	AJ002303	Homo sapiens	synaptogyrin lc	1020	100
639	AJ002304	Homo sapiens	synaptogyrin 1b	1002	100
640	AJ002303	Homo sapiens	synaptogyrin 1c	933	94 100
641	D87682	Homo sapiens	similar to a C.elegans protein encoded in cosmid T26A5.	2676	100
642	M14660	Homo sapiens	ISG-K54	2473	99
643	X06661	Homo sapiens	calbindin (AA 1-261)	1358	100
644	AF119900	Homo sapiens	PRO2822	185	76
645	AB031048	Drosophila melanogaster	microtubule associated- protein orbit	738	27
646	AF250842	Drosophila melanogaster	multiple asters	834	29
647	X86691	Homo sapiens	Mi-2 protein	10110	99
648	Ü67934	Homo sapiens	44.9 kDa protein C18Bl1 homolog	827	96
649	AF236061	Oryctolagus cuniculus	RING-finger binding protein	3830	91
650	AL034553	Homo sapiens	dJ914P20.2 (KIAA0784 protein similar to Mus musculus activity-dependent neuroprotective protein (Adnp))	5708	100
653	X14766	Homo sapiens	GABA-A receptor alpha 1 subunit	2388	99
654	AC004614	Homo sapiens	similar to f-spondin proteins AB006086 (PID:g2529225)	3026	99
655	Y57908	Homo sapiens	Human transmembrane protein HTMPN-32.	608	99
656	234975	Homo sapiens	ldlCp	3733	100
658	AL050306	Homo sapiens	dJ475B7.2 (novel protein)	1942	99
659	W76734	Homo sapiens	Human mDia Rho targeting protein.	781	34
660	AF202724	Homo sapiens	Sadl unc-84 domain protein 1	2172	100
661	Z21966	Homo sapiens	mPOU homeobox protein	1529	100
662	AJ242954	Mus musculus	dysferlin	4752	99
663	AF182316 AL161516	Homo sapiens Arabidopsis	myoferlin hypothetical protein	209	30
665		thaliana			99
667	X59303	Homo sapiens	valyl-tRNA synthetase Amino acid sequence of	3393 3692	100
668	Y13355	Homo sapiens	protein PRO220.	611	52
669	AB010692	Arabidopsis thaliana	contains similarity to endo- beta-N-acetylglucosaminidase gene		
671	X56123	Mus musculus	talin	4474	76
672	AB039371	Homo sapiens	mitochondrial ABC transporter	2902	99
673	AF269223	Homo sapiens	TCP11	806	42
674	AF229633	Mus musculus	groucho-related protein 4	4053	99
675	L14463	Rattus	'transducin	3619	92

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	* IDENTITY
	 	norvegicus		SCORE	
676	AC005757	Homo sapiens	R32611 1	2779	100
677	S61069	Homo sapiens	reverse transcriptase	252	65
			homolog=pol {retroviral element}		
678	AF271388	Homo sapiens	CMP-N-acetylneuraminic acid synthase	2273	100
679	X79066	Homo sapiens	ERF-1	1783	100
680	AF118566	Mus musculus	hematopoietic zinc finger protein	769	50
681	Y51415	Homo sapiens	Human wild type pKe83 , protein.	2621	99
682	AL133545	Homo sapiens	bA386N14.1 (novel protein similar to a dual specificity phosphatase)	700	68
683	Y86214	Homo sapiens	Nuclear transport protein clone hfb341 protein sequence.	5888	99 .
684	Y94952	Homo sapiens	Human secreted protein clone fh116_11 protein sequence SEQ ID NO:110.	354	98
685	AL021878	Homo sapiens	dJ257120.4 (transcription factor 20 (AR1) (KIAA0292) (isoform 2))	154	67
686	AE000198	Escherichia coli	orf, hypothetical protein	628	100
687	M58378	Homo sapiens	synapsin I	3730	99
688	AF039697	Homo sapiens	antigen NY-CO-31	508	98
689	U09355	Oryctolagus cuniculus	protein phosphatase 2A1 B gamma subunit	2356	99
690	AF155106	Homo sapiens	NY-REN-36 antigen	265	50
691	AC004774	Homo sapiens	Dlx-5	1542	100
692	X90530	Homo sapiens	ragB	1926	99
693	X90530	Homo sapiens	ragB	1405	99
694	X90530	Homo sapiens	ragB	1590	85
695	G01563	Homo sapiens	Human secreted protein, SEQ ID NO: 5644.	330	100
696	AC011810	Arabidopsis thaliana	Putative methionine aminopeptidase	669	52
697	AJ250425	Rattus norvegicus	Collybistin I	2455	98
698	AB037901	Homo sapiens	gene amplified in squamous cell carcinoma-1	5364	99
699	Y99401	Homo sapiens	Human PRO1327 (UNQ687) amino acid sequence SEQ ID NO:218.	1386	100
701	AF221712	Homo sapiens	Smad- and Olf-interacting zinc finger protein	6705	100
702	X83573	Homo sapiens	ARSE	3184	99
703	АЈ243274	Homo sapiens	AP-2rep protein	2078	99
704	Y71262	Homo sapiens	Human chondromodulin-like protein, Zchml.	1697	94
705	Y71262	Homo sapiens	Human chondromodulin-like protein, Zchml.	1736	99
706	¥41257	Homo sapiens	Amino acid sequence of long human FAIM.	1060	100
707	AL022237	Homo sapiens	bK1191B2.3 (PUTATIVE novel Acyl Transferase similar to C. elegans C50D2.7) (isoform 1))	2030	100
708	AJ006266	Homo sapiens	AND-1 protein	5942	100
709	G01571	Homo sapiens	Human secreted protein, SEQ ID NO: 5652.	777	99
710	Y08698	Homo sapiens	ranbp3	2849	98
711	Y68770	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-2.	754	99

SEQ ID NO:	ACCESSION	SPECIES	DESCRIPTION	SMITH-	T
NO:	NUMBER	Si Ecile	DB5CK11115K	WATERMAN	IDENTITY
				SCORE	150011111
712	U93574	Homo sapiens	putative p150	799	59
713	AC004531	Homo sapiens	Gene with similaity to DEAD	2715	99
			box helicases	1 - 1 - 2	""
714	D89016	Homo sapiens	Neuroblastoma	538	48
715	Y92175	Homo sapiens	Human cardiovascular system	734	98
		John Departure	associated protein tyrosine	/31	1 -0
			phosphatase 2.		1
716	AL137013	Homo sapiens	bA311P8.3 (probable uracil	862	100
, 20	AD13 / 013	nomo Bapiens	phosphoribosyltranferase)	002	100
717	AB035123	Mus musculus	GD1 alpha/GT1a alpha/GO1b	1696	93
, _ ,	10033123	mas mascaras	alpha synthase	1030	33
718	Y96290	Homo >P40254	Human IGFAM-2 immunoglobulin.	2345	85
.10	150250	P40254 25-	naman zarra z mananogrobutin.	2343	05
		OCT-1984 09-			
		APR-1983			
		Human IgD.	1		
		[Homo			
		sapiens			
719	X07979	Homo sapiens	integrin beta 1 subunit	4347	99
113	X07373	nollo saprens	precursor	4347	99
720	AJ224819	Homo sapiens	tumor suppressor	10140	- · · · · · · · · · · · · · · · · · · ·
721	Y07595			2149	99
721	W41565	Homo sapiens	transcription factor TFIIH	2373	100
122	W41565	Ното	Human calpain.	1591	99
		sapiens] >W41564			
		W41564 08-		1	1
		OCT-1997 05-			1
		APR-1996			
		Human	·	j	
		calpain. [Homo			ļ
		sapiens			
723	AF161341	Homo sapiens	HSPC078	1097	
724	AF187318	Homo sapiens	F-box protein Fbx2	1607	98
725	AC006708	Caenorhabdit	contains similarity to		100
123	ACOUOTOS	is elegans	Saccharomyces cerevisiae pre-	1143	46
		15 cregaiis	mRNA splicing protein PRP31		1
]	(GB:Z72876)	J	1
		Caenorhabdit	contains simlarity to		1
726			Concains Simiaticy to	1 000	16
726	AC006708			988	46
726	AC006708	is elegans	Saccharomyces cerevisiae pre-	988	46
726	AC006708		Saccharomyces cerevisiae pre- mRNA splicing protein PRP31	988	46
		is elegans	Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)		
726	AC006708	is elegans	Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam	988	46
		is elegans	Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain,		
		is elegans	Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8,		
727	AC024818	is elegans Caenorhabdit is elegans	Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3	950	44
727	AC024818 AJ005897	is elegans Caenorhabdit is elegans Homo sapiens	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS	950	44
727	AC024818	is elegans Caenorhabdit is elegans	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JM5 Human secreted protein	950	44
727	AC024818 AJ005897	is elegans Caenorhabdit is elegans Homo sapiens	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene	950	44
727 728 729	AC024818 AJ005897 Y45377	Caenorhabdit is elegans Homo sapiens Homo sapiens	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27.	950 831 908	44
727	AC024818 AJ005897	is elegans Caenorhabdit is elegans Homo sapiens	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JM5 Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ	950	44
727 728 729	AC024818 AJ005897 Y45377 G03931	Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JM5 Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012.	950 831 908	47 97
727 728 729	AC024818 AJ005897 Y45377	Caenorhabdit is elegans Homo sapiens Homo sapiens Oncorhynchus	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JM5 Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ	950 831 908	44
727 728 729 730	AC024818 AJ005897 Y45377 G03931 AB012720	Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens Oncorhynchus masou	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein	950 831 908 578	47 97 100
727 728 729	AC024818 AJ005897 Y45377 G03931	Caenorhabdit is elegans Homo sapiens Homo sapiens Oncorhynchus	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JM5 Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein	950 831 908	47 97
727 728 729 730 731	AC024818 AJ005897 Y45377 G03931 AB012720 W73404	Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JM5 Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8.	950 831 908 578 3865	47 97 100 76
727 728 729 730	AC024818 AJ005897 Y45377 G03931 AB012720	Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens Oncorhynchus masou	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ	950 831 908 578	47 97 100
727 728 729 730 731 732	AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650	is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Homo sapiens	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731.	950 831 908 578 3865 862 644	44 47 97 100 76 97
727 728 729 730 731	AC024818 AJ005897 Y45377 G03931 AB012720 W73404	is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Homo sapiens Caenorhabdit	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein	950 831 908 578 3865	47 97 100 76
727 728 729 730 731 732 733 734	AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813	is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Homo sapiens Caenorhabdit is elegans	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a	950 831 908 578 3865 862 644	44 47 97 100 76 97
727 728 729 730 731 732	AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650	is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Homo sapiens Caenorhabdit	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein	950 831 908 578 3865 862 644	44 47 97 100 76 97
727 728 729 730 731 732 733 734	AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813	is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Homo sapiens Caenorhabdit is elegans	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a	950 831 908 578 3865 862 644 152	47 97 100 76 97 97
727 728 729 730 731 732 733 734	AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813	is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Homo sapiens Caenorhabdit is elegans	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a dJ967N21.6 (novel CDP-alcohol	950 831 908 578 3865 862 644 152	47 97 100 76 97 97
727 728 729 730 731 732 733 734	AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813	is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Homo sapiens Caenorhabdit is elegans	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase	950 831 908 578 3865 862 644 152	47 97 100 76 97 97
727 728 729 730 731 732 733 734	AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813 AL035461	is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Homo sapiens Caenorhabdit is elegans Homo sapiens	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JM5 Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein)	950 831 908 578 3865 862 644 152	44 47 97 100 76 97 97 24
727 728 729 730 731 732 733 734	AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813 AL035461	is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Caenorhabdit is elegans Homo sapiens Caenorhabdit caenorhabdit caenorhabdit caenorhabdit caenorhabdit	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein) similar to S. cerevisiae YJU2	950 831 908 578 3865 862 644 152	44 47 97 100 76 97 97 24

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
738	AJ131712	Homo sapiens	nucleolar RNA-helicase	2793	100
739	AJ133115	Homo sapiens	TSC-22-like protein	2054	99
740	X98258	Homo sapiens	M-phase phosphoprotein 9	953	100
741	X98258	Homo sapiens	M-phase phosphoprotein 9	564	74
742	U97191	Caenorhabdit	strong similarity to the YPT1	960	85
172	03/131	is elegans	sub-family of RAS proteins		
743	X76057	Homo sapiens	phosphomannose isomerase	2191	100
744	G03209	Homo sapiens	Human secreted protein, SEQ	496	98
/44	G03209	HOMO Sapiens	ID NO: 7290.	1300	1 70
745	X97064	Homo sapiens	Sec23 protein	4034	99
	1		Human regulatory molecule	994	100
746	W93946	Homo sapiens	HRM-2 protein.	223	100
	1102220	17	HTRM clone 3376404 protein	1565	99
747	Y73388	Homo sapiens		1363	33
			sequence.	1906	98
748	M19529	Sus scrofa	follistatin A		
749	AJ249457	Trichomonas	centrin, putative	183	28
		vaginalis			
750	AC004410	Homo sapiens	fos39554_1	2094	100
751	AF074968	Homo sapiens	p47ING3 protein	2167	100
752	AF252284	Homo sapiens	transcription specificity	4005	100
			factor Sp1		
753	AB049629	Homo sapiens	phospholysine	1375	99
			phosphohistidine inorganic		
			pyrophosphate phosphatase	ļ	
754	D79205	Homo sapiens	ribosomal protein L39	160	77
755	AB008430	Homo sapiens	CDEP	142	29
758	L32162	Homo sapiens	transcription factor	574	80
759	AF037204	Homo sapiens	RING zinc finger protein	295	54
760	Y44250	Homo Sapiens	Human cell signalling	625	100
760	144250	sapiens	protein-13.	023	1 -00
-	1 2010506	Homo sapiens	Cide-b	1136	100
761	AF218586		histone H2A	625	97
762	U38934	Gallus	nistone HZA	025	31
		gallus	110101 0	606	32
763	AF226053	Homo sapiens	HSKM-B	3626	100
764	X13403	Homo sapiens			38
765	D87446	Homo sapiens	Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)	568	38
766	AL023828	Caenorhabdit is elegans	Y17G7B.14	200	27
767	Y82777	Homo sapiens	Human chordin related protein (Clone dw665_4).	2551	99
768	X92475	Homo sapiens	ITBA1	1429	100
769	Y42752	Homo sapiens	Human calcium binding protein 3 (CaBP-3).	1426	100
770	X51416	Homo sapiens	hormone receptor hERR1 (AA 1- 521)	2641	97
771	AJ006591	Homo sapiens	cysteine-rich protein	1793	100
772	A08695	Homo sapiens	rap2	935	100
773	Z12173	Homo sapiens	N-acetylglucosamine-6- sulphatase	2970	100
774	Y91950	Homo sapiens	Human cytoskeleton associated protein 5 (CYSKP-5).	565	43
776	AL023799	Homo sapiens	dJ322P7.1 (zinc finger)	855	56
777	AL023799	Homo sapiens	dJ322P7.1 (zinc finger)	855	56
778	G01880	Homo sapiens	Human secreted protein, SEQ ID NO: 5961.	849	98
770	AJ012590	Homo sapiens	glucose 1-dehydrogenase	4155	99
779	AL078582	Homo sapiens	dJ130E4.2 (KIAA0796)	1321	68
780			similar to mitochondrial	384	34
	275955	Caenorhabdit is elegans			
780		is elegans	dJi121G12.2 (SCAN domain-	900	100
780 781	275955	is elegans	carrier protein		100

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
			ID NO: 7954.		<u> </u>
785	Y84441	Homo sapiens	Amino acid sequence of a human RNA-associated protein.	2074	100
786	Y00918	Homo sapiens	Human Rab protein, RABP-1, protein sequence.	1048	99
787	Z97029	Homo sapiens	ribonuclease HI large subunit	1548	99 ·
788	AB035384	Homo sapiens	SRp25 nuclear protein	962	94
789	AF024631	Homo sapiens	ANG2	2644	100
790	AJ006710	Rattus norvegicus	phosphatidylinositol 3-kinase	4508	97
792	V00638	bacteriophag e lambda	reading frame eal0	600	100
793	AF049103	Homo sapiens	Huntingtin interacting protein	819	100
795	Z26317	Homo sapiens	desmoglein 2	4810	99
796	Y76884	Homo sapiens	Retinoblastoma binding protein-7sequence.	5080	99
797	U15155	Gallus gallus	trypsinogen	372	37
798	U97189	Caenorhabdit is elegans	strong similarity to thw P13/P14 family of kinases	227	28
799	AF112201	Homo sapiens	neuronal protein NP25	1053 958	100
800	AF234765	Rattus norvegicus	serine-arginine-rich splicing regulatory protein SRRP86	743	99
801	AF267852	Homo sapiens	placental protein 13-like protein	766	80
802	AF208851	Homo sapiens	BM-009 Similarity to Human	152	27
803	Z81097	is elegans	retinoblastoma-binding protein RBAP46 yk662d12.5 comes from this gene Human secreted protein, SEQ	496	98
804	G02113		ID NO: 6194. bA305P22.1 (novel protein)	1160	100
805	AL121673	Homo sapiens Arabidopsis	putative GTPase activator	264	30
806	AC013483	thaliana Arabidopsis	protein putative GTPase activator	264	30
		thaliana	protein beta-ureidopropionase	1494	100
808	AB013885	Homo sapiens	HOTTL protein	1581	99
809	AF078842	Homo sapiens	HSPC303	2134	96
810 811	AF161421 AF261689	Homo sapiens	DNA polymerase epsilon p17 subunit	734	100
812	274029	Caenorhabdit is elegans	Similarity to C.elegans alcohol dehydrogenase comes from this gene	610	71
813	273497	Homo sapiens	cU240C2.2 (Core histone H2A/H2B/H3/H4)	324	100
814	W87689	Homo sapiens	Human HTXFT19 polypeptide.	1484	99
815	X16282	Homo sapiens	zinc finger protein (217 AA) (1 is 2nd base in codon)	1109	99
816	Z92539	Mycobacteriu m tuberculosis	pth	300	36
818	AB030483	Mus musculus	В9	197	27
819	AL117555	Homo sapiens	hypothetical protein	321	94
	AC005328 G03951	Homo sapiens	R26660_2, partial CDS Human secreted protein, SEQ	865 700	97
820 821	0007		ID NO: 8032.		1
	L34807	Musca	transposase	174	20
821		Musca domestica Homo sapiens		174 558	78

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	ł
ID NO:	NUMBER			WATERMAN SCORE	IDENTITY
		romyces	protein 1		
825	AJ006692	Homo sapiens	ultra high sulfer keratin	693	68
826	U23037	Oryctolagus	eIF-2Bepsilon	3406	90
827	G03412	Homo sapiens	Human secreted protein, SEQ ID NO: 7493.	464	100
828	Y30827	Homo sapiens	Human secreted protein	113	44
829	Y32199	Homo sapiens	encoded from gene 17. Human receptor molecule (REC) encoded by Incyte clone	1012	100
830	W78279	Homo sapiens	2022379. Fragment of human secreted	1264	99
	1		protein encoded by gene 33.		
832	AB011542	Homo sapiens	MEGF9	2097	100
833	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	223	70
834	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	1574	100
835	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	1144	89
836	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	1448	94
837	X12517	Homo sapiens	C protein (AA 1-159)	918	100
838	U32865	Drosophila melanogaster	linotte protein	164	24
839	AF067730	Homo sapiens	TLS-associated protein TASR-2	631	56
840	U27831	Homo sapiens	striatum-enriched phosphatase	2840	98
841	AF286366	Homo sapiens	CamKI-like protein kinase	1796	100
842	G02309	Homo sapiens	Human secreted protein, SEQ ID NO: 6390.	278	98
843	AE003615	Drosophila melanogaster	ade3 gene product	113	48
844	G01350	Homo sapiens	Human secreted protein, SEQ ID NO: 5431.	629	100
845	U27838	Mus musculus	glycosyl-phosphatidyl- inositol-anchored protein homolog	3305	96
847	Y87788	Homo sapiens	Human RBP-26 protein.	2026	100
848	AF164794	Homo sapiens	Diff33 protein homolog	2398	100
849	U41315	Homo sapiens	ZNF127-Xp	2458	93
850	AF192784	Homo sapiens	makorin 1	2062	97
851	Y58628	Homo sapiens	Protein regulating gene expression PRGE-21.	1548	100
852	Z22968	Homo sapiens	M130 antigen	6205	100
853	Z22971	Homo sapiens	M130 antigen extracellular variant	6380	100
854	G03362	Homo sapiens	Human secreted protein, SEQ ID NO: 7443.	330	96
855	G03362	Homo sapiens	Human secreted protein, SEQ ID NO: 7443.	203	100
856	AF285118	Homo sapiens	CGI-203	452	100
857	AC006069	Arabidopsis thaliana	putative cleavage and polyadenylation specifity factor	1383	55
858	AL021546	Homo sapiens	Cytochrome C Oxidase Polypeptide VIa-liver precursor (EC 1.9.3.1)	593	100
859	L02956	Xenopus laevis	ribonucleoprotein	1664	85
860	AF201947	Homo sapiens	MEK binding partner 1	616	100
861	L31783	Mus musculus	uridine kinase	1266	92
862	AF161472	Homo sapiens	HSPC123	602	73
863	Z49068	Caenorhabdit is elegans	mitochondrial carrier protein	370	43
864	AF154108	Homo sapiens	tumor necrosis factor type 1	3559	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	1DENTITY
NO:		ļ	receptor associated protein		
865	AE001530	Helicobacter	putative	230	32
	AECOISSO	pylori J99	pataozio		
866	X57807	Homo sapiens	immunoglobulin lambda light chain	699	91
867	AL031673	Homo sapiens	dJ694B14.1 (PUTATIVE novel KRAB box protein with 18 C2H2	4066	99
	İ		type Zinc finger domains)		
868	Y11652	Homo sapiens	phosphate cyclase	238	100
869	AF192968	Homo sapiens	high-glucose-regulated protein 8	3041	99
B70	AB020648	Homo sapiens	KIAA0841 protein	3237	99
871	AL031427	Homo sapiens	dJ167A19.1 (novel protein)	1608	100
872	AF151534	Homo sapiens	core histone macroH2A2.2	1866	100
873	AL021331	Homo sapiens	dJ366N23.1 (putative C. elegans UNC-93 (protein 1, C46F:1.1) LIKE protein)	1129	100
874	X14608	Homo sapiens	propionyl-CoA carboxylase	3579	100
875	AL:117334	Homo sapiens	dJ687F11.1 (novel protein (part of translation of cDNA DKFZp434N061, Em:AL110249))	306	100
-002	X79489	Saccharomyce	E-925 protein	446	35
876	Y/3483	saccharomyce s cerevisiae	•	1	
877	Y53001	Homo sapiens	Human secreted protein clone dn834_1 protein sequence SEQ ID NO:8.	811	100
878	AF281064	Homo sapiens	CHMP1.5	957	100
879	X79417	Sus scrofa	40S ribosomal protein S12	687	100
880	AF001317	Saccharomyce	Soilp	478	28
880	AF001317	s cerevisiae			
881	Y87275	Homo sapiens	Human signal peptide containing protein HSPP-52 SEQ ID NO:52.	2547	100
882	M14036	Homo sapiens	C1-inhibitor	598	77
883	AB041261	Homo sapiens	calcium-independent phospholipase A2	2903	100
884	AF020313	Mus musculus	proline-rich protein 48	999	84
885	Y10936	Homo sapiens	hypothetical protein	1104	99
886	AF073997	Mus musculus	myotubularin related protein	866	36
887	Y57893	Homo sapiens	Human transmembrane protein HTMPN-17.	1099	94
888	AL117635	Homo sapiens	hypothetical protein	929	99
889	AF210317	Homo sapiens	facilitative glucose transporter family member GLUT9	2046	99
890	Y36031	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 416.	583	100
891	Y36031	Homo sapiens	Extended human secreted protein sequence, SEQ ID No. 416.	192	57
892	AF237631	Homo sapiens	ubiquitous tropomodulin U- Tmod	1798	100
893	AF090929	Homo sapiens	PRO0477p	653	99
894	AL031228	Homo sapiens		3196	100
895	AL031228	Homo sapiens	dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1)	2825	96
896	AF171102	Homo sapiens	retinal degeneration B beta	1302	95
896	AE003551	Drosophila	CG18176 gene product	633	33
1 00,	1	melanogaster	_		1

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	*
ID:	NUMBER			WATERMAN SCORE	IDENTITY
898	AJ237946	Homo sapiens	DEAD Box Protein 5	2443	100
899	Z97184	Homo sapiens	HKE2	624	100
900	Z97184	Homo sapiens	HKE2	409	98
901	AJ245587	Homo sapiens	Kruppel-type zinc finger	1942	100
902	AF091034	Homo sapiens	GTP-binding protein RAB22A	1011	100
903	R95953	Homo sapiens	Eukaryotic cell growth	414	96
303	K93933	nomo saptens	inhibiting factor.	47.4	36
904	L04733	Wana and and		1.03	-
	1	Homo sapiens	kinesin light chain	1936	72
905	AE003540	Drosophila melanogaster	CG10984 gene product	446	33
906	M55542	Homo sapiens	guanylate binding protein isoform I	2993	98
907	M55542	Homo sapiens	guanylate binding protein isoform I	2901	96
908	W84085	Homo sapiens	Human membrane fusion protein WDProl.	1889	100
909	AF168676	Homo	TNF intracellular domain-	647	100
	1	sapiens	interacting protein	1	1
910	AB029150	Homo sapiens	KRAB zinc finger protein	2196	100
			HFB101L		
911	G02871	Homo sapiens	Human secreted protein, SEQ ID NO: 6952.	521	100
912	G03162	Homo sapiens	Human secreted protein, SEQ ID NO: 7243.	387	87
913	AJ243721	Homo	dTDP-4-keto-6-deoxy-D-glucose	1710	100
		sapiens)	4-reductase		
		>Y92508		1	
	ľ	Y92508 13-		ł	
		APR-2000 06-		ì	,
		OCT-1998		1	
	1	Human OXRE-			
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		5. [Homo	·		
01.6	U24189	sapiens	l linear black days	1	
914	024189	Caenorhabdit	hypothetical protein 1207-1;	244	41
	}	is elegans	Method: conceptual		
	1	j	translation supplied by	1	ļ
			authors		1
915	Y02591	Homo sapiens	A human progesterone receptor	843	99
			complex p23-like protein.		
916	AE000984	Archaeoglobu	dinitrogenase reductase	171	26
		s fulgidus	activating glycohydrolase	1	1
		_	(draG)	1	I
918	M23159	Cricetus	DHFR-coamplified protein	163	30
		cricetus	• • •		1
919	L12018	Caenorhabdit	putative	1232	41
		is elegans		1	
920	AF102177	Homo sapiens	tumor antiqen SLP-8p	1260	97
921	AL096712				
121	AUV30/12	Homo sapiens	dJ744I24.2 (similar to a	1017	78
			novel human gene mapping to		
000	1		Activator)		
922	AL161495	Arabidopsis	putative WD-repeat protein	866	42
		thaliana			
923	AL161495	Arabidopsis	putative WD-repeat protein	442	36
	ļ	thaliana			<u> </u>
924	U97001	Caenorhabdit	similar to	605	51
		is elegans	Schizosaccharomyces pombe	1]
925	X71978	Mus musculus	Fif	1503	95
926	M92288	Drosophila	beta-spectrin	290	51
		melanogaster		J	}
927	Y27575	Homo sapiens	Human secreted protein	1392	100
221	12/3/3	women sabrens	_	1392	100
	V22760	110000 0000	encoded by gene No. 9.	2242	
928	Y22499	Homo sapiens	Human secreted protein	2249	100
928	1				
			sequence clone mh703_1.		
	AJ224326	Homo sapiens	ribulose-5-phosphate-	912	100
928 930 931	AJ224326	Homo sapiens		912	100

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:		is elegans	cm21c7	DOURL	
	AL080065	Homo sapiens	hypothetical protein	210	25
932	G01884	Homo sapiens	Human secreted protein, SEQ	767	98
933			ID NO: 5965.	1200	100
934	AJ276485	Homo sapiens	integral membrane transporter protein		
935	AL035681	Homo sapiens	dJ756G23.3 (novel protein similar to drosophila transcriptional repressor)	1142	80
936	AB026808	Mus musculus	synaptotagmin XI	2142	95
937	AB020000	Homo sapiens	HRIHFB2216	2601	99
938	X65724	Homo sapiens	ORF2	498	100
939	W89024	Homo sapiens	Polypeptide fragment encoded	1487	100
940	G04047	Homo sapiens	by gene 156. Human secreted protein, SEQ	117	100
941	AF094583	Homo sapiens	ID NO: 8128. putative HIV-1 infection	452	100
			related protein	1250	+
942	AC024200	Caenorhabdit is elegans	contains similarity to several zinc finger proteins but not to the zinc finger domains	350	69
943	AF129756	Homo sapiens	G5c	273	100
944	M23765	Rattus norvegicus	alpha-tropomyosin	133	96
945	AC009917	Arabidopsis thaliana	Contains similarity to	583	47
946	AF223468	Homo sapiens	AD021 protein	551	44
947	AF055473	Homo sapiens	GAGE-8	273	51
948	X75756	Homo sapiens	protein kinase C mu	2019	68
949	AF143956	Mus musculus	coronin-2	2300	93
950	Y36729	Homo sapiens	Human PG1 protein sequence.	1861	99
951	W49041	Homo sapiens	Human low density lipoprotein binding protein LBP-2.	282	67
952	AB016881	Arabidopsis thaliana	gene_id:MXC17.7~	203	46
953	Y01785	Homo sapiens	Human ubiquitin-conjugating enzyme >Y25341 Y25341 01-JUL- 1999 12-AUG-1998 Human NCE-2 protein.	365	100
954	AF145615	Drosophila melanogaster	BcDNA.GH03377	823	46
955	U09410	Homo sapiens	zinc finger protein ZNF131	2483	99
956	U09410	Homo sapiens	zinc finger protein ZNF131	1853	99
957	AF195623	Homo sapiens	cholinephosphotransferase 1 alpha	2126	99
958	X94917	Drosophila melanogaster	head-elevated expression in 0.9 kb	155	32
959	U54807	Rattus	GTP-binding protein	1167	97
960	AF058807	Bos taurus	GTP-binding protein rah	606	97
961	G03244	Homo sapiens	Human secreted protein, SEQ ID NO: 7325.	471	100
962	AF078850	Homo sapiens	steroid dehydrogenase homolog	583	40
963	AP001754	Homo sapiens	transient receptor potential- related channel 7, a novel putative Ca2+ channel protein	317	30
964	AL035419	Homo sapiens	dJ1100H13.1 (putative novel protein)	1129	100
965	X61381	Rattus	interferon-induced protein	202	46
966	D38169	Homo sapiens	inositol 1,4,5-trisphosphate 3-kinase isoenzyme	3278	100
657	AL031432	Homo	dJ465N24.2.1 (PUTATIVE novel	893	100
967	AD031432	sapiens	protein) (isoform 1)		

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
968	U79275	Homo sapiens	unknown	611	100
969	AJ011306	Homo sapiens	guanine nucleotide exchange factor (long isoform)	2752	99
970	AF281134	Homo sapiens	exosome component Rrp46	1186	100
971	U53336	Caenorhabdit is elegans	weak similarity over a short region to myosin heavy chain	536	23
972	AC018749	Leishmania major	L8840.12	589	53
973	AF188504	Mus musculus	LNV	544	85
974	U25801	Homo sapiens	Tax1 binding protein	852	98
975	AF049523	Homo sapiens	huntingtin-interacting protein HYPA/FBP11	1390	97
976	AF161530	Homo sapiens	HSPC182	1040	100
977	G04020	Homo sapiens	Human secreted protein, SEQ ID NO: 8101.	626	100
978	AF164797	Homo sapiens	ribosomal protein L17 isolog	908	100
979	U94991	Xenopus laevis	transcription factor XLMO1	795	97
980	\$73775	Homo sapiens	calmitine; calsequestrine	2029	100
981	Y94888	Homo sapiens	Human protein clone HP01462.	2501	100
982	AJ243191	Homo sapiens	heat shock protein	827	96
983	X65020	Bos taurus	PSST subunit of the NADH: ubiquinone oxidoreductase complex	964	85
984	AJ249207	Rhodococcus sp. AD45	putative racemase	351	43
985	Z30093	Homo sapiens	basic transcription factor 2, 35 kD subunit	1576	99
986	AB030835	Homo sapiens	contains two glutamine rich domains, three zinc-finger domains, and matrin 3 homologous domain 3 (MH3)	4697	99
987	AF227258	Bos taurus	RPGR-interacting protein-1	1262	38
988	AL022238	Homo sapiens	dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE)	4048	99
989	AL022238	Homo sapiens	dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE)	2321	99
990	AF161426	Homo sapiens	HSPC308	448	92
991	AF161426	Homo sapiens	HSPC308	448	92
992	AF161426	Homo sapiens	HSPC308	453	92
993	AL023859	Schizosaccha romyces pombe	trna-splicing endonuclease subunit	172	42
994	AL049631	Homo sapiens	dJ513M9.1 (novel Homeobox domain protein)	241	47
995	AC005253	Homo sapiens	R26445_1	902	100
996	AF265206	Homo sapiens	MOG1 isoform A	974	100
997	AJ248285	Pyrococcus abyssi	sarcosine oxidase, subunit beta (soxB)	195	28
998	AE003641	Drosophila melanogaster	BG:DS00941.3 gene product	218	58
999	W69343	Homo sapiens	Secreted protein of clone CR930_1.	1340	98
1000	AY007135	Homo sapiens	similar to bovine ADP/ATP translocase T1 mRNA with GenBank Accession Number M24102.1	1543	100
1001	Y73381	Homo sapiens	HTRM clone 1877278 protein sequence.	1668	100
1002	AF208844	Homo sapiens	BM-002	428	100
1003	AE004944	Pseudomonas aeruginosa	hypothetical protein	134	35
1004	AL031431	Homo sapiens	dJ462023.2 (novel protein)	2058	100
1005	S45367	Canis	centractin	1949	100
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TABLE 2

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TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
1040	AF290204	Homo sapiens	blood group carrier molecule DOK1	1637	99
1041	Y96730	Homo sapiens	PR0539, a Costal-2 homologue.	162	22
1042	AF140683	Mus musculus	F-box protein FWD2	2397	98
1043	AF151023	Homo sapiens	HSPC189	1104	100
1044	AF181631	Drosophila melanogaster	BcDNA.GH04929	204	37
1045	Y77985	Homo sapiens	Human collectin amino acid sequence.	1940	100
1046	AJ243972	Homo sapiens	6-phosphogluconolactonase	1317	100
1047	AB035863	Homo sapiens	ATP specific succinyl CoA synthetase beta subunit precursor	2324	99
1048	AL034550	Homo sapiens	dJ1184F4.2 (novel protein similar to nucleolar protein 4 (NOL4) (NOLP))	981	92
1049	AF163825	Homo sapiens	pre-B lymphocyte protein 3	634	100
1050	AF201949	Homo sapiens	60S ribosomal protein L30 isolog	868	100
1051	AF190624	Mus musculus	mdgl-1	236	85
1052	AE003529	Drosophila melanogaster	CG6151 gene product	160	44
1053	G01191	Homo sapiens	Human secreted protein, SEQ ID NO: 5272.	646	98
1054	AL162756	Neisseria meningitidis	Glu-tRNA(Gln) amidotransferase subunit A	682	44
1055	AF181856	Rattus norvegicus	tRNA selenocysteine associated protein	1525	99
1056	U89649	Chlamydomona s reinhardtii	Mr19,000 outer arm dynein light chain	244	34
1057	AF159141	Homo sapiens	breast cancer metastasis- suppressor 1	663	53
1058	AF230929	Homo sapiens	keratinocyte annexin-like protein pemphaxin	1710	99
1059	AJ270952	Homo sapiens	putative membrane protein	1363	100
1060	AF224263	Heterodontus francisci	HoxD8	742	83
1061	X63417	Homo sapiens	IRLB	1037	100
1062	AL079345	Streptomyces coelicolor A3(2)	hypothetical protein	143	27
1063	Y71112	Homo sapiens	Human Hydrolase protein-10 (HYDRL-10).	2547	100
1064	AF263614	Homo sapiens	acetyl-CoA synthetase	3493	99
1065	Y13356	Homo sapiens	Amino acid sequence of protein PRO221.	1363	100
1066	AC006153	Homo sapiens	similar to Aquifex aeolicus GTP-binding protein; similar to AE000771 (PID:g2984292)	662	98
1067	Y18930	Sulfolobus solfataricus	hypothetical protein	162	29
1068	R65969	Homo sapiens T98G	Glioblastoma-derived polypeptide.	887	100
1069	Y07964	Homo sapiens	Human secreted protein fragment	863	96
1070	AF177476	Rattus norvegicus	CDK5 activator-binding protein	1995	86
1071	AF245505	Homo sapiens	adlican	3109	99
1072	U92794	Mus musculus	alpha glucosidase II, beta subunit	147	36
1073	G03889	Homo sapiens	Human secreted protein, SEQ ID NO: 7970.	698	98
1074	U15779	Homo sapiens	p70	380	28
1075	Y13392	Homo sapiens	Amino acid sequence of	1271	91

TABLE 2

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	* IDENTITY
NO:	, and about	ļ		SCORE	{
	 		protein PRO328.		
1076	AF161457	Homo sapiens	HSPC339	571	100
1077	Y79509	Homo sapiens	Human carbohydrate-associated	2151	98
	}	110	protein CRBAP-5.		
1078	AF223466	Homo sapiens	HT015 protein	831	66
1079	AL132965	Arabidopsis	putative WD-40 repeat-protein	286	29
1075	1 232703	thaliana	patatite me it ispain process.	1 200	
1080	AB024937	Homo sapiens	LUNX	1284	100
1081	Y14768	Homo sapiens	V-ATPase G-subunit like	579	100
1001	114700	nomo saprems	protein	1 3,73	100
1082	AF016416	Caenorhabdit	F29A7.4 gene product	141	31
1002	ALOTO410	is elegans	PESA7:4 gene product	111	
1083	L13291	Homo sapiens	ADP-ribosylarginine hydrolase	802	45
1084	AB041541	Mus musculus	unnamed protein product	151	44
			Human secreted protein, SEQ	202	97
1085	G01922	Homo sapiens		202	97
		L.,	ID NO: 6003.	833	100
1086	AB030814	Homo sapiens	H-REV107 protein homolog)
1087	AF151638	Homo sapiens	phosphatidylcholine transfer	1142	100
			protein	-	L
1088	Y84432	Homo sapiens	Amino acid sequence of a	2783	100
			human RNA-associated		}
			protein.		
1089	Y94867	Homo	Human protein clone HP10563.	613	100
		sapiens		<u> </u>	
1090	AK023982	Homo sapiens	unnamed protein product	130	49
1091	AB041586	Mus musculus	unnamed protein product	1103	81
1092	¥71277	Homo sapiens	Human Zlipo3 protein.	606	100
1093	U34973	Mus musculus	protein tyrosine phosphatase-	1131	95
			like]
1094	Y66677	Homo	Membrane-bound protein	522 .	56
	ļ	sapiens	PRO828.		
1095	Y87276	Homo sapiens	Human signal peptide containing protein HSPP-53 SEQ ID NO:53.	1029	99
1096	Y87276	Homo sapiens	Human signal peptide	863	98
1096	187276	HOMO Sapiens	containing protein HSPP-53 SEQ ID NO:53.	""	
1097	AF161455	Homo sapiens	HSPC337	742	98
1098	U80029	Caenorhabdit	similar to thioredoxin	242	39
1050	000027	is elegans			
1099	AJ005866	Homo sapiens	Sqv-7-like protein	1321	99
1100	AJ005866	Homo sapiens	Sqv-7-like protein	1118	99
1101	AJ005866	Homo sapiens	Sqv-7-like protein	891	99
1101	AJ005866	Homo sapiens	Sqv-7-like protein	1016	99
1102		Homo sapiens	hypothetical protein	299	31
	AL110244	· · · · · · · · · · · · · · · · · · ·	hrakeless-B	147	52
1104	AF242194	Drosophila	brakeless-B	14/	52
		melanogaster		<u> </u>	
1105	AL031010	Homo sapiens	dJ422F24.1 (PUTATIVE novel	968	100
			protein similar to C. elegans		1
	L		C02C2.5)		
1106	U28016	Mus musculus	parathion hydrolase	1624	87
	1		(phosphotriesterase) -related		İ
		<u> </u>	protein	<u> </u>	
1107	AJ278150	Homo sapiens	putative lipid kinase	2207	99
1108	G03733	Homo sapiens	Human secreted protein, SEQ	495	98
		1	ID NO: 7814.		l _
1109	AF217287	Drosophila melanogaster	G protein RhoBTB	834	54
1110	Y28921	Homo	Human regulatory protein	941	48
		sapiens	HRGP-7.		
1111	Y28921	Homo	Human regulatory protein	1331	51
	1	sapiens	HRGP-7.		1
	AF176704	Homo sapiens	F-box protein FBX9	2027	99
1117		, Daprens	I Process sous	1	1
1112		Homo	dlioma tumor gunnreggor	2418	100
1112	AF182076	Homo	glioma tumor suppressor	2418	100
		Homo sapiens Homo sapiens	glioma tumor suppressor candidate region protein 2 Human secreted protein, SEQ	2418	96

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
			ID NO: 8120.		
1115	AF229439	Mus musculus	zinc finger protein 289	1697	91
1116	L40357	Homo sapiens	thyroid receptor interactor	509	100
1117	L40357	Homo sapiens	thyroid receptor interactor	404	85
1118	A12155	Homo sapiens	Human X5L cDNA.	1673	100
1119	AL161542	Arabidopsis thaliana	isomerase like protein	607	53
1120	AL023754	Homo sapiens	dJ272L16.1 (Rat Ca2+/Calmodulin dependent Protein Kinase LIKE protein)	2341	98
1121	Y57901	Homo sapiens	Human transmembrane protein HTMPN-25.	321	36
1122	Z14122	Xenopus laevis	XLCL2	455	77
1123	AF225418	Homo sapiens	lipase	1531	97
1124	Y06518	Homo sapiens	Zen GTPase interacting protein ZIP.	3227	100
1125	AL035690	Homo sapiens	dJ202121.1 (novel protein)	952	100
1126	AJ000217	Homo sapiens	CLIC2	1286	99
1127	AB030505	Mus musculus	UBE-1c2	1069	79
1128	Y73375	Homo sapiens	HTRM clone 1427838 protein sequence.	874	100
1129	Y78941	Homo sapiens	Cyclophilin-type peptidyl prolyl cis/trans isomerase amino acid sequence.	877	100
1130	AL023553	Homo sapiens	dJ347H13.4 (novel protein)	557	100
1131	Y91945	Homo sapiens	Human chaperone protein 6 (HCHP-6).	1408	100
1132	Z68197	Schizosaccha romyces pombe	putative nuclear pore protein	596	39
1133	Z68197	Schizosaccha romyces pombe	putative nuclear pore protein	389	35
1134	AF180681	Homo sapiens	guanine nucleotide exchange factor	3597	100
1135	AF079765	Mus musculus	enhancer of polycomb	264	41
1136	M62419	Mus musculus	clathrin-associated protein	2189	99
1137	AJ006219	Drosophila melanogaster	clathrin-associated protein	1254	78
1138	Y76218	Homo sapiens	Human secreted protein encoded by gene 95.	440	98
1139	W88104	Homo sapiens	A Rab protein designated HRABS-2.	1065	99
1140	Y13401	Homo sapiens	Amino acid sequence of protein PRO339.	3979	98
1141	W85026	Chimeric - Homo sapiens	Green fluorescent protein- Zap70 fusion product.	3309	100
1142	Y13402	Homo sapiens	Amino acid sequence of protein PRO310.	1694	99
1143	G03875	Homo sapiens	Human secreted protein, SEQ ID NO: 7956.	660	99
1144	Y12917	Homo sapiens	Amino acid sequence of a human secreted peptide.	750	98
1145	Y12917	Homo sapiens	Amino acid sequence of a human secreted peptide.	1096	100
1146	AL022157	Homo sapiens	SPIN (SPINDLIN HOMOLOG (PROTEIN DXF34))	1233	100
1147	AL022157	Homo sapiens	SPIN (SPINDLIN HOMOLOG (PROTEIN DXF34))	1233	100
1148	G02548	Homo sapiens	Human secreted protein, SEQ ID NO: 6629.	370	98
1149	Y73338	Homo sapiens	HTRM clone 2019742 protein sequence.	1492	100
1150	W74841	Homo sapiens	Human secreted protein encoded by gene 113 clone	228	55

TABLE 2

	ACCESSION	SPECIES	DESCRIPTION	SMITH-	1
SEQ	NUMBER	Dr. Berbe	225001212201	WATERMAN	IDENTITY
NO:	NONDER			SCORE	10000
			HEAAR60.		
1151	AF044201	Rattus	neural membrane protein 35;	1570	92
4454	111111111	norvegicus	NMP35	20.0	
1152	AF156774	Homo	lysophosphatidic acid	1855	99
1132	111 135771	sapiens	acyltransferase-gamma1		
1153	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein	872	64
1133	ADITOSOI	none suprem	(translation of the cDNA	" "	••
			DKFZp566A0946, Em:AL050069))	1	
1154	AF131852	Homo sapiens	Unknown	473	100
1155	Y41705	Homo	Human PRO352 protein	1381	97
1155	141705	sapiens	sequence.	1301	3 '
1156	G04036	Homo sapiens	Human secreted protein, SEQ	607	99
1126	G04036	nomo sapiens	ID NO: 8117.	807	33
1157	AF112444	Lupinus	L-asparaginase	287	43
1127	AFIIZ444	luteus	l -asparaginase	201	43
1150	37751040		CCT CC TOTAL	232	32
1158	AF151848	Homo sapiens	CGI-90 protein	1	
1159	AJ272267	Homo sapiens	choline dehydrogenase	2449	100
1160	AB001773	Ciona	PEM-6	196	33
- 2 2 2 2 2 2	1100000	savignyi	**************************************	1776	
1161	¥87330	Homo sapiens	Human signal peptide	746	83
		Í	containing protein HSPP-107		1
			SEQ ID NO:107.		
1162	Y87330	Homo sapiens	Human signal peptide	746	83
		~	containing protein HSPP-107	1	
			SEQ ID NO:107.		
1163	AF113534	Homo sapiens	HP1-BP74 protein	2723	96
1164	AF232226	Danio rerio	Dedd1	191	41
1165	65 AL118501 Homo sapie	Homo sapiens	dJ1191N16.1 (A novel protein	1051	71
			(translation of the cDNA		
			DKFZp566A0946, Em:AL050069))		
1166	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein	945	76
			(translation of the cDNA		
			DKFZp566A0946, Em:AL050069))		
1167	AF187733	Homo sapiens	syntaphilin	831	42
1168	AB019435	Homo sapiens	phospholipase	951	55
1169	AF064604	Homo sapiens	KE03 protein	324	33
1170	Y01164	Homo sapiens	Polypeptide fragment encoded	1191	100
			by gene 6.		
1171	L03188	Saccharomyce	putative	180	22
		s cerevisiae	<u> </u>		
1172	AF113751	Mus musculus	nuclear pore membrane	3941	81
			glycoprotein POM210		
1173	AJ245417	Homo sapiens	G5b protein	794	100
1174	AL022238	Homo sapiens	dJ1042K10.3 (novel protein)	1285	100
1175	U41278	Caenorhabdit	F33G12.3 gene product	332	28
		is elegans			<u> </u>
					83
1176	M35617	Homo sapiens	T-cell receptor V-alpha-J-	284	1 63
1176	M35617	-	alpha region	284	63
1176	M35617 AC012680	Homo sapiens Arabidopsis	alpha region putative protein phosphatase	284	37
		-	alpha region putative protein phosphatase 2C; 55455-56414		
		Arabidopsis	alpha region putative protein phosphatase		
1177	AC012680	Arabidopsis thaliana	alpha region putative protein phosphatase 2C; 55455-56414 Human secreted protein, SEQ ID NO: 5426.	209	37
1177	AC012680	Arabidopsis thaliana	alpha region putative protein phosphatase 2C; 55455-56414 Human secreted protein, SEQ	209	37
1177	AC012680 G01345	Arabidopsis thaliana Homo sapiens	alpha region putative protein phosphatase 2C; 55455-56414 Human secreted protein, SEQ ID NO: 5426.	209	37
1177	AC012680 G01345	Arabidopsis thaliana Homo sapiens	alpha region putative protein phosphatase 2C; 55455-56414 Human secreted protein, SEQ ID NO: 5426. dJ579N16.3 (novel protein similar to worm, Arabidopsis and pine proteins)	209	37
1177	AC012680 G01345	Arabidopsis thaliana Homo sapiens	alpha region putative protein phosphatase 2C; 55455-56414 Human secreted protein, SEQ ID NO: 5426. dJ579N16.3 (novel protein similar to worm, Arabidopsis	209	37
1177 1178 1179	AC012680 G01345 AL096767	Arabidopsis thaliana Homo sapiens Homo sapiens	alpha region putative protein phosphatase 2C; 55455-56414 Human secreted protein, SEQ ID NO: 5426. dJ579N16.3 (novel protein similar to worm, Arabidopsis and pine proteins)	209 692 1342	37 99 100
1177 1178 1179	AC012680 G01345 AL096767	Arabidopsis thaliana Homo sapiens Homo sapiens Caenorhabdit is elegans	alpha region putative protein phosphatase 2C; 55455-56414 Human secreted protein, SEQ ID NO: 5426. dJ579N16.3 (novel protein similar to worm, Arabidopsis and pine proteins) similar to ATP synthase B chain	209 692 1342	37 99 100
1177 1178 1179 1180	AC012680 G01345 AL096767 AF039716 Y11710	Arabidopsis thaliana Homo sapiens Homo sapiens Caenorhabdit is elegans Homo sapiens	alpha region putative protein phosphatase 2C; 55455-56414 Human secreted protein, SEQ ID NO: 5426. dJ579N16.3 (novel protein similar to worm, Arabidopsis and pine proteins) similar to ATP synthase B chain collagen type XIV	209 692 1342	37 99 100
1177 1178 1179	AC012680 G01345 AL096767 AF039716	Arabidopsis thaliana Homo sapiens Homo sapiens Caenorhabdit is elegans Homo sapiens	alpha region putative protein phosphatase 2C; 55455-56414 Human secreted protein, SEQ ID NO: 5426. dJ579N16.3 (novel protein similar to worm, Arabidopsis and pine proteins) similar to ATP synthase B chain	209 692 1342 496	37 99 100 55
1177 1178 1179 1180	AC012680 G01345 AL096767 AF039716 Y11710	Arabidopsis thaliana Homo sapiens Homo sapiens Caenorhabdit is elegans Homo sapiens Homo sapiens	alpha region putative protein phosphatase 2C; 55455-56414 Human secreted protein, SEQ ID NO: 5426. dJ579N16.3 (novel protein similar to worm, Arabidopsis and pine proteins) similar to ATP synthase B chain collagen type XIV	209 692 1342 496	37 99 100 55
1177 1178 1179 1180	AC012680 G01345 AL096767 AF039716 Y11710	Arabidopsis thaliana Homo sapiens Homo sapiens Caenorhabdit is elegans Homo sapiens Homo sapiens >R94974	alpha region putative protein phosphatase 2C; 55455-56414 Human secreted protein, SEQ ID NO: 5426. dJ579N16.3 (novel protein similar to worm, Arabidopsis and pine proteins) similar to ATP synthase B chain collagen type XIV	209 692 1342 496	37 99 100 55
1177 1178 1179 1180	AC012680 G01345 AL096767 AF039716 Y11710	Arabidopsis thaliana Homo sapiens Homo sapiens Caenorhabdit is elegans Homo sapiens Homo sapiens >R94974 R94974 09-	alpha region putative protein phosphatase 2C; 55455-56414 Human secreted protein, SEQ ID NO: 5426. dJ579N16.3 (novel protein similar to worm, Arabidopsis and pine proteins) similar to ATP synthase B chain collagen type XIV	209 692 1342 496	37 99 100 55
1177 1178 1179 1180	AC012680 G01345 AL096767 AF039716 Y11710	Arabidopsis thaliana Homo sapiens Homo sapiens Caenorhabdit is elegans Homo sapiens Homo sapiens 3 >R94974 R94974 09- MAY-1996 27-	alpha region putative protein phosphatase 2C; 55455-56414 Human secreted protein, SEQ ID NO: 5426. dJ579N16.3 (novel protein similar to worm, Arabidopsis and pine proteins) similar to ATP synthase B chain collagen type XIV	209 692 1342 496	37 99 100 55
1177 1178 1179 1180	AC012680 G01345 AL096767 AF039716 Y11710	Arabidopsis thaliana Homo sapiens Homo sapiens Caenorhabdit is elegans Homo sapiens Homo sapiens >R94974 R94974 09-	alpha region putative protein phosphatase 2C; 55455-56414 Human secreted protein, SEQ ID NO: 5426. dJ579N16.3 (novel protein similar to worm, Arabidopsis and pine proteins) similar to ATP synthase B chain collagen type XIV	209 692 1342 496	37 99 100 55

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
		[Homo sapiens			
1183	U42841	Caenorhabdit is elegans	short region of weak similarity to collagen	161	33
1185	AJ131613	Homo sapiens	dicarboxylate carrier protein	1470	99
1186	L27645	Danio rerio	growth-associated protein	130	36
1187	Y02738	Homo sapiens	Human secreted protein encoded by gene 89 clone HLHFP03.	636	100
1188	AF217544	Xenopus laevis	ornithine decarboxylase-2	1459	60
1189	AL136307	Homo sapiens	dJ380B8.2 (Neuritin, a protein which promotes neurite outgrowth)	182 .	33 .
1190	X89602	Homo sapiens	rTSbeta	197	100
1191	U32828	Haemophilus influenzae Rd	ribosomal protein S6 modification protein (rimK)	268	31
1192	AF154831	Rattus norvegicus	PV-1	1403	60
1193	Y50926	Homo sapiens	Human fetal brain cDNA clone vc16_1 derived protein.	918	100
1194	AF026530	Rattus norvegicus	stathmin-like-protein splice variant RB3''	1093	97
1195	U35244	Rattus norvegicus	vacuolar protein sorting homolog r-vps33a	2981	96
1196	Y70470	Homo sapiens	Human p53 target molecule, PRG3 protein.	1680	100
1197	AF157318	Homo sapiens	AD-017 protein	912	47
1198	AF125443	Caenorhabdit is elegans	contains similarity to S. pombe phosphatidyl synthase (GB:Z28295)	460	39
1199	AF201934	Homo sapiens	DC12	1649	88
1200	AL031775	Homo sapiens	dJ30M3.3 (novel protein similar to C. elegans Y63D3A.4)	1902	100
1201	M21103	Ovis aries	BIIIB4 high-sulfur keratin	484	82
1202	Z85986	Homo sapiens	dJ108K11.3 (similar to yeast suppressor protein SRP40)	1143	75
1203	U18762	Rattus norvegicus	retinol dehydrogenase type I	890	52
1204	U35730	Mus musculus	jerky	2235	76
1205	AB002327	Homo sapiens	KIAA0329	151	24
1206	AB019233	Arabidopsis thaliana	ubiquinone/menaquinone biosynthesis methyltransferase-like	762	56
1207	AL136307	Homo sapiens	dJ380B8.2 (Neuritin, a protein which promotes neurite outgrowth)	742	100
1208	AF207989	Homo sapiens	orphan G-protein coupled receptor	2326	100
1209	297630	Homo sapiens	dJ466N1.4 (novel protein similar to ANK3 (ankyrin 3, node of Ranvier (ankyrin G)))	181	44
1210	U21549	Mus musculus	Ac39/physophilin	1280	68
1211	Y27700	Homo sapiens	Human secreted protein encoded by gene No. 12.	1267	100
1212	AF117814	Mus musculus	odd-skipped related 1 protein	945	66
1213	AF277233	Naegleria fowleri	calcineurin B	222	39
1214	D14849	Mus musculus	meiosis-specific nuclear structural protein 1	1950	77
1215	G03022	Homo sapiens	Human secreted protein, SEQ ID NO: 7103.	590	100
1216	272510	Caenorhabdit	similarity to yeast UTR3	634	49

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	1
ID NO:	NUMBER			WATERMAN SCORE	IDENTITY
	 	is elegans	protein (Swiss Prot accession		
			yk677h11.5 comes from this gene		
1217	249703	Saccharomyce s cerevisiae	unknown	134	22
1218	AC013430	Arabidopsis thaliana	F3F9.18	199	29
1219	L10910	Homo sapiens	splicing factor	1026	71
1220	270750	Caenorhabdit is elegans	similar to vanadate resistance protein transmembranous comes from this gene	965	58
1221	AL163815	Arabidopsis thaliana	putative protein	653	61
1222	AF155100	Homo sapiens	zinc finger protein NY-REN-21 antigen	2261	100
1223	J05071	Bos taurus	GTP-binding regulatory protein gamma-6 subunit	356	100
1224	Y73364	Homo sapiens	HTRM clone 2765991 protein sequence.	1169	99
1225	AL050170	Homo sapiens	hypothetical protein	714	100
1226	X64002	Homo sapiens	RAP74	2661	99
1227	X04085	Homo sapiens	catalase	2846	100
1228	AJ005620 AF045564	Mus musculus Rattus	skeletal muscle-specific gene development-related protein	1416	90
		norvegicus			93
1230	X97571	Mus musculus	HCMV-interacting protein	479	96
231	L08239	Homo sapiens	located at OATL1	2274	100
232	AF121863 AF121863	Homo sapiens	sorting nexin 14	1964	100
1233	AC024805	Homo sapiens Caenorhabdit	contains similarity to	744	31
		is elegans	TR:004595		
1235	AC006634	Caenorhabdit is elegans	contains similarity to Saccharomyces cerevisiae probable membrane protein YLR418c (GB:U20162)	357	33
1236	Y18101	Mus musculus	macrophage actin-associated- tyrosine-phosphorylated protein	1559	87
1237	AB042646	Homo sapiens	TGIF2	1224	100
1238	AB026264	Homo sapiens	IMPACT	1694	100
1239	AB026264	Homo sapiens	IMPACT	1123	100
1240	G00429	Homo sapiens	Human secreted protein, SEQ ID NO: 4510.	324	100
1241	Y76144	Homo sapiens	Human secreted protein encoded by gene 21.	1363	53
1242	AL035602	Arabidopsis thaliana	putative protein	499	28
1243		Gallus gallus	Yes-associated protein (65kDa)	574	48
1244	AF220186	Homo sapiens	uncharacterized hypothalamus protein HT012	503	100
1245	AL021453 AJ276003	Homo sapiens	dJ821D11.3 (PUTATIVE protein) GAR1 protein	856 1216	100
1247	Y57910	Homo sapiens	Human transmembrane protein HTMPN-34.	1369	98
1248	AC004874	Homo sapiens	similar to N- acetylgalactosaminyltransfera se; similar to Q07537 (PID:q1171989)	957	100
1249	AF199597	Homo sapiens	A-type potassium channel modulatory protein 1	1139	100
1250	Y13148	Rattus norvegicus	PAG608	1350	88
1251	M24852	Rattus	neuron-specific protein PBP-	124	46

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
1252	AF146738	Rattus norvegicus	testis specific protein	771	83
1253	G02725	Homo sapiens	Human secreted protein, SEQ ID NO: 6806.	419	97
1254	W44375	Homo sapiens	Human ubiquitin-conjugating enzyme polypeptide.	1045	99
1255	AC006538	Homo sapiens	BC41195_1	831	78
1256	AB004316	Bos taurus	mitochondrial methionyl-tRNA transformylase	1556	88
1257	235094	Homo sapiens	SURF-2	1354	97
1258	Y13362	Homo sapiens	Amino acid sequence of protein PRO214.	2383	100
1259	AC006014	Homo sapiens	similar to RFP transforming protein; similar to P14373 (PID:g132517)	1299	100
1260	AC005099	Homo sapiens	match to AI222572 (NID:g3804775)	469	100
1261	V00507	Homo sapiens	coding sequence of DHFR (1 is lst base in codon) (561 is 3rd base in codon)	984	100
1262	X15443	Rattus sp.	gamma-glutamyltranspeptidase (AA 1-568)	697	32
1263	AF173871	Mus musculus	neuronal PAS3	977	94
1264	AF178983	Homo sapiens	Ras-associated protein Rapl	433	97
1265	Y70473	Homo sapiens	Human cyclic nucleotide- associated protein-1 (CNAP- 1).	2785	99
1266	Y41738	Homo sapiens	Human PRO541 protein sequence.	1622	100
1267	AF061346	Mus musculus	Edpl protein	1077	64
1268	U97006	Caenorhabdit is elegans	C13F10.4 gene product	154	23
1269	AF233582	Mus musculus	GTPase Rab37	942	95
1270	AF195951	Homo sapiens	signal recognition particle	3127	98
1271	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	1150	55
1272	AF201933	Homo sapiens	DC11	650	100
1273	AF201933	Homo sapiens	DC11	346	98
1274	AL021710	Arabidopsis thaliana	putative protein	348	
1275	AC004449	Homo sapiens	R33683_3	556 1920	100
1276	Y86295	Homo sapiens	Human secreted protein HL2AG87, SEQ ID NO:210.	1576	99
1277	Y71111	Homo sapiens	Human Hydrolase protein-9 (HYDRL-9).		
1278	S94421	Homo sapiens	T cell receptor eta-exon	1909	100
1279	Y66695	Homo sapiens	Membrane-bound protein PRO1344.	772	100
1280	AF161380	Homo sapiens	HSPC262	779	100
1281	Y48610	Homo sapiens	Human breast tumour- associated protein 71.		35
1282	AC015446	Arabidopsis thaliana	Similar to AIG1 protein	406	
1283	AK024432	Homo sapiens	FLJ00022 protein	1825	35 81
1284	W96153	Homo sapiens	Human FADD-interacting protein (FIP).	1301	100
1285	AJ001019	Homo sapiens	ring finger protein		
1286	AE003823	Drosophila melanogaster	CG13178 gene product	195	29
1287	AF178632	Homo sapiens	FEM-1-like death receptor binding protein	3261	100
1288	AC006033	Homo sapiens	similar to MLN 64; similar to I38027 (PID:g2135214)	1195	100
1289	AC006033	Homo sapiens	similar to MLN 64; similar to 138027 (PID:g2135214)	668	93
1290	AB023811	Homo sapiens	TU3A	351	54

TABLE 2

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:				SCORE	IDENTITI
1291	273424	Caenorhabdit is elegans	C44B9.1	235	36
1292	Y94871	Homo sapiens	Human protein clone HP02551.	1222	100
1293	AF180425	Homo sapiens	retinoblastoma-associated protein RAP140	489	29
1294	G03856	Homo sapiens	Human secreted protein, SEQ ID NO: 7937.	538	99
1295	AF133670	Mus musculus	ARL-6 interacting protein-2	367	51
1296	AJ249735	Homo sapiens	claudin-6	1142	100
1297	X57560	Escherichia coli	pspE protein	535	100
1298	AF169284	Homo sapiens	LIM and cysteine-rich domains protein 1	1997	100
1299	U41023	Caenorhabdit is elegans	coded for by C. elegans cDNA yk61f1.3; coded for by C. yk109h8.5	324	29
1300	AB024523	Homo sapiens	basic kruppel like factor	1206	100
1301	X55989	Homo sapiens	eosinophil cationic-related protein	737	99
1302	AF007151	Homo sapiens	unknown	1481	100
1303	X52904	Escherichia coli	open reading frame (AA 1-65)	359	100
1304	U19577	Escherichia coli	galactonate dehydratase	242	93
1305	AF266508	Mus musculus	NELF protein	1409	97
1306	Y57901	Homo sapiens	Human transmembrane protein HTMPN-25.	932	100
1307	U58750	Caenorhabdit is elegans	similar to the mitochondrial carrier family	365	54
1308	AF044774	Homo sapiens	breakpoint cluster region protein 2	2681	99
1309	AL078593	Homo sapiens	dJ210B1.1 (KIAA0680)	267	34
1310	X82693	Homo sapiens	E48 antigen	620	96
1311	Z82263	Caenorhabdit is elegans	C47A4.1	283	35
1312	AF131218	Homo sapiens	chromosome 16 open reading frame 5	1493	100
1313	Y41763	Homo sapiens	Human PRO938 protein sequence.	1636	100
1314	AF196972	Homo sapiens	JM24 protein	2239	100
1315	AF053356	Homo sapiens	insulin receptor substrate like protein	228	97
1316	Y66695	Homo sapiens	Membrane-bound protein PRO1344.	1909	100
1317	AF153127	Gallus gallus	SAPK interacting protein	2442	89
1318	AF153127	Gallus gallus	SAPK interacting protein	1477	83
1319	AF153127	Gallus gallus	SAPK interacting protein	1651	86
1320	X56932	Homo sapiens	23 kD highly basic protein	1044	100
1321	AF174605	Homo sapiens] >Y83086 Y83086 09- MAR-2000 28- AUG-1998 F- box protein FBP-18. [Homo sapiens	F-box protein Fbx25	467	70
1322	M61732	Trypanosoma cruzi	neuraminidase	214	24
1323	Y17013	porcine endogenous	pol	304	64

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	*
ID	NUMBER			WATERMAN	IDENTITY
NO:				SCORE	
		retrovirus		1	
1324	AL138655	Arabidopsis thaliana	putative protein	1174	37
1325	AL138655	Arabidopsis	putative protein	946	35
1505	12230033	thaliana	paradara paradara		33
1326	AL133215	Homo sapiens	bA108L7.2 (novel protein	1322	99 -
			similar to rat tricarboxylate		1
			carrier)		<u> </u>
1327	AF161541	Homo sapiens	HSPC056	1357	99
1328	Y73346	Homo sapiens	HTRM clone 619699 protein	785	96
			sequence.		
1329	L10910	Homo sapiens	splicing factor MIL1 protein	912 1936	100
1330	AF146568 W87772	Homo sapiens	Human serum glucocorticoid-	232	39
1331	W8///2	Homo sapiens	regulated kinase (H-SGK2)	232	39
			polypeptide.		
1332	Y41741	Homo	Human PRO704 protein	1860	100
		sapiens	sequence.		
1333	AF295096	Homo sapiens	zinc-finger protein ZBRK1	411	91
1334	Z82271	Caenorhabdit	Similarity to Mouse kinensin-	578	44
		is elegans	like protein KIF4 comes from		
	<u> </u>		this gene		
1335	AE000810	Methanobacte	conserved protein	290	43
		rium	·		
	ł	thermoautotr			
1336	Y68779	ophicum Homo sapiens	Amino acid sequence of a	1019	91
1336	168//9	Homo Bapiens	human phosphorylation	1019	1 31
	ĺ		effector PHSP-11.		
1337	AB027003	Mus musculus	protein phosphatase	378	84
1338	U64856	Caenorhabdit	weak similarity to TPR	215	40
2000		is elegans	domains		
1339	AE001394	Plasmodium	protein of the YMR7 family	170	29
		falciparum			
1340	X76717	Homo sapiens	MT-11 protein	204	89
1341	AC011914	Arabidopsis	putative mutT protein; 68398-	289	45
		thaliana	67881		
1342	AJ276171	Homo sapiens	ASPIC	2122	100
1343	AF187016	Homo sapiens	myosin regulatory light chain interacting protein MIR	2303	99
1344	AC006963	Homo sapiens	similar to Kelch proteins;	894	35
1344	ACCOUGGES	nomo sapiens	similar to BAA77027	6,54	33
	ì		(PID:q4650844)		
1345	AF257466	Homo sapiens	N-acetylneuraminic acid	1880	99
		1	phosphate synthase		
1346	Y25896	Homo sapiens	Human secreted protein	1148	100
			fragment encoded from gene		Į
	1		64.		
1347	AJ272073	Torpedo	male sterility protein 2-like	1664	58
3340	1 N D 2 C 2 C 4 C 2	marmorata	protein	1010	
1348	AF161548	Homo sapiens	HSPC063 Human secreted protein	1018	98
1349	W78128	Homo sapiens	encoded by gene 3 clone	1117	100
			HOSBI96.		
1351	G02144	Homo sapiens	Human secreted protein, SEQ	418	100
			ID NO: 6225.		
1352	D90869	Escherichia	similar to	2047	100
		coli			
1353	A12029	Homo sapiens	MRP-14	613	100
1354	AC005328	Homo sapiens	R26660_1, partial CDS	870	74
1355	AC024876	Caenorhabdit	contains similarity to	829	61
		is elegans	SW:RPB1_CRIGR		
1356	AF077226	Homo sapiens	copine III	1876	64
1359	AF217188	Mus musculus	YIPIB	801	63
1360	AC074331	Homo sapiens	ZNF234	3869	100
1361	AL163279	Homo sapiens	homolog to cAMP response	5035	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	1DENTITY
NO.			element binding and beta transducin family proteins		
362	248475	Homo sapiens	glucokinase regulator	3160	99
363	Z48475	Homo sapiens	glucokinase regulator	2682	97
364	AF195764	Homo sapiens	megakaryocyte-enhanced gene transcript 1 protein; MEGT1 protein	2055	99 .
1365	AF116609	Homo sapiens	PR00915	581	100
1366	AF116609	Homo sapiens	PR00915	581	100
1367	AL117352	Homo sapiens	dJ876B10.3 (novel protein similar to C. elegans T19B10.6 (Tr:Q22557))	2581	99
1368	Y34124	Homo sapiens	Human potassium channel K+Hnov15.	1342	100
1369	AJ245621	Homo sapiens	CTL2 protein	3728	99
1370	AF008220	Bacillus subtilis	YtaG	429	45
1371	X05562	Homo sapiens	alpha-2 chain precursor (AA - 25 to 1018) (3416 is 2nd base in codon)	5908	99
1372	Z98048	Homo sapiens	dJ408N23.4 (novel DnaJ domain protein)	1296	99
1373	AF154415	Homo sapiens	FLASH	10253	100
1374	U20286	Rattus norvegicus	lamina associated polypeptide 1C	1567	69
1375	U53445	Homo sapiens	DOC1	1645	46
1376	AL117337	Homo sapiens	bA393J16.1 (zinc finger protein 33a (KOX 31))	250	60
1377	AC005328	Homo sapiens	R26660_1, partial CDS	1126	100
1378	U35113	Homo sapiens	metastasis-associated gene	1823	69
1379	L15313	Caenorhabdit is elegans	putative	858	58
1380	Y25756	Homo sapiens	Human secreted protein encoded from gene 46.	1508	100
1381	AB037360	Homo sapiens	ANKHZN	5734	95
1382	AB037360	Homo sapiens	ANKHZN	959	97
1383	AF237676	Mus musculus	G beta-like protein GBL	1721	70
1384	AF237676	Mus musculus	G beta-like protein GBL	715	100
1385	¥58793	Homo sapiens	Human calcium regulatory protein CaREG-1.	10369	99
1386	AF212162	Homo sapiens	ninein	337	33
1387 1388	AL031685 AC004890	Homo sapiens Homo sapiens	dJ963K23.2 (novel protein) similar to zinc finger proteins; similar to BAA24380 >W06316 W06316 03-OCT-1996 27-APR-1995 TRP-1 protein.	542	86
1389	AF187989	Homo sapiens	zinc finger protein ZNF223	2665	99
1390	AC035150	Homo sapiens	Zinc finger protein ZNF221	3459	100
1391	AF287894	Homo sapiens	PIST	1410	97
1392	AF282265	Homo sapiens	inner centromere protein INCENP	1794	99
1393	X90840	Homo sapiens	axonal transporter of synaptic vesicles	4584	99
1394	AF076249	Homo sapiens	zinc finger protein SBBIZ1	3208	99
1395	G02224	Homo sapiens	Human secreted protein, SEQ ID NO: 6305.	299	75
1396	AC004809	Arabidopsis thaliana	Similar to	130	34
1398	AF242519	Homo sapiens	zinc finger protein SBZF3	181	66
1399	AL133396	Homo sapiens	dJ1068H6.4 (prion protein like protein doppel)	962	100
1400	Y48611	Homo sapiens	Human breast tumour- associated protein 72.	817	99
1401	AC004472	Homo sapiens	P1.11659_5	280	54
		Saccharomyce	.l	164	27
1402	X91489	Daccitatom ce	Padada in in in in in in in in in in in in in	·	

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
1403 ,	Y79222	Homo sapiens	Human transferase TRNSFS-14.	2842	100
1404	X81058	Mus musculus	tex261	1010	99
1405	AB012084	Mus musculus	ITM	194	29
1406	AB030251	Homo sapiens	GTPase activating protein	3233	99
		Rattus	PTB-like protein	2684	99
1407	AJ010585	rattus			
1408	X75760	Drosophila melanogaster	LRR47	364	29
1409	U76618	Mus musculus	N-RAP	804	48
1410	AC00557B	Homo sapiens	P20887_1, partial CDS	835	63
1411	AE000284	Escherichia coli	orf, hypothetical protein.	360	100
1412	X01563	Escherichia coli	L5 (rplE) (aa 1-179)	911	100
1413	W78279	Homo sapiens	Fragment of human secreted protein encoded by gene 33.	1264	99
1414	AB031051	Homo sapiens	organic anion transporter OATP-E	3832	100
1415	M17466	Homo sapiens	coagulation factor XII	3455	100
1416	AF097994	Homo	L-kynurenine/alpha-	2202	99
		sapiens	aminoadipate aminotransferase		
1417	AF151077	Homo sapiens	HSPC243	1262	99
1418	Y09945	Rattus norvegicus	putative integral membrane transport protein	1098	61
1419	U13152	Mesocricetus	guanine nucleotide-binding protein beta 5	2179	76
1420	AI:162458	Homo sapiens	bA465L10.5 (KIAA1176 (novel	5696	100
1120	AB102430	Albana Bapana	protein, presumed ortholog of mouse K-Cl cotransporter KCC2))		
1421	Y99426	Homo sapiens	Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.	152	29
1422	Y94923	Homo sapiens	Human secreted protein clone qs14_3 protein sequence SEQ ID NO:52.	4039	99
1423	AF177388	Homo sapiens	cancer-amplified transcriptional coactivator ASC-2	10748	99
1424	Y48517	Homo sapiens	Human breast tumour- associated protein 62.	1851	99
1425	AF208848	Homo sapiens	BM-006	1454	89
1426	AF208848	Homo sapiens	BM-006	853	79
1427	AF112886	Bos taurus	differentiation enhancing factor 1	4693	95
1428	U41387	Homo sapiens		1372	63
1429	AF161534	Homo sapiens	HSPC049	2853	78
1430	AF125043	Mus musculus	bisphosphate 3'-nucleotidase	275	30
1431	Y66718	Homo sapiens	Membrane-bound protein PRO1106.	1886	100
1432	AF193613	Homo sapiens	cell recognition molecule Caspr2	568	100
1433	AB044560	Mus musculus	Gliacolin	192	34
1434	R99800	Homo sapiens	NTII-1 nerve protein, facilitates regeneration of	707	51
1435	AF220530	Homo sapiens	nerve cells. myo-inositol 1-phosphate	2904	100
1436	X70944	Homo sapiens	synthase Al	1261	72
		Homo sapiens	factor bridging integrator-3	1282	100
1437	AF271732		Human secreted protein	595	98
1438	Y30811	Homo sapiens	encoded from gene 1.		97
1439	AJ293659	Homo sapiens	mucolipidin	628	100
1440	AF219138	Homo sapiens		3083	100
1441	AF21913B	Homo sapiens	GGA3 long isoform	3346	1 700

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	*
ID	NUMBER			WATERMAN	IDENTITY
NO:				SCORE	
1442	AB039669	Homo sapiens	ALEX3	1944	100
1443	AF237711	Drosophila	Diablo .	191	27
		melanogaster		ļ	
1444	AJ011896	Homo sapiens	Nafl beta protein	439	39
1445	X73874	Homo sapiens	phosphorylase kinase	6233	98
1446	AF214114	Homo sapiens	breast carcinoma-associated	3999	99
			antigen BCAA		ļ.,
1447	AF003924	Homo sapiens	ANC_2H01	2645	99
1448	AF003136	Caenorhabdit	contains weak similarity to	2843	52
		is elegans	an AMP-binding motif		<u> </u>
1449	AF155112	Homo sapiens	NY-REN-50 antigen	1184	100
1450	Y95004	Homo sapiens	Human secreted protein	985	100
			vc54_1, SBQ ID NO:48.	688	57
1451	AF107203	Homo sapiens	ataxin 2-binding protein	456	78
1452	AF107203	Homo sapiens	ataxin 2-binding protein	882	56
1453	Z38011	Mus musculus	DMR-N9	510	28
1454	X90568	Homo sapiens	Protein sequence and	210	28
			annotation available soon via		
			dJ564M11.3 (similar to	1356	100
1455	AL035409	Homo sapiens	dJ564M11.3 (Similar to sialyltranferase)	1356	100
1156		Mus musculus	MATH-2 protein	272	100
1456	D44480	Homo sapiens	RNA helicase HDB/DICE1	478	45
1458	AF141326		retinovin	945	34
1459	AF242552	Gallus gallus	retinovin	345	34
	Ü11036	Homo sapiens	Ibd1	724	84
1460 1461	AB025258	Mus musculus	granuphilin-a	545	39
1461	Y08134	Homo sapiens	acid sphingomyelinase-like	2428	99
1462	108134	nomo sapiens	phosphodiesterase	2420	1 33
1463	AC004997	Homo sapiens	match to ESTs Z43979	869	98
1403	ACUU4991	noulo saptens	(NID:q573097), R19699	1 003	1 30
	}		(NID:9774333)		1
1464	AC004997	Homo sapiens	match to ESTs Z43979	869	98
1101	ACCOUNTY	nome supreme	(NID:g573097), R19699	1	
			(NID:g774333)	ļ	
1465	U32743	Haemophilus	fucose operon protein (fucU)	315	50
		influenzae	-	1	
		Rd	1	}	1
1466	Y09022	Homo sapiens	Not56-like protein	2342	100
1467	AC003034	Homo sapiens	Homolog of rat kidney-	1072	99
		•	specific (KS) gene		
1468	AF071544	Spinacia	ribulose-1,5-bisphosphate	333	26
		oleracea	carboxylase/oxygenase small		1
		(subunit N-methyltransferase I		
1469	Y57930	Homo sapiens	Human transmembrane protein	1053	100
		_	HTMPN-54.		
1470	AF032666	Rattus	rsec5	4504	93
		norvegicus			1
1471	¥70467	Homo sapiens	Human membrane channel	452	74
			protein-17 (MECHP-17).		1
1472	AL031033	Homo sapiens	C321D2.1 (Ribosomal Large	1694	100
			Subunit Pseudouridine		1
			Synthase protein)		<u> </u>
1473	AF177292	Homo sapiens	genethonin 3	4026	98
1474	\$45936	Homo sapiens	HTS1	1101	50
1475	¥86241	Homo sapiens	Human secreted protein	1879	98
		<u></u> _	HOABR60, SEQ ID NO:156.		
1476	AJ010317	Fugu	Sand	1278	68
		rubripes		L	
1477	U42831	Caenorhabdit	coded for by C. elegans cDNA	846	44
		is elegans	yk99b4.3; similar to human		I
			transforming protein		1
			(PIR:S22157)		
1478	X62447	Homo sapiens	PR 264	543	61
1479	X82209	Homo sapiens	MN1	7116	100
1480	U10536	Pan paniscus	MHC class I A	675	84

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
1481	AL078599	Homo sapiens	dJ991C6.1 (novel protein similar to C. elegans	1274	65
			F55A12.9 (Tr:P91086))		
1482	298977	Schizosaccha romyces pombe	putative vacuolar protein	256	29
1483	AB005662	Mus musculus	JNK/SAPK-associated protein-1	4968	92
1484	AL050120	Homo sapiens	hypothetical protein	716	100
1485	M27878	Homo sapiens	DNA binding protein	1006	53
1486	Y69161	Homo sapiens	Amino acid sequence of a partial protein kinase.	575	99
1487	X84156	Saccharomyce s cerevisiae	ATH1	341	29
1488	AF038963	Homo sapiens	RNA helicase	446	34
1489	U56966	Caenorhabdit is elegans	coded for by C. elegans cDNA yk30b3.5; coded for by C. elegans cDNA yk30b3.3	620	42
1490	AE000989	Archaeoglobu s fulgidus	enoyl-CoA hydratase (fad-4)	533	46
1491	MB0633	Rattus norvegicus	adenylyl cyclase type IV	707	95
1492	Y73342	Homo sapiens	HTRM clone 2709055 protein sequence.	3513	99
1493	Y17220	Homo sapiens	Human secreted protein (clone fj283-11).	462	37
1494	AF133670	Mus musculus	ARL-6 interacting protein-2	701	97
1495	Y94897	Homo sapiens	Human protein clone HP10574.	1371	100
1496	AL049699	Homo sapiens	dJ747H23.2 (novel protein)	1550	100
1497	AF037447	Homo sapiens	ribosomal S6 protein kinase	2427	100
1498	AL445067	Thermoplasma acidophilum	putative target YPL207w of the HAP2 transcriptional complex related protein	269	35
1499	AB039947	Homo sapiens	X11L-binding protein 51	227	36
1500	AJ277750	Homo sapiens	UBASH3A protein	3509	100
1501	AL050333	Homo sapiens	dJ93K22.1 (novel protein (contains DKFZP564B116))	2439	100
1502	AF179896	Homo sapiens	TALE homeobox protein Meis2b	1140	100
1503	AF178948	Homo sapiens	TALE homeobox protein Meis2a	1177	100
1504	¥53005	Homo sapiens	Human secreted protein clone pm749_8 protein sequence SEQ ID NO:16.	1442	99
1505	X82494	Homo sapiens	fibulin-2	3580	99
1506	X98296	Homo sapiens	ubiquitin hydrolase	783	42
1507	AL034548	Homo sapiens	dJ1103G7.6 (novel protein)	1098	100
1508	Y76144	Homo sapiens	Human secreted protein encoded by gene 21.	1736	100
1509	AF220182	Homo sapiens	protein HT008	1181	98
1510	U64601	Caenorhabdit is elegans	Gene probably begins in the next cosmid	415	58
1511	AL356192	Neurospora crassa	related to MDM1 protein	196	29
1512	D17629	Homo sapiens	N-acetylgalactosamine 6- sulfate sulfatase (GALNS)	1829	100
1513	AF168717	Homo sapiens	x 009 protein	694	99
1514 1515	AJ243531 AC003672	Homo sapiens Arabidopsis	nM15 protein putative C3HC4-type RING zinc	735 407	30
1516	AF115435	Rattus	finger protein syntaxin 17	1374	90
	_	norvegicus		<u> </u>	
1517	AF003140	Caenorhabdit is elegans	C44E4.5 gene product	274	31
1518	AB002584	Rattus norvegicus	beta-alanine-pyruvate aminotransferase	2238	82
1519	AL121764	Schizosaccha	yeast atp12 protein precursor	270	30

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	*
ID	NUMBER			WATERMAN	IDENTITY
NO:				SCORE	
		romyces	homolog		
1520	AF255910	pombe Homo	vascular endothelial	547	100-
1520	AF255910	sapiens	junction-associated molecule	547	100
1521	D31764	Homo sapiens	KIAA0064	170	27
1522	Y66634	Homo	Membrane-bound protein	985	100
		sapiens	PRO190.		
1523	Y94450	Homo sapiens	Human inflammation associated	250	43
			protein		
1524	AC000107	Arabidopsis	F17F8.22	277	37
1525	AF109377	thaliana Mus musculus	117.	1000	
1525	AL031427	Homo sapiens	dJ167A19.4 (novel protein)	1277	99
1527	Y08135	Mus musculus	acid sphingomyelinase-like	1496	79
1321	100155	Inas mascaras	phosphodiesterase	1430	'3
1528	AK024423	Homo sapiens	FLJ00012 protein	611	100
1529	AF154502	Homo sapiens	quiescent cell proline	679	100
	•	,	dipeptidase		
1530	AF205598	Homo sapiens	transposase-like protein	1368	100
1531	AF251039	Homo sapiens	putative zinc finger protein	1420	50
1532	W74805	Homo sapiens	Human secreted protein	493	57
	ļ.		encoded by gene 77 clone		
2522	3 F02 0 0 2 2	Homo sapiens	HOEAS24.		<u> </u>
1533	AF039023	Homo sapiens	Ran-GTP binding protein; RanBP6	5707	99
1534	AC007190	Arabidopsis	F23N19.9	374	37
1331	HCCO/1250	thaliana	125113.5	374] 3 /
1535	AB027564	Homo sapiens	DINB1	4482	100
1536	Y36178	Homo sapiens	Human secreted protein	377	87
1537	Y50907	Homo sapiens	Human fetal brain cDNA clone	3693	99
			vb3_1 derived protein.		
1538	AF017368	Mus musculus	faciogenital dysplasia	177	47
			protein 2		
1539 1540	AF266756 Z48804	Homo sapiens	sphingosine kinase OA1	2011	99
1541	AF000195	Caenorhabdit	Contains similarity to Pfam	2238 379	100
1311	74 000233	is elegans	domain: PF00169 (PH), Score=20.6, E-value=1.9e-05, N=1	379	42
1542	Y71159	Homo sapiens	Human phosphodiesterase	9415	99
			interacting protein, myomegalin.	3113	33
1543	X76092	Homo sapiens	DNA binding protein RFX3	3327	100
1544	AB015330	Homo sapiens	HRIHFB2007	631	50
1545	AF198487	Homo sapiens	transcription factor LBP-1b	2822	100
1546	AF016417	Caenorhabdit	Similar to BZIP transcription	518	42
1547	X55885	is elegans Homo sapiens	factor KDEL receptor	1106	100
1548	AB035495	Carassius	ubiquitin-activating enzyme	836	100
~~=0		auratus	B1	""	34
1549	AL021707	Homo sapiens	dJ508I15.4 (KIAA0668)	3688	100
1550	AJ223978	Bacillus	YvqK protein	292	42
		subtilis		Ì	
1551	AF145615	Drosophila	BcDNA.GH03377	822	44
		melanogaster		L	
1552	AL157734	Schizosaccha romyces pombe	putative mannosyltransferase involved in N-glycosylation	435	37
1553	AF079527	Mus musculus	IER5	691	63
1554	AB026291	Rattus norvegicus	acetoacetyl-CoA synthetase	1099	88
1555	Y44722	Homo sapiens	Human immune system molecule, ISMO-3.	1780	99
1556	AF116553	Drosophila melanogaster	antennal-specific short-chain dehydrogenase/reductase	277	32
1557	Y71056	Homo sapiens	Human membrane transport	1975	99

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:				SCORE	
			protein, MTRP-1.	1975	99
1558	Y71056	Homo sapiens	Human membrane transport protein, MTRP-1.		
1559	Y71056	Homo sapiens	Human membrane transport protein, MTRP-1.	1894	97
1560	AF092050	Mus musculus	beta-1,3-N- acetylglucosaminyltransferase	262	44
1561	AL109827	Homo sapiens	dJ309K20.2 (acrosomal protein	1607	97
1501			ACR55 (similar to rat sperm antiqen 4 (SPAG4)))	43	
1562	AJ131890	Homo sapiens	DNA polymerase lambda	3002	100
1563	AL035424	Homo sapiens	dA22D12.1 (novel protein	3015	100 /
			similar to Drosophila Kelch proteins)		
1564	AC002400	Homo sapiens	Gene product with similarity to Ubiquitin binding enzyme	2790	100
1565	AC005306	Homo sapiens	R27216 1	919	82
1566	AF000195	Caenorhabdit	Contains similarity to Pfam	550	45
		is elegans	domain: PF00169 (PH),		
			Score=20.6, E-value=1.9e-05, N=1	1	
1563	AB033281	Homo	F-box and WD-repeats protein	2879	100
1567	ABU33281	Homo sapiens	beta-TRCP2 isoform C	1	
1568	D49473	Mus musculus	truncated form of Sox17	1047	78
1569	AK025270	Homo sapiens	unnamed protein product	210	91
1570	X75756	Homo sapiens	protein kinase C mu	4797	99
1571	AF145713	Homo sapiens	SCHIP-1	2388 .	100
1572	AE003831	Drosophila melanogaster	CG18445 gene product	180	31
1573	AF074603	Streptomyces	NonF	205	38
		griseus	·		
	İ .	subsp.			
		griseus	F22D3.3 gene product	144	27
1574	U28993	Caenorhabdit is elegans	F22D3.3 gene product	144	
1575	AF129507	Homo sapiens	transcription factor ICBP90	287	68
1576	X64878	Homo sapiens	oxytocin receptor	2002	100
1577	AF237711	Drosophila	Diablo	421	54
		melanogaster		1.00	1.00
1578	G00975	Homo sapiens	Human secreted protein, SEQ ID NO: 5056.	480	100
1579	AF248744	Cryptosporid ium parvum	thrombospondin-related adhesive protein	123	3.3
1580	AL121782	Homo sapiens	dJ585I14.2 (novel protein	663	100
			(translation of cDNA Em:AK000219))		
1581	AF041853	Homo sapiens	kinesin family member protein KIF3A	345	33
1582	AF025441	Homo sapiens	Opa-interacting protein OIP5	1198	100
1583	AE001803	Thermotoga maritima	glycerate kinase, putative	349	34
1584	AF252283	Homo sapiens	Kelch-like 1 protein	3973	100
1585	AF169675	Homo sapiens	leucine-rich repeat transmembrane protein FLRT1	3494	99
1586	AF118274	Homo sapiens	DNb-5	2628	97
1587	X79440	Homo sapiens	NADP+-dependent malic enzyme	3167	99
1588	X99802	Homo sapiens	ZYG homologue	3966	99
1589	AF169803	Homo sapiens	flavohemoprotein b5+b5R	2563	100
1590	Y29861	Homo sapiens	Human secreted protein clone cb98_4.	181	47
1591	225535	Homo sapiens	nuclear pore complex protein	7567	99
1592	X13293	Homo sapiens	B-myb protein (AA 1-700)	3678	99
1593	M74027	Homo sapiens	mucin	242	27
1594	AL139314	Schizosaccha	hypothetical protein	235	54
	1	romyces		1	1

TABLE 2

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:		pombe			
<u> </u>	W78324	Homo sapiens	Fragment of human secreted	1318	98
.595		-	protein encoded by gene 81.	2236	98
.596	Y94906	Homo sapiens	Human secreted protein clone rb649_3 protein sequence SEQ ID NO:18.	2236	30
.597	AF174605	Homo sapiens	F-box protein Fbx25	1408	99
598	AB032254	Homo	bromodomain adjacent to zinc	9676	98
598	AB032234	sapiens	finger domain 2A		
599	X73114	Homo sapiens	slow MyBP-C	5568	95
600	X82200	Homo sapiens	qpStaf50	2305	100
601	Y00876	Homo	Human LAPH-1 protein	1149	98
. POT	100876	sapiens	sequence.		
1602	AJ223351	Homo sapiens	HIRA-interacting protein 3	2821	99
602	AJ222801	Homo sapiens	neutral sphingomyelinase	2268	99
604	AJ222801	Homo sapiens	neutral sphingomyelinase	1601	99
605	AF185576	Mus musculus	POZ/zinc finger transcription	3435	97
1605	AF 1055/6	Mus musculus	factor ODA-8		
	AF093744	Homo sapiens	unknown	131	100
606	A12142	synthetic	IFN-pseudo-omega 2	800	98
1607	A12142	construct	The product of the second		
L60B	Y57949	Homo sapiens	Human transmembrane protein	1868	100
			HTMPN-73.	681	97
1609	AF151044	Homo sapiens	HSPC210		100
1610	X15218	Homo sapiens	ski protein (AA 1 - 728)	3765	
1611	Y08200	Homo sapiens	rab geranylgeranyl transferase	2976	100
1612	AF220560	Homo sapiens	B/K protein	2486	99
1613	AC004481	Arabidopsis	nodulin-like protein	371	26
		thaliana	NADH-cytochrome-b5 reductase	1607	100
1614	Y09501	Homo sapiens	start position 1	3150	97
1615	Y15521	Homo sapiens		890	62
1616	AJ010750	Rattus norvegicus	Castration induced prostatic apoptosis related protein-1, (CIPAR-1)	850	02
1617	X58079	Homo sapiens	S100 alpha protein	481	100
1618	Y66678	Ното	Membrane-bound protein	967	100
1010	1000	sapiens	PRO1009.		ļ
1619	AJ242973	Homo sapiens	peptide methionine sulfoxide reductase	929	100
		Wasa sanians	AD-014 protein	288	100
1620	AF150733	Homo sapiens	E1B-55kDa-associated protein	4646	98
1621	AJ007509		metallothionein	380	100
1622	X64177	Homo sapiens	A. fulgidus predicted coding	240	36
1623	AE001045	Archaeoglobu s fulgidus	region AF0859		
1624	AL355013	Schizosaccha romyces pombe	mitochondrial carrier protein	403	34
1625	Y66746	Homo	Membrane-bound protein PRO1198.	1184	100
1606	700053	sapiens Sus scrofa	destrin	863	100
1626	D90053	Homo sapiens	Extended human secreted	756	100
1627	¥35954	Homo sapiens	protein sequence, SEQ ID NO. 203.		
1628	AL031775	Homo sapiens		470	100
1629	AF132484	Mus musculus		286	68
1630	AF017096	Drosophila melanogaster	similar to C. elegans R10H10.6 and S. cerevisiae YD8419.03c	493	61
	V00000	Vomo contant		1704	100
1631	X03077	Homo sapiens		763	100
1632	AF151084	Homo sapiens		255	97
1633 1634	AJ001874 AC012187	Homo sapiens Arabidopsis thaliana	Contains weak similarity to GATA-6 DNA-binding protein gb H36135, gb Z26200 come	143	38

TABLE 2

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:			tionic Production	411	90
1635	AF026246	Homo sapiens	HERV-E integrase	1	95
1636	Y50943	Homo sapiens	Human adult brain cDNA clone ve8_1 derived protein.	1126	
1637	AF134593	Homo sapiens	L-pipecolic acid oxidase	2068	99
1638	AJ238247	Mus musculus	putative phosphatase subunit	1948	96
1639	Y94942	Homo sapiens	Human secreted protein clone yk251_1 protein sequence SEQ ID NO:90.	1320	100
1640	AF235030	Homo sapiens	BM88 antigen	766	99
1641	AF233288	Drosophila melanogaster	WDS	358	26
1642	M19351	Mus musculus	immunoglobulin heavy chain binding protein	145	34
1643	Y70452	Homo sapiens	Human membrane channel protein-2 (MECHP-2).	1352	100
1644	AF176520	Mus musculus	WD repeat-containing F-box protein FBW5	2676	88
1645	W67816	Homo sapiens	Human secreted protein encoded by gene 10 clone HCEMU42.	1156	100
1646	X67155	Homo sapiens	mitotic kinase-like protein-1	4456	99
1647	M63180	Homo sapiens	threonyl-tRNA synthetase	1040	61
1648	Y87342	Homo sapiens	Human signal peptide containing protein HSPP-119 SEQ ID NO:119.	1566	93
1649	R95332	Homo sapiens	Tumor necrosis factor receptor 1 death domain ligand (clone 3TW).	4137	100
1650	AC007136	Homo sapiens	Putative map kinase interacting kinase	856	99
1651	AB015346	Homo sapiens	Eps15R	4464	99
1652	AL161576	Arabidopsis thaliana	putative protein	1341	48
1653	AC005313	Arabidopsis thaliana	putative calmodulin	288	28
1654	AL031428	Homo sapiens	dJ184J9.1 (KIAA0601 protein)	3526	100
1655	AL031428	Homo sapiens	dJ184J9.1 (KIAA0601 protein)	3526	100
1656	AB017910	Dictyosteliu m discoideum	туом	297	32
1657	Y28919	Homo sapiens	Human regulatory protein HRGP-5.	2251	99
1658	AF056191	Homo sapiens	TPA inducible protein	2744	98
1659	U76846	Arabidopsis thaliana	ubiquitin-specific protease	137	35
1660	AL078627	Schizosaccha romyces pombe	actin-like protein; (2 actin domains)	320	34
1662	X52022	Homo sapiens	collagen type VI, alpha 3 chain	16274	99
1663	AF300648	Homo sapiens	guanine nucleotide binding protein beta subunit 4	1811	100
1664	AF214736	Homo sapiens	EH domain containing protein 2	2774	100
1665	248613	Saccharomyce s cerevisiae	unknown	138	26
1666	AF177385	Homo sapiens	cytochrome c oxidase assembly protein isoform 2	1395	99
1667	AC007842	Homo sapiens	BC331191 1	1581	47
1668	S67513	Borna disease virus BDV, WT-1, Halle Bl/91, horse brain, field	p40	397	43
		isolate, Peptide, 370			

TABLE 2

ID NO:	ACCESSION	SPECIES	DESCRIPTION	SMITH-	1
	NUMBER	5120120		WATERMAN	IDENTITY
1669				SCORE	
1669	700F3	aa	putative NOL1-NOP2-sun family	569	47
ı	299753	Schizosaccha romyces	nucleolar protein	303	1,
		pombe	Paragram Paragram		
1670	G03130	Homo sapiens	Human secreted protein, SEQ	427	97
			ID NO: 7211.		
1671	M96625	Gallus	cardiac muscle tensin	1185	54
	X 214400	gallus	polycomb 3	2005	99
	AF174482 Y51846	Homo sapiens	Human 18.1 homolog protein	233	29
16/3	131040 .	nono sapiens	fragment.		
1674	AF255334	Homo sapiens	EXP35	152	29
1675	Y94867	Homo	Human protein clone HP10563.	109	30
		sapiens			
1676	Y25712	Homo sapiens	Human secreted protein	3043	99
1.555	V05710	Homo sapiens	encoded from gene 2. Human secreted protein	1580	91
1677	Y25712	HOMO Sapiens	encoded from gene 2.	1	1
1678	AF163151	Homo sapiens	dentin sialophosphoprotein	170	17
			precursor		
1679	AF163151	Homo sapiens	dentin sialophosphoprotein	170	17
			precursor	1349	100
- 1	AK024453 AF019236	Homo sapiens	FLJ00045 protein TipD	613	34
1681	AF019236	Dictyosteliu m discoideum	Tipo	013	1 3 2
1682	AJ243459	Leishmania	proteophosphoglycan	153	26
1002	710243433	major			
1683	Z69369	Schizosaccha	putative GTP-binding protein	560	46
		romyces			
		pombe		1334	100
1684	X94910	Homo sapiens Takifugu	ERp28 retinitis pigmentosa GTPase	196	19
1685	AF286475	rubripes	regulator-like protein	130	1
1686	AF191298	Homo sapiens	vacuolar sorting protein 35	4087	100
1687	AJ275986	Homo sapiens	transcription factor	2958	100
1688	AJ275986	Homo sapiens	transcription factor	1886	88
1689	X07311	Drosophila	heat shock protein	138	43
		melanogaster	TTG: /sking protoin	1383	83
1690	AF240463	Rattus norvegicus	LIS1-interacting protein	1303	63
1691	AJ272078	Homo sapiens	APOBEC-1 stimulating protein	1256	68
1692	AJ272079	Homo sapiens	APOBEC-1 stimulating protein	1336	60
1693	AF177942	Xenopus	katanin p60	1664	66
		laevis			
1694 •	AF263539	Homo sapiens	arginine N-methyltransferase	1774	81
1695	AF222689	Homo	protein arginine N- methyltransferase 1-variant 2	1182	**
1696	AK000193	sapiens Homo sapiens	unnamed protein product	1060	100
1696	AB041035	Homo sapiens	kidney superoxide-producing	3122	100
1001		Suprem	NADPH oxidase		
1698	AB041035	Homo sapiens	kidney superoxide-producing	2181	100
Ll			NADPH oxidase	1.00	1
1.600	AF025772	Homo sapiens	C2H2 zinc finger protein	488	97
1699	Y44676	Homo sapiens	Human ARF-Related Protein-1 (HARP-1).	938	"
1700	AKC22407	Homo sapiens	unnamed protein product	315	98
1700	AB024574	Homo sapiens	GTP-binding like protein 2	1172	100
1700		Homo sapiens	zinc finger protein 42	421	52
1700 1701 1702	AF055078) HOMO Sabiens	·		77
1700 1701 1702 1703		Mus musculus	RP42	1057	1
1700 1701 1702	AF055078	· -	RP42 CG12474 gene product	1057	33
1700 1701 1702 1703 1704 1705	AF055078 AF198092 AE003573	Mus musculus Drosophila melanogaster	CG12474 gene product	161	33
1700 1701 1702 1703 1704	AF055078 AF198092	Mus musculus Drosophila melanogaster Drosophila			1
1700 1701 1702 1703 1704 1705	AF055078 AF198092 AE003573 AB036345	Mus musculus Drosophila melanogaster Drosophila melanogaster	CG12474 gene product aquaporin	161	33
1700 1701 1702 1703 1704 1705	AF055078 AF198092 AE003573	Mus musculus Drosophila melanogaster Drosophila	CG12474 gene product	161	33

TABLE 2

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION .	SMITH- WATERMAN	IDENTITY
NO:	NONBER	1		SCORE	ļ
NO:		thaliana			
210	B01311	Homo sapiens	Human PRO241 polypeptide.	1649	97
710	U40750	Mus musculus	formin binding protein 30	4561	85
711		Mus musculus	skeletal muscle and cardiac	1490	89
712	AJ011118		protein	4416	99
713	AF255303	Homo sapiens	membrane-associated nucleic acid binding protein		_
1714	AF255303	Homo sapiens	membrane-associated nucleic acid binding protein	2960	100
1715	U08227	Rattus norvegicus	Ras-related protein	511	51
1716	AF168795	Rattus	schlafen-4	1129	44
	AF196304	Homo sapiens	SUMO-1-specific protease	5804	99
1717		Homo sapiens	HMG20A	1782	100
1718	AL355737		HrPET-1	1069	46
1719	AB029333	Halocynthia roretzi			
1720	AF071317	Mus musculus	COP9 complex subunit 7b	1297	97
1721	AJ272215	Homo sapiens	HEYL protein	1681	99
1722	G01982	Homo sapiens	Human secreted protein, SEQ ID NO: 6063.	718	100
1723	AL032643	Caenorhabdit is elegans	similar to Uncharacterized protein family UPF0034,	825	41
1724	G01972	Homo sapiens	Human secreted protein, SEQ ID NO: 6053.	586	92
1725	Y94441	Homo sapiens	Human Adipose Specific Protein 1.	1231	100
1726	AF255443	Homo sapiens	CGI-201 protein	4397	99
1727	AF183426	Homo sapiens	HT004 protein	1810	99
1728	D10884	Bos taurus	neurocalcin	1002	99
1729	Z18529	Gallus	tensin	1411	84
		gallus		233	41
1730	273423	Caenorhabdit is elegans	cDNA EST EMBL: Z14908 comes from this gene-cDNA EST this gene	233	1
	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	Homo sapiens	PR00105	470	30
1732	AF090891	Homo sapiens		2015	100
1733	AJ277724		Human secreted protein, SEQ	503	95
1734	G04050	Homo sapiens	TD NO: 8131.		
1735	D45913	Mus musculus	leucine-rich-repeat protein	3531	94
1736	AF096709	Drosophila virilis	failed axon connections protein	276	32
1737	AF195120	Homo sapiens	dynactin p62 subunit	2417	99
1738	L15314	Caenorhabdit is elegans	contains similarity to Pfam family PF01772 N=1	206	37
1739	X54618	Listeria monocytogene	phosphadidylinositol specific phospholipase C	134	27
1740	AL031658	Homo sapiens	dJ310013.4 (novel protein similar to predicted C. elegans an C. intestinalis proteins)	123	31
1741	Y35924	Homo sapiens		1013	99
1742	AC013354	Arabidopsis thaliana	F15H18.15	202	32
1743	W75771	Homo sapiens	Human GTP binding protein APD08.	1932	59
1744	W75771	Homo sapiens	Human GTP binding protein APD08.	1854	61
1745	AF221098	Homo sapiens	Ral guanine nucleotide exchange factor RalGPS1A	1224	70
1746	Y99372	Homo sapiens	Human PRO1430 (UNQ736) amino acid sequence SEQ ID NO:116.	1332	99
	1	Homo sapiens		842	100

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	*
ID	NUMBER	5120120	220 01121 22 011	WATERMAN	IDENTITY
NO:	Norman		•	SCORE	
			enzyme CoAEN-2.	 	
1748	AK024436	Homo sapiens	FLJ00026 protein	1619	100
1749	AE000877	Methanobacte	conserved protein	231	36
-, -,		rium	• • • • • • • • • • • • • • • • • • •		
		thermoautotr			1
		ophicum			l .
1750	AF101361	Drosophila	Abnormal X segregation	193	33
		melanogaster			
1751	Y15067	Homo sapiens	ZNF232	889	100
1752	AF251038	Homo sapiens	GAP-like protein	822	100
1753	AC003093	Homo sapiens	OXYSTEROL-BINDING PROTEIN;	352	57
1.55	1		45% similarity to P22059		}
	ļ		(PID:q129308)	ł	
1754	X69089	Homo sapiens	165kD protein	5703	99
1755	AL049795	Homo sapiens	dJ622L5.3 (novel protein)	1039	100
1756	AL031393	Homo sapiens	dJ733D15.1 (Zinc-finger	2765	100
1/26	ALUSIS 93	Nomo sapiens	protein)	2,03	100
1757	AB040672	Homo sapiens	UDP-GalNAc: polypeptide N-	2020	99
1/5/	AB040672	Nome Bapiens	acetylgalactosaminyltransfera	2020	"
			se		
1758	AL022238	Homo sapiens	dJ1042Kl0.4 (novel protein)	776	43
1759	AF117653	Homo sapiens	double homeobox protein	375	54
1760	Y12065	Homo sapiens	hNop56	2959	99
1761	AL049712	Homo sapiens	dJ686C3.2 (nucleolar protein	2595	99
1/61	AL049/12	nomo sapiens	hNop56)	2333	33
1762	AC002394	Homo	Gene product with similarity	1542	51
1/62	AC002394	sapiens	to dynein beta subunit	1542	1 32
1763	AF169017	Homo sapiens	formiminotransferase	877	100
1/63	AF16901/	NOMO Saprems	cyclodeaminase	""	100
1764	U91541	Homo sapiens	human formiminotransferase	596	100
1/64	091241	Homo Bapiens	cyclodeaminase (ftcd)protein,	330	100
			carboxy-terminal end	•	i
1765	AB013365	Bacillus	'YlqF	350	34
1/65	AB013365	halodurans	11qr	330	34
1766	Y38421	Homo sapiens	Human secreted protein	145	71
1/66	130421	HOMO Baptens	encoded by gene No. 36.		1.
1767	AC009176	Arabidopsis	putative ribulose-1,5-	216	27
1/6/	AC009176	thaliana	bisphosphate	1	-
		Charlana	carboxylase/oxygenase small		
			subunit N-methyltransferase I		1
1768	AK000647	Homo sapiens	unnamed protein product	737	99
1769	AJ238982	Homo sapiens	VNN3 protein	2665	99
		Homo sapiens	AMSH	1214	56
1770	U73522		unknown	829	86
1771	U89435	Mus musculus			95
1772	S70011	Rattus sp.	tricarboxylate carrier	1604	1
1773	AL035086	Homo sapiens	dJ44A20.2 (novel protein)	2036	100
1774	Y99426	Homo sapiens	Human PRO1604 (UNQ785) amino	1057 .	99
	1.5	I	acid sequence SEQ ID NO:308.	3116	100
1775	AF110330	Homo sapiens	glutaminase	3146	100
1776	AJ269529	Homo sapiens	glycercl 3-phosphate permease	2787	100
1777	Z81579	Caenorhabdit	cDNA EST yk76f1.5 comes from	232	31
	J	is elegans	this gene	1.055	
1778	AY007239	Homo sapiens	monooxygenase X	1875	99
1779	AL109608	Schizosaccha	oxysterol-binding protein	644	38
		romyces	family	1	
		pombe			
1780	AF254260	Homo sapiens	tuftelin 1	1729	100
1781	L07924	Mus musculus	guanine nucleotide	247	50
		/Aga	dissociation stimulator		<u> </u>
1782	AF295773	Homo	ral guanine nucleotide	142	49.
		sapiens	dissociation stimulator		<u> </u>
1783	AK024475	Homo sapiens	FLJ00068 protein	4333	100
1784	AK024475	Homo sapiens	FLJ00068 protein	3996	93
1785	G03933	Homo sapiens	Human secreted protein, SEQ	570	100
			ID NO: 8014.		
		Homo sapiens	Ig lambda-like gene/beta-	247	100

TABLE 2

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:			glucuronidase exon 11 homolog		

TRADOCS:1416280.1(%CT401!.DOC)

TABLE 3

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
2	BL00240	Receptor tyrosine kinase	BL00240B 24.70 8.250e-
2	BL00240	class III proteins.	12 157-181
3	PR00109	TYROSINE KINASE	PR00109D 17.04 B.085e-
		CATALYTIC DOMAIN SIGNATURE	13 358-381
4	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 9.400e-
•	2200020	domain proteins.	10 1129-1146 BL00028
			16.07 1.257e-09 820-
5	BL00023	Type II fibronectin	BL00023 24.31 8,920e-
3	BECCCES	collagen-binding domain	33 413-450 BL00023
	1	proteins.	24.31 4.545e-27 353-
			390
6	BL00023	Type II fibronectin	BL00023 24.31 8.920e-
		collagen-binding domain	33 413-450 BL00023
		proteins.	24.31 4.545e-27 353-
			390
7	BL00023	Type II fibronectin	BL00023 24.31 B.920e-
		collagen-binding domain	33 413-450 BL00023
	}	proteins.	24.31 4.545e-27 353-
8	DI COCCO	Type II fibronectin	390 BL00023 24.31 8.920e-
0	BL00023	collagen-binding domain	33 413-450 BL00023
		proteins.	24.31 4.545e-27 353-
		Process.	390
9	BL01160	Kinesin light chain	BL01160B 19.54 5.119e-
		repeat proteins.	09 863-917
10	PR00464	E-CLASS P450 GROUP II	PR00464D 17.40 6.182e-
		SIGNATURE	12 294-312 PR00464G
		ì	12.41 4.231e-11 377-
			393
11	PR00734	GLYCOSYL HYDROLASE FAMILY 7 SIGNATURE	PR00734I 11.46 4.296e- 09 502-520
12	PF00023	Ank repeat proteins.	PF00023B 14.20 6.500e-
	1100023	Tapear processo.	10 89-99 PF00023B
			14.20 2.636e-09 56-66
14	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 3.848e-
			09 79-113
15	PR00208	GLIADIN AND LMW GLUTENIN	PR00208A 12.59 9.868e-
		SUPERFAMILY SIGNATURE	10 517-535 PR00208A
	1		12.59 2.233e-09 520-
	77700065	DROWNIN GING BINGER	538
17	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e- 14 282-295 PD00066
		PISTAU-BINDI.	13.92 9.400e-14 477-
			490 PD00066 13.92
			6.500e-13 505-518
			PD00066 13.92 9.500e-
			13 254-267 PD00066
			13.92 1.429e-12 393-
		1	406 PD00066 13.92
			6.571e-12 421-434
18	BL00845	CAP-Gly domain proteins.	BL00845 16.43 2.200e- 25 55-80
20	BL00487	IMP dehydrogenase / GMP	BL00487E 16.12 5.737e-
		reductase proteins.	26 154-199 BL00487F
		P - 1 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2	18.79 8.984e-22 235-
			276 BL00487G 26.82
			4.082e-12 287-329
21	BL00487	IMP dehydrogenase / GMP	BL00487E 16.12 5.737e-
		reductase proteins.	26 154-199 BL00487F
			18.79 8.984e-22 235-
			276 BL00487G 26.82
22	B1 001 02	Durchain lains 2000	4.082e-12 348-390 BL00107A 18.39 3.250e-
22	BL00107	Protein kinases ATP-	26 302-333
	5	binding region proteins.	40 204-333

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
23	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 3.250e- 26 302-333
25	DI 00115	Eukaryotic RNA	BL00115T 8.45 7.273e-
25	BL00115	, polymerase II	29 1208-1242 BL00115Q
		, ~ -	
	į ·	heptapeptide repeat	18.08 2.776e-21 953-
		proteins.	983 BL00115Y 11.86
	ŀ		8.000e-17 1604-1650
			BL00115M 19.19 8.130e-
			16 731-774 BL00115H
			14.34 9.392e-16 463-
		1	496 BL00115A 15.44
	Ì		7.414e-15 43-82
			BL00115R 6.50 6.128e-
	<u> </u>	40.	14 983-1010 BL00115J
	•	4	16.71 9.289e-14 591-
			617 BL00115I 8.33
		}	4.336e-13 535-590
			BL00115L 12.25 5.939e-
	1		13 662-694 BL00115G
			11.65 6.011e-13 435-
			463 BL00115K 15.03
			3.417e-10 617-659
			BL001150 16.76 5.805e-
1			10 863-913 BL00115P
	1		11.54 7.538e-10 913-
			953 BL00115S 18.24
	1		7.968e-10 1010-1052
0		i	BL00115U 10.34 4.475e-
			09 1242-1265
26	BL00420	Speract receptor repeat	BL00420A 20.42 4.109e-
		proteins domain	11 81-110 BL00420A
	<u></u>	proteins.	20.42 8.820e-10 84-113
27	BL00050	Ribosomal protein L23	BL00050A 23.71 9.250e-
		proteins.	27 94-127 BL00050B
		\	14.81 8.125e-12 133-
			147
28	PR00925	NONHISTONE CHROMOSOMAL	PR00925B 3.73 3.089e-
	1	PROTEIN HMG17 FAMILY	10 41-54
		SIGNATURE	***************************************
29	PF00756	Putative esterase.	PF00756C 14.12 1.108e-
			09 486-516
32	BL00557	FMN-dependent alpha-	BL00557D 17.76 5.065e-
		hydroxy acid	37 274-316 BL00557A
[dehydrogenases proteins.	35.08 8.909e-29 24-73
			BL00557C 15.59 1.000e-
		1	28 227-257 BL00557B
!		}	21.27 8.898e-22 130-
<u> </u>	DD00505	LOVE PROGRAMOWYPOCETY	169 PR00629E 9.90 5.886e-
34	PR00629	SHC PHOSPHOTYROSINE	
	1	INTERACTION DOMAIN	35 299-328 PR00629F 10.95 8.364e-32 334-
1		SIGNATURE	361 PR00629B 13.66
1		1	3.786e-27 224-247
I			PR00629A 13.45 8.364e-
1			21 206-222 PR00629C
			3.80 4.000e-12 249-261
1			PR00629D 12.45 3.739e-
1			11 276-286
35	PD01270	RECEPTOR FC	PD01270A 17.22 1.000e-
1	12012.0	IMMUNOGLOBULIN AFFIN.	40 39-79 PD01270B
1		2	22.18 2.875e-38 94-131
			PD01270D 24.66 3.700e-
	}	1	34 171-207 PD01270C
1			19.54 3.455e-30 137-
1			166
36	PD01270	RECEPTOR FC	PD01270A 17.22 1.000e-
1		IMMUNOGLOBULIN AFFIN.	40 39-79 PD01270B
			22.18 2.875e-38 94-131
L		<u> </u>	1

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		PD01270D 24.66 3.700e-
	İ		34 171-207 PD01270C
			19.54 3.455e-30 137-
			166
7.0	BL00412	Neuromodulin (GAP-43)	BL00412C 10.28 9.241e-
37	BD00412	proteins.	10 264-298
38	BL00412	Neuromodulin (GAP-43)	BL00412C 10.28 9.241e-
36	2200122	proteins.	10 264-298
39	BL00412	Neuromodulin (GAP-43)	BL00412C 10.28 9.241e-
33	1	proteins.	10 264-298
40	PR00380	KINESIN HEAVY CHAIN	PR00380B 12.64 7.366e-
		SIGNATURE	14 342-360 PR00380C 13.18 6.927e-13 375-
			394 PR003B0D 9.93
		i e	2.180e-12 429-451
	İ		PR00380A 14.18 5.154e-
			12 143-165
	71.003.45	Ets-domain proteins.	BL00345B 21.28 1.000e-
44	BL00345	BCB-domain production	40 239-290 BL00345A
		1	13.96 2.452e-14 204-
			223
45	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e-
3.5		_	40 215-266 BL00345A
			13.96 2.452e-14 180-
			199
46	DM01551	kw OSTEOINDUCTIVE YOPM	DM01551A 15.63 3.538e-
		MEMBRANE OUTER.	26 172-202 DM01551C
			14.62 3.571e-17 232- 252 DM01551B 8.84
			4.750e-11 214-226
		NEMATODE METALLOTHIONEIN	PRO0876B 7.66 9.328e-
47	PR00876		11 246-260
	5007.000	SIGNATURE PROTEIN ZINC FINGER	PD01066 19.43 4.231e-
48	5D01066	ZINC-FINGER METAL-	33 6-45
	ļ.	BINDING NU.	
50	BL00972	Ubiquitin carboxyl-	BL00972D 22.55 7.750e-
1 30	BESSIE	terminal hydrolases	19 994-1019 BL00972A
		family 2 proteins.	11.93 7.120e-18 216-
]			234 BL00972E 20.72
			9.471e-14 1020-1042 BL00972C 16.48 7.000e-
1			13 360-375 BL00972B
	1	•	9.45 8.269e-10 302-312
		Ubiquitin carboxyl-	BL00972D 22.55 7.750e-
51	BL00972	terminal hydrolases	19 990-1015 BL00972A
1		family 2 proteins.	11.93 7.120e-18 216-
		Lamily 2 processar.	234 BL00972E 20.72
	1		9.471e-14 1016-1038
			BL00972C 16.48 7.000e-
1	1	•	13 360-375 BL00972B
			9.45 8.269e-10 302-312
52	BL01115	GTP-binding nuclear	BL01115A 10.22 3.063e-
	1	protein ran proteins.	14 10-54
53	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 8.500e-
1			17 20-38 PR00988F 12.23 7.828e-15 196-
		i	210 PR00988C 13.64
	•		6.108e-14 104-120
			PR00988E 8.27 3.872e-
1			11 174-186 PR00988D
1			5.95 6.878e-10 160-171
			PR00988B 11.60 2.915e-
1	1	\	09 57-69
	PR00762	CHLORIDE CHANNEL	PR00762C 9.29 4.682e-
55	FROUTEZ	SIGNATURE	21 294-314 PR00762D
1			11.29 4.103e-19 509-
1		1	530 PR00762A 14.22
			9.333e-18 199-217

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
-	NO.		
			PR00762F 15.12 3.100e-
			16 563-583 PR00762B
			12.12 6.063e-16 230-
			250 PR00762E 12.07 2.286e-15 545-562
	ľ		PR00762G 14.13 6.276e-
			13 601-616
56	BL00216	Sugar transport	BL00216B 27.64 8.800e-
20	2200220	proteins.	10 153-203
58	PF00791	Domain present in ZO-1	PF00791B 28.49 2.049e-
	1	and Unc5-like netrin	10 1080-1135
		receptors.	
59	PF00791	Domain present in ZO-1	PF00791B 28.49 2.049e-
		and Unc5-like netrin	10 1062-1117
		receptors.	
61	PD01929	KINASE TYPE RESISTANCE	PD01929E 10.76 9.018e-
		ANTIBIOTIC TRANSFERASE	09 206-221
		AM.	
68	PR00360	C2 DOMAIN SIGNATURE	PR00360A 14.59 7.395e-
·			09 680-693
69	PR00360	C2 DOMAIN SIGNATURE	PR00360A 14.59 7.395e-
	1		09 670-683
70	PF00651	BTB (also known as BR-	PF00651 15.00 8.714e-
	- Buggara	C/Ttk) domain proteins. w KINASE ALPHA ADHESION	10 51-64
72	DM00179	T-CELL.	DM00179 13.97 5.304e-
73	BL00239	Receptor tyrosine kinase	09 108-118 BL00239B 25.15 7.075e-
/3	8100239	class II proteins.	12 118-166
74	BL00790	Receptor tyrosine kinase	BL00790N 13.25 6.116e-
/ 1	BD00730	class V proteins.	10 93-120
76	DM00471	0 PROKARYOTIC DNA	DM00471A 11.73 9.357e-
70	D1400471	TOPOISOMERASE I.	13 53-66 DM00471B
		101010011111111111111111111111111111111	8.45 4.857e-12 70-81
80	PD02876	DECARBOXYLASE	PD02876C 8.80 2.723e-
		PHOSPHATIDYLSERINE.	13 223-236 PD02876D
			12.13 2.588e-12 334-
			351
81	PD02876	DECARBOXYLASE	PD02876C 8.80 2.723e-
		PHOSPHATIDYLSERINE.	13 282-295 PD02876D
			12.13 2.588e-12 393-
			410
83	BL00708	Prolyl endopeptidase	BL00708B 24.91 7.197e-
		family serine proteins. FIBRONECTIN TYPE III	12 570-601
84	PR00014		PR00014C 15.44 8.043e-
86	PR00678	REPEAT SIGNATURE PI3 KINASE P85	09 985-1004 PR00678H 9.13 1.379e-
00	PROUGTS	REGULATORY SUBUNIT	09 246-269
		SIGNATURE	UJ 240-203
89	PR00320	G-PROTEIN BETA WD-40	PR00320C 13.01 8.200e-
	1	REPEAT SIGNATURE	09 264-279 PR00320B
			12.19 8.650e-09 264-
			279
93	BL00455	Putative AMP-binding	BL00455 13.31 2.588e-
		domain proteins.	14 316-332
95	BL00107	Protein kinases ATP-	BL00107A 18.39 4.000e-
		binding region proteins.	10 123-154
96	BL00107	Protein kinases ATP-	BL00107A 18.39 4.000e-
	<u></u>	binding region proteins.	10 212-243
97	PR00081	GLUCOSE/RIBITOL	PR00081B 10.38 6.318e-
		DEHYDROGENASE FAMILY	13 134-146 PR00081A
		SIGNATURE	10.53 2.500e-12 54-72
98	PR00380	KINESIN HEAVY CHAIN	PR00380A 14.18 5.500e-
		SIGNATURE	24 401-423 PR00380D
			9.93 7.188e-20 613-635
			PR00380B 12.64 7.517e-
		·	16 529-547 PR00380C
		·	13.18 2.756e-13 560- 579
	1		1 212

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SEQ ID NO	NO.	DESCRIPTION	RESULTS*
102	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-BINDING	PR00300A 9.56 7.545e- 14 289-308
104	BL00479	SUBUNIT SIGNATURE Phorbol esters /	BL00479B 12.57 6.786e-
		diacylglycerol binding domain proteins.	18 298-314 BL00479A 19.86 4.913e-16 155-
		•	178 BL00479A 19.86 4.300e-13 272-295
			BL00479B 12.57 6.294e-
106	BL01019	ADP-ribosylation factors	BL01019A 13.20 8.013e-
107	DM01970	family proteins. 0 kw 2K632.12 YDR313C	DM01970B 8.60 5.000e-
108	BL00191	ENDOSOMAL III. Cytochrome b5 family,	16 403-416 BL00191K 17.38 4.951e-
		heme-binding domain proteins.	27 238-282 BL00191J 11.37 6.447e-17 182- 204
109	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 4.938e-
		ZINC-FINGER METAL- BINDING NU.	37 8-47
110	BL01138	Scorpion short toxins proteins.	BL01138A 10.96 B.297e- 10 38-50
113	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 5.800e- 23 156-187 BL00107B
			13.31 9.100e-14 225- 241
117	BL00214	Cytosolic fatty-acid binding proteins.	BL00214B 26.51 1.000e- 17 46-91 BL00214A 21.17 7.052e-11 5-31
118	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 8.560e-
119	PR00529	GONADOTROPHIN RELEASING HORMONE RECEPTOR SIGNATURE	PR00529C 11.03 7.506e- 10 158-177
120	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 9.400e-
121	PR00320	G-PROTEIN BETA WD-40	PR00320C 13.01 9.400e-
127	BL00215	REPEAT SIGNATURE Mitochondrial energy	09 80-95 BL00215A 15.82 7.158e-
128	BL01032	transfer proteins. Protein phosphatase 2C	13 216-241 BL01032C 6.14 3.195e-
120	2202032	proteins.	12 147-157 BL01032H 11.25 5.680e-11 318-
			331 BL01032G 8.33
			8.932e-11 282-296 BL01032I 10.42 8.902e-
129	BL01310	ATP1G1 / PLM / MAT8	09 379-389 BL01310 14.74 6.694e-
		family proteins.	26 28-64
130	PR00990	RIBOKINASE SIGNATURE	PR00990B 12.32 9.534e- 15 47-67 PR00990A
			16.23 5.500e-14 20-42 PR00990C 12.62 2.412e-
122	DY 00000	Doub Cop biledia	09 119-133
133	BL00880	Acyl-CoA-binding protein.	BL00880 17.52 5.576e- 26 72-122
134	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 9.308e- 14 18-37
135	PR00215	NEUROMODULIN SIGNATURE	PR00215C 13.98 6.779e- 10 475-496
136	BL01310	ATPIG1 / PLM / MAT8 family proteins.	BL01310 14.74 2.432e- 29 71-107
140	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 7.882e-
		domain proteins.	14 214-231 BL00028 16.07 9.471e-14 102-
			119 BL00028 16.07 2.800e-13 18-35
·			

EQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		BL00028 16.07 5.500e-
		i	13 74-91 BL00028
			16.07 9.100e-13 186-
		}	203 BL00028 16.07
		l l	8.043e-12 46-63
			Вьооо28 16.07 8.435е-
			12 130-147 BL00028
			16.07 9.217e-12 270-
		l i	287 BL00028 16.07
	1		6.192e-11 242-259
	1	İ	BL00028 16.07 4.000e-
			10 158-175
		Signal peptidases I	BL00501D 16.69 9.538e-
141	BL00501		14 113-133 BL00501C
	\	serine proteins.	9.61 8.688e-10 89-101
143	BL01020	SAR1 family proteins.	BL01020C 15.35 7.722e-
			20 79-130
146	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 6.400e-
140	150100	ZINC-FINGER METAL-	25 335-374
	{	BINDING NU.	
	Dr. 003 36	3'5'-cyclic nucleotide	BL00126C 22.07 1.450e-
149	BL00126	phosphodiesterases	25 509-550 BL00126E
	1		35.22 3.951e-16 654-
	1	proteins.	709 BL00126D 25.50
	1		1.360e-15 565-604
			BL00126B 15.20 8.200e-
	ŀ		11 483-495 BL00126A
			27.56 8.269e-11 442-
			479
	5-00-00	Ribosomal protein S4	BL00632 23.79 5.271e-
151	BL00632		20 106-149
		proteins.	BL00559I 13.63 5.304e-
154	BL00559	Eukaryotic molybdopterin	19 29-58 BL00559K
		oxidoreductases	
		proteins.	13.17 2.957e-18 172-
			199 BL00559J 19.63
			8.385e-13 99-151
			BL00559L 13.60 5.814e-
	1		12 241-259
155	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 1.692e-
155	FROUTES .	RAS SIGNATURE	13 13-35
	DY 00406	Actins proteins.	BL00406D 12.58 2.547e-
157	BL00406	Actins processes.	18 275-330 BL00406A
	})	9.95 5.776e-16 15-50
			BL00406B 5.47 7.429e-
			12 69-124 BL00406C
			6.75 9.682e-12 128-183
		Zinc carboxypeptidases,	BL00132A 26.07 7.000e-
160	BL00132		
160	BL00132	zinc-binding region 1	14 22-63 BL00132C
160	BL00132	zinc-binding region 1	
160	BL00132		14 22-63 BL00132C
		zinc-binding region 1 proteins.	14 22-63 BL00132C 21.35 3.466e-12 104- 145
160	BL00132	zinc-binding region 1 proteins. TYROSINE KINASE	14 22-63 BL00132C 21.35 3.466e-12 104- 145 PR00109B 12.27 9.043e-
		zinc-binding region 1 proteins. TYROSINE KINASE CATALYTIC DOMAIN	14 22-63 BL00132C 21.35 3.466e-12 104- 145
	PR00109	zinc-binding region 1 proteins. TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	14 22-63 BL00132C 21.35 3.466e-12 104- 145 PR00109B 12.27 9.043e- 13 139-158
		zinc-binding region 1 proteins. TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE Ribosomal protein S15	14 22-63 BL00132C 21.35 3.466e-12 104- 145 PR00109B 12.27 9.043e- 13 139-158 BL00362 24.67 9.700e-
165	PR00109	zinc-binding region 1 proteins. TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE Ribosomal protein S15 proteins.	14 22-63 BL00132C 21.35 3.466e-12 104- 145 PR00109B 12.27 9.043e- 13 139-158 BL00362 24.67 9.700e- 15 129-172
165	PR00109	zinc-binding region 1 proteins. TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE Ribosomal protein S15 proteins. DEAD-box subfamily ATP-	14 22-63 BL00132C 21.35 3.466e-12 104- 145 PR00109B 12.27 9.043e- 13 139-158 BL00362 24.67 9.700e- 15 129-172 BL00039D 21.67 1.000e-
165	PR00109	zinc-binding region 1 proteins. TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE Ribosomal protein S15 proteins. DEAD-box subfamily ATP-	14 22-63 BL00132C 21.35 3.466e-12 104- 145 PR00109B 12.27 9.043e- 13 139-158 BL00362 24.67 9.700e- 15 129-172 BL00039D 21.67 1.000e- 35 640-686 BL00039A
165	PR00109	zinc-binding region 1 proteins. TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE Ribosomal protein S15 proteins. DEAD-box subfamily ATP- dependent helicases	14 22-63 BL00132C 21.35 3.466e-12 104- 145 PR00109B 12.27 9.043e- 13 139-158 BL00362 24.67 9.700e- 15 129-172 BL00039D 21.67 1.000e- 35 640-686 BL00039A 18.44 1.964e-13 212-
165	PR00109	zinc-binding region 1 proteins. TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE Ribosomal protein S15 proteins. DEAD-box subfamily ATP-	14 22-63 BL00132C 21.35 3.466e-12 104- 145 PR00109B 12.27 9.043e- 13 139-158 BL00362 24.67 9.700e- 15 129-172 BL00039D 21.67 1.000e- 35 640-686 BL00039A 18.44 1.964e-13 212-
165	PR00109	zinc-binding region 1 proteins. TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE Ribosomal protein S15 proteins. DEAD-box subfamily ATP- dependent helicases	14 22-63 BL00132C 21.35 3.466e-12 104- 145 PR00109B 12.27 9.043e- 13 139-158 BL00362 24.67 9.700e- 15 129-172 BL00039D 21.67 1.000e- 35 640-686 BL00039A 18.44 1.964e-13 212- 251 BL00039B 19.19
165	PR00109	zinc-binding region 1 proteins. TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE Ribosomal protein S15 proteins. DEAD-box subfamily ATP- dependent helicases	14 22-63 BL00132C 21.35 3.466e-12 104- 145 PR00109B 12.27 9.043e- 13 139-158 BL00362 24.67 9.700e- 15 129-172 BL00039D 21.67 1.000e- 35 640-686 BL00039A 18.44 1.964e-13 212- 251 BL00039B 19.19 4.553e-13 378-404
165	PR00109	zinc-binding region 1 proteins. TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE Ribosomal protein S15 proteins. DEAD-box subfamily ATP- dependent helicases	14 22-63 BL00132C 21.35 3.466e-12 104- 145 PR00109B 12.27 9.043e- 13 139-158 BL00362 24.67 9.700e- 15 129-172 BL00039D 21.67 1.000e- 35 640-686 BL00039A 18.44 1.964e-13 212- 251 BL00039B 19.19 4.553e-13 378-404 BL00039C 15.63 8.773e-
165	PR00109	zinc-binding region 1 proteins. TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE Ribosomal protein S15 proteins. DEAD-box subfamily ATP- dependent helicases proteins.	14 22-63 BL00132C 21.35 3.466e-12 104- 145 PR00109B 12.27 9.043e- 13 139-158 BL00362 24.67 9.700e- 15 129-172 BL00039D 21.67 1.000e- 35 640-686 BL00039A 18.44 1.964e-13 212- 251 BL00039B 19.19 4.553e-13 378-404 BL00039C 15.63 8.773e- 12 465-489
165	PR00109	zinc-binding region 1 proteins. TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE Ribosomal protein S15 proteins. DEAD-box subfamily ATP- dependent helicases	14 22-63 BL00132C 21.35 3.466e-12 104- 145 PR00109B 12.27 9.043e- 13 139-158 BL00362 24.67 9.700e- 15 129-172 BL00039D 21.67 1.000e- 35 640-686 BL00039A 18.44 1.964e-13 212- 251 BL00039B 19.19 4.553e-13 378-404 BL00039C 15.63 8.773e- 12 465-489 PR00449A 13.20 3.721e-
168	PR00109 BL00362 BL00039	zinc-binding region 1 proteins. TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE Ribosomal protein S15 proteins. DEAD-box subfamily ATP- dependent helicases proteins. TRANSFORMING PROTEIN P21 RAS SIGNATURE	14 22-63 BL00132C 21.35 3.466e-12 104- 145 PR00109B 12.27 9.043e- 13 139-158 BL000362 24.67 9.700e- 15 129-172 BL00039D 21.67 1.000e- 35 640-686 BL00039A 18.44 1.964e-13 212- 251 BL00039B 19.19 4.553e-13 378-404 BL00039C 15.63 8.773e- 12 465-489 PR00449A 13.20 3.721e- 12 14-36
165 168 169	PR00109 BL00362 BL00039 PR00449	zinc-binding region 1 proteins. TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE Ribosomal protein S15 proteins. DEAD-box subfamily ATP- dependent helicases proteins. TRANSFORMING PROTEIN P21	14 22-63 BL00132C 21.35 3.466e-12 104- 145 PR00109B 12.27 9.043e- 13 139-158 BL00362 24.67 9.700e- 15 129-172 BL00039D 21.67 1.000e- 35 640-686 BL00039A 18.44 1.964e-13 212- 251 BL00039B 19.19 4.553e-13 378-404 BL00039C 15.63 8.773e- 12 465-489 PR00449A 13.20 3.721e- 12 14-36 BL001310 14.74 2.432e-
168	PR00109 BL00362 BL00039	zinc-binding region 1 proteins. TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE Ribosomal protein S15 proteins. DEAD-box subfamily ATP- dependent helicases proteins. TRANSFORMING PROTEIN P21 RAS SIGNATURE ATPIGI / PLM / MAT8	14 22-63 BL00132C 21.35 3.466e-12 104- 145 PR00109B 12.27 9.043e- 13 139-158 BL00362 24.67 9.700e- 15 129-172 BL00039D 21.67 1.000e- 35 640-686 BL00039A 18.44 1.964e-13 212- 251 BL00039B 19.19 4.553e-13 378-404 BL00039C 15.63 8.773e- 12 465-489 PR00449A 13.20 3.721e- 12 14-36 BL01310 14.74 2.432e- 29 133-169
165 168 169	PR00109 BL00362 BL00039 PR00449	zinc-binding region 1 proteins. TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE Ribosomal protein S15 proteins. DEAD-box subfamily ATP- dependent helicases proteins. TRANSFORMING PROTEIN P21 RAS SIGNATURE	14 22-63 BL00132C 21.35 3.466e-12 104- 145 PR00109B 12.27 9.043e- 13 139-158 BL00362 24.67 9.700e- 15 129-172 BL00039D 21.67 1.000e- 35 640-686 BL00039A 18.44 1.964e-13 212- 251 BL00039B 19.19 4.553e-13 378-404 BL00039C 15.63 8.773e- 12 465-489 PR00449A 13.20 3.721e- 12 14-36 BL001310 14.74 2.432e-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
		BINDING NU.	
180	PR00007	COMPLEMENT C1Q DOMAIN	PR00007B 14.16 7.429e-
		SIGNATURE	20 160-180 PR00007A
			19.33 4.938e-19 133-
			160 PR00007C 15.60
			1.225e-15 206-228
			PR00007D 9.64 6.885e-
			11 238-249
181	BL00027	'Homeobox' domain	BL00027 26.43 9.526e- 24 280-323
		proteins.	BL00027 26.43 9.526e-
182	BL00027	'Homeobox' domain	24 263-306
	-	proteins. 'Homeobox' domain	BL00027 26.43 9.526e-
183	BL00027	proteins.	24 280-323
104	DECOGG	'Homeobox' domain	BL00027 26.43 9.526e-
184	BL00027	proteins.	24 263-306
		AT-HOOK-LIKE DOMAIN	PR00929C 5.26 3.328e-
188	PR00929	SIGNATURE	09 460-471
		AT-HOOK-LIKE DOMAIN	PR00929C 5.26 3.328e-
189	PR00929	SIGNATURE	09 440-451
100	DY 00702	Tyrosine specific	BL00383F 15.51 7.188e-
190	BL00383	protein phosphatases	17 666-682 BL00383A
		protein phosphacases	13.34 8.714e-17 162-
		process:	177 BL00383E 10.35
			1.000e-14 333-344
			BL00383E 10.35 7.300e-
		İ	14 628-639 BL00383F
			15.51 1.720e-13 371-
			387 BL00383C 10.10
			3.000e-13 217-228
	1		BL00383D 11.92 7.000e-
			13 295-308 BL00383B
			7.61 1.692e-11 187-196
			BL00383C 10.10 1.750e-
			09 509-520 BL00383D
	1		11.92 4.000e-09 589-
			602 BL00383B 7.61
		-	8.000e-09 479-488
191	PR00450	RECOVERIN FAMILY	PR00450C 12.22 7.911e-
	1	SIGNATURE	15 83-105 PR00450C
			12.22 6.286e-13 47-69
193	PF00564	Octicosapeptide repeat	PF00564B 24.74 6.164e-
		proteins.	16 227-278
194	PR00503	BROMODOMAIN SIGNATURE	PR00503D 20.81 9.156e-
		i i	15 204-224 PR00503B
			9.96 9.571e-13 170-187
195	BL00901	Cysteine	BL00901C 20.63 3.429e-
		synthase/cystathionine	1.0 0/-11/
		beta-synthase P-	1
107	Pt 00636	phosphate att.	BL00636A 8.07 6.211e-
197	BL00636	Nt-dnaJ domain proteins.	17 40-57 BL00636B
1	1	1	15.11 2.000e-13 67-88
100	PROCESS	ADHESIN FAMILY SIGNATURE	PR00690A 10.86 9.866e-
198	PR00690	ADDESIN FAMILI SIGNATURE	09 463-482
100	DI.01121	Ribosomal RNA adenine	BL01131A 26.62 2.343e-
199	BL01131	dimethylases proteins.	12 84-130
201	PR00910	LUTEOVIRUS CRF6 PROTEIN	PR00910A 2.51 8.352e-
201	LKOOJIO	SIGNATURE	12 509-522
203	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.286e-
203	50,00213	TROUGHD RICH PROTEIN 3.	10 39-72
206	PR00261	LOW DENSITY LIPOPROTEIN	PR00261A 11.02 4.462e-
200	1100201	(LDL) RECEPTOR SIGNATURE	19 65-87 PR00261C
		ADDI RECEPTOR SIGNATURE	11.37 9.308e-19 65-87
		1	PR00261D 12.47 2.667e-
1			18 65-87 PR00261B
			14.12 4.000e-18 143-
			165 PR00261A 11.02
t			1

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			4.833e-18 143-165 PR00261D 12.47 7.500e- 18 143-165 PR00261B 14.12 5.065e-16 65-87 PR00261C 11.37 8.967e- 16 143-165 PR00261F 11.57 4.938e-13 143- 165 PR00261E 11.08 7.188e-13 65-87 PR00261F 11.57 7.188e- 13 65-87 PR00261E 11.08 1.643e-11 143- 165
209	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 6.143e- 13 118-173 PF00791C 20.98 7.680e-10 132- 171
211	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007A 19.33 5.781e- 19 131-158 PR00007B 14.16 4.115e-18 158- 178 PR00007C 15.60 1.675e-15 201-223 PR00007D 9.64 7.231e- 11 233-244
212	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 1.545e- 30 43-91
213	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 1.545e- 30 43-91
215	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 1.900e- 29 568-614 BL00039A 18.44 1.871e-23 21-60 BL00039C 15.63 1.720e- 11 364-388 BL00039B 19.19 4.064e-11 277- 303
217	BL00100	Chloramphenicol acetyltransferase proteins.	BL00100D 17.22 8.484e- 09 68-106
219	PR00213	MYELIN PO PROTEIN SIGNATURE	PR00213C 15.94 3.969e- 11 199-227
222	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 1.947e-09
224	PR00875	MOLLUSC METALLOTHIONEIN SIGNATURE	PR00875A 5.83 1.000e- 09 901-913
225	BL00636	Nt-dnaJ domain proteins.	BL00636B 15.11 8.200e- 19 18-39
226	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 1.000e- 21 21-38 BL00636B 15.11 8.200e-19 45-66
229	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE	PR00301F 13.98 7.563e- 13 329-346 PR00301G 13.78 4.300e-12 361- 382
230	BL00460	Glutathione peroxidases selenocysteine proteins.	BL00460A 28.67 8.773e- 20 35-70 BL00460B 9.73 7.429e-16 78-96 BL00460C 14.35 2.831e- 12 111-134 BL00460D 16.89 8.773e-11 140- 160
231	PR00647	SENR ORPHAN RECEPTOR SIGNATURE	PR00647B 10.19 8.522e- 09 273-287
233	BL00292	Cyclins proteins.	BL00292B 20.31 7.429e-
			27 244-275 BL00292A 22.87 7.750e-27 201- 235

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			17.27 4.462e-11 47-70 PR00449D 10.79 7.120e- 11 109-123
235	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 7.300e- 10 251-265 PR00019B 11.36 5.320e-09 119- 133 PR00019B 11.36 1.000e-08 229-243
236	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 7.300e- 10 245-259 PR00019B 11.36 5.320e-09 113- 127 PR00019B 11.36 1.000e-08 223-237
237	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESYNA.	PD00289 9.97 8.448e-09 67-81
240	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 3.492e- 10 616-635
241	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 3.492e- 10 616-635
244	BL00903	Cytidine and deoxycytidylate deaminases zinc-binding region s.	BL00903 12.93 8.941e- 12 54-64
245	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 8.043e- 09 124-134
248	BL00246	Wnt-1 family proteins.	BL00246D 23.97 1.000e- 40 186-239 BL00246E 20.32 1.000e-40 305- 351 BL00246B 13.69 4.176e-36 105-140 BL00246A 15.75 2.286e- 24 70-90 BL00246C 15.56 4.857e-22 150- 175
250	PR00927	ADENINE NUCLEOTIDE TRANSLOCATOR 1 SIGNATURE	PR00927E 14.93 5.114e- 10 253-275
254	BL00674	AAA-protein family proteins.	BL00674B 4.46 1.000e- 09 223-245
255	PD01796	PROTEIN TRANSMEMBRANE COBALT ZINC CADMIU.	PD01796 15.01 6.045e- 09 61-88
256	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002B 15.18 2.800e- 10 421-435
258	PR00094	ADENYLATE KINASE SIGNATURE	PR00094C 12.94 2.200e- 18 87-104 PR00094D 12.52 2.731e-14 161- 177 PR00094A 10.31 5.500e-14 11-25 PR00094B 11.01 4.115e- 13 39-54 PR00094E 11.25 7.333e-13 178- 193
259	BL00892	HIT family proteins.	BL00892A 18.17 5.500e- 13 60-91
262	BL00388	Proteasome A-type subunits proteins.	BL00388A 23.14 1.000e- 40 8-54 BL00388B 31.38 3.864e-33 66-108 BL00388D 20.71 1.000e- 21 153-184 BL00388C 18.79 8.147e-16 126- 148
264	BL00903	Cytidine and deoxycytidylate deaminases zinc-binding region s.	BL00903 12.93 5.821e- 09 91-101
267	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.529e- 09 241-257
270	BL00226	Intermediate filaments proteins.	BL00226D 19.10 1.000e- 37 362-409 BL00226B

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	NO.		23.86 8.043e-35 196- 244 BL00226C 13.23 7.000e-20 261-292 BL00226A 12.77 6.143e- 15 96-111
271	PD02952	KINASE TRANSFERASE CHOLINE PROTEIN MULTIGENE FAMI.	PD02952C 15.76 9.731e- 16 235-265 PD02952B 15.57 5.625e-09 215- 229
272	PD02929	ADHESION GLYCOPROTEIN PRECURSOR I.	PD02929A 28.27 1.000e- 40 106-160 PD02929B 18.36 8.800e-17 179- 199
274	BL01027	Glycosyl hydrolases family 39 proteins.	BL01027B 15.34 3.486e- 09 213-250
275	PR00424	ADENOSINE RECEPTOR SIGNATURE	PR00424D 14.32 6.451e- 11 39-59
277	BL00052	Ribosomal protein S7 proteins.	BL00052A 27.85 6.000e- 13 137-184 BL00052B 15.17 5.143e-12 208- 235
279	BL00790	Receptor tyrosine kinase class V proteins.	BL00790N 13.25 5.659e- 13 267-294
280	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 107-125 PR00319C 13.41 1.000e-21 89-105 PR00319A 15.27 8.364e- 21 51-68 PR00319B 11.47 8.200e-19 70-85
281	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 94-112 PR00319C 13.41 1.000e-21 76-92 PR00319A 15.27 8.364e- 21 38-55 PR00319B 11.47 8.200e-19 57-72
287	PF00929	Exonuclease.	PF00929D 16.17 7.366e- 09 149-163
291	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e- 09 93-127
292	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e- 09 93-127
294	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.714e- 12 203-216
295	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.500e- 15 322-339 BL00028 16.07 9.471e-14 433- 450 BL00028 16.07 4.600e-13 648-665 BL00028 16.07 5.500e- 13 760-777 BL00028 16.07 9.550e-13 788- 805 BL00028 16.07 3.348e-12 704-721 BL00028 16.07 6.478e- 12 461-478 BL00028 16.07 8.435e-12 844- 861 BL00028 16.07 1.692e-11 593-610 BL00028 16.07 2.038e- 11 211-228 BL00028 16.07 5.154e-11 732- 749 BL00028 16.07 5.846e-11 377-394 BL00028 16.07 6.885e- 11 816-833 BL00028 16.07 7.231e-11 676- 693 BL00028 16.07 9.654e-11 564-581

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			BL00028 16.07 4.086e-
			09 517-534 BL00028 16.07 7.429e-09 489-
			506
		Wheelerdrial energy	BL00215A 15.82 8.333e-
296	BL00215	Mitochondrial energy transfer proteins.	16 111-136 BL00215A
	}	cranster process.	15.82 2.723e-11 10-35
			BL00215B 10.44 9.526e-
			11 152-165 BL00215B
			10.44 7.375e-10 59-72
	ĺ	1	BL00215A 15.82 9.824e-
			10 205-230
302	PF00953	Glycosyl transferase.	PF00953C 19.70 8.773e-
	1		34 236-269 PF00953A
			19.68 5.000e-25 102- 129 PF00953B 6.17
			1.000e-13 182-194
		tRNA synthetases class	PF00152D 21.30 8.364e-
304	PF00152	II.	28 422-461 PF00152C
		11.	28.03 9.250e-21 220-
			257 PF00152B 15.67
			2.658e-13 159-184
			PF00152A 19.68 5.714e-
	ļ	<u> </u>	11 44-67
305	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 8.250e-
		ZINC-FINGER METAL-	35 37-76
		BINDING NU.	PD02784B 26.46 5.840e-
306	PD02784	PROTEIN NUCLEAR	09 92-135
		RIBONUCLEOPROTEIN. ETS DOMAIN SIGNATURE	PR00454C 11.24 7.808e-
307	PR00454	ETS DOMAIN SIGNATURE	09 1167-1186
200	PR00237	RHODOPSIN-LIKE GPCR	PR00237E 13.03 5.091e-
308	PR00237	SUPERFAMILY SIGNATURE	13 188-212 PR00237G
	1		19.63 7.207e-13 268-
			295 PR00237A 11.48
			4.375e-11 24-49
			PR00237C 15.69 3.057e-
			10 101-124 PR00237D 8.94 4.750e-10 137-159
			PR00237F 13.57 5.364e-
			10 230-255 PR00237B
	ļ		13.50 9.438e-10 57-79
309	BL00522	DNA polymerase family X	BL00522C 11.90 7.577e-
209	3250322	proteins.	24 315-339 BL00522F
		1	14.90 1.310e-15 470-
		1	494 BL00522A 25.52
			1.265e-14 179-226 BL00522E-19.63 8.615e-
		,	14 430~460 BL00522B
	1	1	27.30 9.625e-12 267-
		ļ	313
	D7.00225	Tropomyosins proteins.	BL00326D 8.76 5.235e-
310	BL00326	TIODOMAORIUS Procesus.	10 856-897
1	1	Immunoglobulins and	BL00290A 20.89 4.706e-
312	BL00290		14 151-174 BL00290B
312	BL00290	major histocompatibility	
312	BL00290	major histocompatibility	13.17 9.000e-12 211-
312	BL00290	major histocompatibility complex proteins.	13.17 9.000e-12 211- 229
312	BL00290 BL00345	major histocompatibility	13.17 9.000e-12 211- 229 BL00345B 21.28 1.000e-
		major histocompatibility complex proteins.	13.17 9.000e-12 211- 229 BL00345B 21.28 1.000e- 40 34-85 BL00345A
	BL00345	major histocompatibility complex proteins. Ets-domain proteins.	13.17 9.000e-12 211- 229 BL00345B 21.28 1.000e- 40 34-85 BL00345A 13.96 9.217e-16 1-20
		major histocompatibility complex proteins. Ets-domain proteins. BTB (also known as BR-	13.17 9.000e-12 211- 229 BL00345B 21.28 1.000e- 40 34-85 BL00345A 13.96 9.217e-16 1-20 PF00651 15.00 5.091e-
313	3L00345	major histocompatibility complex proteins. Ets-domain proteins. BTB (also known as BR-C/Ttk) domain proteins.	13.17 9.000e-12 211- 229 BL00345B 21.28 1.000e- 40 34-85 BL00345A 13.96 9.217e-16 1-20 PF00651 15.00 5.091e- 15 63-76
313	BL00345	major histocompatibility complex proteins. Ets-domain proteins. BTB (also known as BR-	13.17 9.000e-12 211- 229 BL00345B 21.28 1.000e- 40 34-85 BL00345A 13.96 9.217e-16 1-20 PF00651 15.00 5.091e- 15 63-76 BL01020C 15.35 3.198e-
313 315 317	BL00345 PF00651 BL01020	major histocompatibility complex proteins. Ets-domain proteins. BTB (also known as BR-C/Ttk) domain proteins. SAR1 family proteins.	13.17 9.000e-12 211- 229 BL00345B 21.28 1.000e- 40 34-85 BL00345A 13.96 9.217e-16 1-20 PF00651 15.00 5.091e- 15 63-76 BL01020C 15.35 3.198e- 17 79-130
313	3L00345	major histocompatibility complex proteins. Ets-domain proteins. BTB (also known as BR-C/Ttk) domain proteins. SAR1 family proteins. Sugar transport	13.17 9.000e-12 211- 229 BL00345B 21.28 1.000e- 40 34-85 BL00345A 13.96 9.217e-16 1-20 PF00651 15.00 5.091e- 15 63-76 BL01020C 15.35 3.198e- 17 79-130 BL00216B 27.64 4.696e-
313 315 317	BL00345 PF00651 BL01020	major histocompatibility complex proteins. Ets-domain proteins. BTB (also known as BR-C/Ttk) domain proteins. SAR1 family proteins.	13.17 9.000e-12 211- 229 BL00345B 21.28 1.000e- 40 34-85 BL00345A 13.96 9.217e-16 1-20 PF00651 15.00 5.091e- 15 63-76 BL01020C 15.35 3.198e- 17 79-130

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	NO.		1.5552.5
		SIGNATURE	
321	BL00027	'Homeobox' domain	BL00027 26.43 5.688e-
		proteins.	10 329-372
322	PR00109	TYROSINE KINASE	PR00109B 12.27 8.765e-
		CATALYTIC DOMAIN	12 558-577
324	- Property	SIGNATURE	
324	BL01241	Link domain proteins.	BL01241 35.81 8.313e-
			30 183-236 BL01241
		\	35.81 3.222e-13 282-
326	BL00412	Nouvendulia (Chp. 42)	335
520	D100412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 4.000e-
		proceins.	12 515-566 BL00412D 16.54 5.705e-11 516-
			567 BL00412D 16.54
		•	7.848e-10 518-569
		1	BL00412D 16.54 1.827e-
			09 514-565 BL00412D
			16.54 1.918e-09 513-
			564 BL00412D 16.54
			2.102e-09 520-571
328	BL00232	Cadherins extracellular	BL00232B 32.79 9.557e-
		repeat proteins domain	20 151-199 BL00232B
		proteins.	32.79 2.246e-18 41-89
			BL00232B 32.79 5.985e-
			18 370-418 BL00232B
			32.79 5.500e-16 258-
			306 BL00232B 32.79
			9.384e-15 475-523
			BL00232C 10.65 2.537e-
			12 256-274 BL00232C
			10.65 4.326e-11 368-
			386 BL00232C 10.65
	ł	1	7.261e-11 473-491
	1		
			BL00232C 10.65 7.457e-
330	PR00454	ETS DOMAIN SIGNATURE	11 39-57
330	PR00454	ETS DOMAIN SIGNATURE	11 39-57 PR00454C 11.24 7.808e-
330	PR00454		11 39-57
331	BL00598	ETS DOMAIN SIGNATURE Chromo domain proteins.	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186
		Chromo domain proteins. Glycoprotease family	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e-
331	BL00598	Chromo domain proteins.	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E
331	BL00598	Chromo domain proteins. Glycoprotease family	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149-
331	BL00598	Chromo domain proteins. Glycoprotease family	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71
331	BL00598	Chromo domain proteins. Glycoprotease family	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301
331	BL00598	Chromo domain proteins. Glycoprotease family	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e-
331	BL00598	Chromo domain proteins. Glycoprotease family	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G
331	BL00598	Chromo domain proteins. Glycoprotease family	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271
331	BL00598	Chromo domain proteins. Glycoprotease family	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e-
331	BL00598	Chromo domain proteins. Glycoprotease family	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016B 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e- 10 4-19 BL01016F
331	BL00598	Chromo domain proteins. Glycoprotease family	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e- 10 4-19 BL01016F 13.34 1.563e-09 200-
331	BL00598	Chromo domain proteins. Glycoprotease family	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e- 10 4-19 BL01016F 13.34 1.563e-09 200- 212 BL01016B 8.93
331	BL00598	Chromo domain proteins. Glycoprotease family	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e- 10 4-19 BL01016F 13.34 1.563e-09 200- 212 BL01016B 8.93 8.855e-09 38-50
331 333 339	BL01016 BL01016	Chromo domain proteins. Glycoprotease family proteins. GTP-binding nuclear protein ran proteins.	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e- 10 4-19 BL01016F 13.34 1.563e-09 200- 212 BL01016B 8.93
333	BL00598	Chromo domain proteins. Glycoprotease family proteins. GTP-binding nuclear protein ran proteins. PROTEIN ZINC FINGER	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e- 10 4-19 BL01016F 13.34 1.563e-09 200- 212 BL01016B 8.93 8.855e-09 38-50 BL01115A 10.22 5.500e- 11 17-61 PD01066 19.43 1.231e-
331 333 339	BL01016 BL01016	GTP-binding nuclear protein ran proteins. GTP-binding nuclear protein ran proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL-	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e- 10 4-19 BL01016F 13.34 1.563e-09 200- 212 BL01016B 8.93 8.855e-09 38-50 BL01115A 10.22 5.500e- 11 17-61
331 333 339 340	BL01016 BL01115 PD01066	Chromo domain proteins. Glycoprotease family proteins. GTP-binding nuclear protein ran proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e- 10 4-19 BL01016F 13.34 1.563e-09 200- 212 BL01016B 8.93 8.855e-09 38-50 BL01115A 10.22 5.500e- 11 17-61 PD01066 19.43 1.231e- 33 10-49
331 333 339	BL01016 BL01016	Chromo domain proteins. Glycoprotease family proteins. GTP-binding nuclear protein ran proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. Kinesin light chain	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e- 10 4-19 BL01016F 13.34 1.563e-09 200- 212 BL01016B 8.93 8.855e-09 38-50 BL01115A 10.22 5.500e- 11 17-61 PD01066 19.43 1.231e- 33 10-49 BL01160B 19.54 5.042e-
331 333 339 340	BL01016 BL01115 PD01066 BL01160	Chromo domain proteins. Glycoprotease family proteins. GTP-binding nuclear protein ran proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. Kinesin light chain repeat proteins.	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e- 10 4-19 BL01016F 13.34 1.563e-09 200- 212 BL01016B 8.93 8.855e-09 38-50 BL01115A 10.22 5.500e- 11 17-61 PD01066 19.43 1.231e- 33 10-49 BL01160B 19.54 5.042e- 09 55-109
331 333 339 340	BL01016 BL01115 PD01066	Chromo domain proteins. Glycoprotease family proteins. GTP-binding nuclear protein ran proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. Kinesin light chain repeat proteins. PROTEIN ZINC FINGER	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e- 10 4-19 BL01016F 13.34 1.563e-09 200- 212 BL01016B 8.93 8.855e-09 38-50 BL01115A 10.22 5.500e- 11 17-61 PD01066 19.43 1.231e- 33 10-49 BL01160B 19.54 5.042e- 09 55-109 PD01066 19.43 2.400e-
331 333 339 340	BL01016 BL01115 PD01066 BL01160	Chromo domain proteins. Glycoprotease family proteins. GTP-binding nuclear protein ran proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. Kinesin light chain repeat proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL-	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e- 10 4-19 BL01016F 13.34 1.563e-09 200- 212 BL01016B 8.93 8.855e-09 38-50 BL01115A 10.22 5.500e- 11 17-61 PD01066 19.43 1.231e- 33 10-49 BL01160B 19.54 5.042e- 09 55-109
331 333 339 340 341	BL01016 BL01016 BL01016 BL01066 PD01066	Chromo domain proteins. Glycoprotease family proteins. GTP-binding nuclear proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. Kinesin light chain repeat proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016B 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e- 10 4-19 BL01016F 13.34 1.563e-09 200- 212 BL01016B 8.93 8.855e-09 38-50 BL01115A 10.22 5.500e- 11 17-61 PD01066 19.43 1.231e- 33 10-49 BL01160B 19.54 5.042e- 09 55-109 PD01066 19.43 2.400e- 30 16-55
331 333 339 340	BL01016 BL01115 PD01066 BL01160	Chromo domain proteins. Glycoprotease family proteins. GTP-binding nuclear protein ran proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. Kinesin light chain repeat proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL-	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e- 10 4-19 BL01016F 13.34 1.563e-09 200- 212 BL01016B 8.93 8.855e-09 38-50 BL01115A 10.22 5.500e- 11 17-61 PD01066 19.43 1.231e- 33 10-49 BL0116OB 19.54 5.042e- 09 55-109 PD01066 19.43 2.400e- 30 16-55
331 333 339 340 341 342	BL01016 BL01115 PD01066 BL01160 PD01066	Chromo domain proteins. Glycoprotease family proteins. GTP-binding nuclear proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU. Kinesin light chain repeat proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU. IMMUNOGLOBULIN V REGION.	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e- 10 4-19 BL01016F 13.34 1.563e-09 200- 212 BL01016B 8.93 8.855e-09 38-50 BL01115A 10.22 5.500e- 11 17-61 PD01066 19.43 1.231e- 33 10-49 BL01160B 19.54 5.042e- 09 55-109 PD01066 19.43 2.400e- 30 16-55 DM00031A 16.80 1.000e- 40 20-68
331 333 339 340 341	BL01016 BL01016 BL01016 BL01066 PD01066	Chromo domain proteins. Glycoprotease family proteins. GTP-binding nuclear proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU. Kinesin light chain repeat proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU. IMMUNOGLOBULIN V REGION.	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e- 10 4-19 BL01016F 13.34 1.563e-09 200- 212 BL01016B 8.93 8.855e-09 38-50 BL01115A 10.22 5.500e- 11 17-61 PD01066 19.43 1.231e- 33 10-49 BL01160B 19.54 5.042e- 09 55-109 PD01066 19.43 2.400e- 30 16-55 DM00031A 16.80 1.000e- 40 20-68 PR00109B 12.27 4.764e-
331 333 339 340 341 342	BL01016 BL01115 PD01066 BL01160 PD01066	Chromo domain proteins. Glycoprotease family proteins. GTP-binding nuclear proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. Kinesin light chain repeat proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. IMMUNOGLOBULIN V REGION. TYROSINE KINASE CATALYTIC DOMAIN	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e- 10 4-19 BL01016F 13.34 1.563e-09 200- 212 BL01016B 8.93 8.855e-09 38-50 BL01115A 10.22 5.500e- 11 17-61 PD01066 19.43 1.231e- 33 10-49 BL01160B 19.54 5.042e- 09 55-109 PD01066 19.43 2.400e- 30 16-55 DM00031A 16.80 1.000e- 40 20-68
331 333 339 340 341 342	BL01016 BL01115 PD01066 BL01160 PD01066	Chromo domain proteins. Glycoprotease family proteins. GTP-binding nuclear proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU. Kinesin light chain repeat proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU. IMMUNOGLOBULIN V REGION.	11 39-57 PR00454C 11.24 7.808e- 09 1167-1186 BL00598 14.45 8.393e- 18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e- 10 4-19 BL01016F 13.34 1.563e-09 200- 212 BL01016B 8.93 8.855e-09 38-50 BL01115A 10.22 5.500e- 11 17-61 PD01066 19.43 1.231e- 33 10-49 BL01160B 19.54 5.042e- 09 55-109 PD01066 19.43 2.400e- 30 16-55 DM00031A 16.80 1.000e- 40 20-68 PR00109B 12.27 4.764e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		CATALYTIC DOMAIN SIGNATURE	11 135-154
351	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 1.783e- 13 100-116 BL01187B 12.04 8.435e-13 276- 292 BL01187B 12.04 8.800e-11 13-29 BL01187B 12.04 7.429e- 10 54-70 BL01187B 12.04 5.725e-09 231- 247 BL01187A 9.98 7.000e-09 255-267
352	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.950e- 10 366-379 PD00078B 13.14 4.522e-09 168- 181
354	BL00380	Rhodanese proteins.	BL00380F 9.76 6.694e- 11 542-553
355	PF00628	PHD-finger.	PF00628 15.84 1.000e- 11 116-131
356	PR00587	SOMATOSTATIN RECEPTOR TYPE 1 SIGNATURE	PR00587A 8.06 9.700e- 09 17-37
359	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 4.462e- 15 261-274 PD00066 13.92 6.500e-13 233- 246 PD00066 13.92 4.300e-09 289-302
361	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 9.604e- 13 54-109 PF00791B 28.49 1.095e-12 21-76 PF00791A 27.85 1.432e- 09 71-126 PF00791B 28.49 7.440e-09 184- 239
362	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 2.273e- 11 279-334
363	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 5.080e- 10 73-95 PR00450C 12.22 3.278e-09 109- 131
364	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242Q 13.51 2.328e- 09 22-68
365	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242Q 13.51 2.328e- 09 22-68
366	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.644e- 09 1038-1092
367	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PRO0019B 11.36 1.360e- 09 229-243 PRO0019B 11.36 6.040e-09 91-105 PR00019A 11.19 8.667e- 09 370-384
368	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 9.000e- 15 30-49 PR00011A 14.06 9.830e-15 30-49 PR00011B 13.08 4.500e- 14 30-49 PR00011C 24.25 5.143e-09 6-35
369	BL01032	Protein phosphatase 2C proteins.	BL01032H 11.25 4.150e- 09 417-430
372	BL00478	LIM domain proteins.	BL00478B 14.79 7.750e- 12 410-425
373	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.757e- 34 26-65
376	PR00170	SODIUM CHANNEL SIGNATURE	PR00170E 6.48 2.739e-

000 TO 100	Lacondator	DECEMENTON	RESULTS*
SEQ ID NO:	ACCESSION NO.	DESCRIPTION	KESULTS*
	140.	 	10 88-118
380	BL00107	Protein kinases ATP-	BL00107A 18.39 1.000e-
300	BEOUTO	binding region proteins.	23 276-307 BL00107B
		zamating regress processis.	13.31 1.692e-12 342-
			358
381	BL00455	Putative AMP-binding	BL00455 13.31 5.714e-
		domain proteins.	12 50-66
382	PR00624	HISTONE H5 SIGNATURE	PR00624G 4.08 4.900e-
			09 524-544
384	PD00078	REPEAT PROTEIN ANK	PD00078B 13.14 5.950e-
		NUCLEAR ANKYR.	10 366-379 PD00078B
			13.14 4.522e-09 168-
			181
385	PR00511	TEKTIN SIGNATURE	PR00511D 7.11 5.371e-
306	5500000	DECEMBED THERE STATES	09 67-80 PD02870B 18.83 6.000e-
386	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	10 97-130
388	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 5.000e-
388	200006	METAL-BINDI.	13 516-529
389	BL00290	Immunoglobulins and	BL00290A 20.89 7.667e-
202	200230	major histocompatibility	09 151-174
		complex proteins.	
390	BL00215	Mitochondrial energy	BL00215A 15.82 5.200e-
		transfer proteins.	15 221-246 BL00215A
		_	15.82 7.618e-14 20-45
			BL00215A 15.82 8.851e-
			11 123-148 BL00215B
			10.44 9.526e-11 69-82
			BL00215B 10.44 7.300e-
			09 272-285 BL00215B
			10.44 8.500e-09 165-
394	BL00674	AAA-protein family	BL00674B 4.46 2.723e-
394	BL008/4	proteins.	16 299-321
397	PR00048	C2H2-TYPE ZINC FINGER	PR00048A 10.52 8.579e-
33,	1.000010	SIGNATURE	11 141-155
398	PR00761	BINDIN PRECURSOR	PR00761B 9.93 6.764e-
		SIGNATURE	09 55-74
399	BL00240	Receptor tyrosine kinase	BL00240B 24.70 7.907e-
ļ		class III proteins.	10 118-142
401	PF00676	Dehydrogenase El	PF00676B 24.71 8.071e-
		component.	18 331-369 PF00676D
			14.40 3.854e-15 486-
			506 PF00676C 16.88
402	PT 00514	Fibrinogen beta and	9.182e-14 454-478 BL00514C 17.41 4.673e-
402	BL00514	gamma chains C-terminal	28 4432-4469 BL00514G
		domain proteins.	15.98 6.092e-14 4555-
ļ		,	4585 BL00514D 15.35
			2.532e-12 4473-4486
1			BL00514F 11.65 4.288e-
			10 4519-4534 BL00514H
		1	14.95 4.955e-10 4584-
<u> </u>			4609
403	PF00992	Troponin.	PF00992A 16.67 5.974e-
			09 105-140
404	PR00019	LEUCINE-RICH REPEAT	PR00019B 11.36 1.450e-
		SIGNATURE	10 73-87 PR00019A
			11.19 8.043e-10 76-90
			PR00019B 11.36 1.000e-
			09 50-64 PR00019B
405	DI 00222	Cadharina out	11.36 1.000e-09 96-110 BL00232B 32.79 9.557e-
405	BL00232	Cadherins extracellular repeat proteins domain	20 139-187 BL00232B
1		proteins.	32.79 2.246e-18 29-77
	1	process.	BL00232B 32.79 5.985e-
1			18 358-406 BL00232B
1			32.79 5.500e-16 246-
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SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		294 BL00232B 32.79
		i	9.384e-15 463-511
	1		BL00232C 10.65 2.537e-
	1	1	12 244-262 BL00232C
			10.65 4.326e-11 356-
		1	374 BL00232C 10.65
			7.261e-11 461-479
			BL00232C 10.65 7.457e-
			11 27-45
407	PF00426	Outer Capsid protein VP4	PF00426S 15.67 5.634e-
		(Hemagglutinin).	09 902-940
409	BL01160	Kinesin light chain	BL01160B 19.54 9.695e- 09 126-180
	71.00741	repeat proteins. Guanine-nucleotide	BL00741B 14.27 2.731e-
410	BL00741	dissociation stimulators	09 252-275
		CDC24 family sign.	05 252 275
411	PF00646	F-box domain proteins.	PF00646A 14.37 6.344e-
411	1100010	I zon zomzu procesu.	09 86-100
412	BL00603	Thymidine kinase	BL00603B 11.39 8.500e-
		cellular-type proteins.	09 542-557
415	BL00866	Carbamoyl-phosphate	BL00866B 36.29 3.571e-
		synthase subdomain	31 245-291 EL00866C
		proteins.	23.26 9.000e-25 331-
			366
418	PR00239	MOLLUSCAN RHODOPSIN C-	PR00239E 1.58 6.114e-
	7,700,701	TERMINAL TAIL SIGNATURE Domain present in ZO-1	09 590-602 PF00791B 28.49 7.955e-
421	PF00791	and Unc5-like netrin	14 23-78 PF00791B
		receptors.	28.49 3.653e-12 273-
		receptors.	328 PF00791B 28.49
			4.273e-11 156-211
			PF00791B 28.49 7.818e-
		\	11 89-144 PF00791B
			28.49 1.524e-10 56-111
	1		PF00791C 20.98 3.559e-
	•		09 37-76 PF00791C
			20.98 5.235e-09 170-
			209 PF00791C 20.98 5.235e-09 381-420
			PF00791B 28.49 6.202e-
			09 189-244 PF00791B
]	28.49 7.028e-09 435-
		1	490 PF00791B 28.49
			8.679e-09 367-422
424	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 7.207e-
			28 1645-1679
425	PR00109	TYROSINE KINASE	PR00109D 17.04 5.881e-
		CATALYTIC DOMAIN	10 228-251
100	D. O.S.	SIGNATURE CONCA TIME	BLOOS 18 12 23 4 600c
429	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 4.600e-
421	BL00039	(RING finger), proteins. DEAD-box subfamily ATP-	BL00039D 21.67 1.844e-
431	פניייים	dependent helicases	34 490-536 BL00039A
1		proteins.	18.44 5.615e-19 205-
		1	244 BL00039B 19.19
İ		1	8.920e-16 251-277
I	1		BL00039C 15.63 5.781e-
1			
			15 333-357
432	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 7.652e-
			PR00452B 11.65 7.652e- 12 169-185
432	PR00452	SH3 DOMAIN SIGNATURE FORMIN SIGNATURE	PR00452B 11.65 7.652e- 12 169-185 PR00828B 5.23 8.218e-
433	PR00828	FORMIN SIGNATURE	PR00452B 11.65 7.652e- 12 169-185 PR00828B 5.23 8.218e- 10 382-405
			PR00452B 11.65 7.652e- 12 169-185 PR00828B 5.23 8.218e- 10 382-405 BL00415N 4.29 8.643e-
433	PR00828	FORMIN SIGNATURE	PR00452B 11.65 7.652e- 12 169-185 PR00828B 5.23 8.218e- 10 382-405 BL00415N 4.29 8.643e- 11 195-239 BL00415N
436	PR00828 BL00415	FORMIN SIGNATURE Synapsins proteins.	PR00452B 11.65 7.652e- 12 169-185 PR00828B 5.23 8.218e- 10 382-405 BL00415N 4.29 8.643e- 11 195-239 BL00415N 4.29 3.036e-09 809-853
433	PR00828	FORMIN SIGNATURE Synapsins proteins. HTRA/DEGQ PROTEASE	PR00452B 11.65 7.652e- 12 169-185 PR00828B 5.23 8.218e- 10 382-405 BL00415N 4.29 8.643e- 11 195-239 BL00415N 4.29 3.036e-09 809-853 PR00834F 10.91 6.040e-
436	PR00828 BL00415	FORMIN SIGNATURE Synapsins proteins.	PR00452B 11.65 7.652e- 12 169-185 PR00828B 5.23 8.218e- 10 382-405 BL00415N 4.29 8.643e- 11 195-239 BL00415N 4.29 3.036e-09 809-853

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		p15.	10 183-218 PF01140D 15.54 3.093e-09 246- 281
449	PR00568	DOPAMINE D3 RECEPTOR SIGNATURE	PR00568G 13.95 5.551e-
451	PF00084	Sushi domain proteins (SCR repeat proteins.	PF00084B 9.45 3.813e- 10 47-59
452	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 2.821e- 09 618-649
456	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 1.000e- 25 77-99 PR00380D 9.93 1.000e-21 281-303 PR00380C 13.18 8.286e- 17 230-249 PR00380B 12.64 4.724e-16 194- 212
457	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 9.143e- 24 246-267 PR00253B 13.47 2.000e-23 272- 294 PR00253C 13.85 7.000e-23 306-328 PR00253D 16.68 5.950e- 21 452-473
467	PR00849	GLYCOSYL HYDROLASE FAMILY 58 SIGNATURE	PR00849D 9.77 9.236e- 09 910-937
471	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 8.200e-12 33-44
472	BL00226	Intermediate filaments proteins.	BL00226B 23.86 3.721e- 09 282-330
473	BL00344	GATA-type zinc finger domain proteins.	BL00344 17.99 7.000e- 12 814-852
474	BL00481	Thiol-activated cytolysins proteins.	BL00481E 13.07 8.909e- 09 173-199
479	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 2.571e- 09 393-408
480	PD01066	FROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 1.900e- 38 8-47
481	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405C 19.41 1.000e- 19 451-473 PR00405B 11.83 4.333e-18 430- 448 PR00405A 17.71 4.971e-18 411-431
482	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.286e- 10 959-974 PR00049D 0.00 9.857e-10 958-973 PR00049D 0.00 1.305e- 09 937-952 PR00049D 0.00 8.322e-09 939-954
496	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007B 14.16 8.615e- 23 653-673 PR00007A 19.33 6.192e-22 626- 653 PR00007C 15.60 5.846e-19 698-720 PR00007D 9.64 3.647e- 13 732-743
487	PD00567	PROTEIN RNA-BINDING RNA REPEAT HYD.	PD00567B 18.23 2.853e- 09 200-214
488	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 4.569e- 12 3-21
489	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 4.882e- 27 30-69 PD01066 19.43 3.430e-10 71-110
490	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.864e-
492	BL01128	Shikimate kinase proteins.	BL01128A 18.84 6.464e- 17 58-92
497	PF00429	ENV polyprotein (coat	PF00429 31.08 7.171e-

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SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
52g 15 NO.	NO.	DESCRIPTION .	RESOLIS.
	 	polyprotein).	15 21-71
498	BL00120	Lipases, serine	BL00120B 11.37 7.923e-
		proteins.	09 185-200
500	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.353e- 11 299-318
501	BL01159	WW/rsp5/WWP domain	BL01159 13.85 8.579e-
		proteins.	12 131-146
505	BL00021	Kringle domain proteins.	BL00021B 13.33 3.739e- 17 492-510
508	PR00120	H+TRANSPORTING ATPASE	PR00120C 9.90 5.800e-
		(PROTON PUMP) SIGNATURE	19 705-722
509	DM01417.	6 kw INDUCING XPMC2 MUSHROOM SPAC22G7.04.	DM01417E 20.62 2.938e-
		MUSHROOM SPAC22G7.U4.	16 362-395 DM01417D 11.08 3.800e-13 322-
			338
510	PF00534	Glycosyl transferases	PF00534B 14.47 6.625e-
		group 1.	09 346-370
511	PF00534	Glycosyl transferases	PF00534B 14.47 6.625e-
<u></u>	DECOSE A	group 1.	09 293-317
512	PF00534	Glycosyl transferases group 1.	PF00534B 14.47 6.625e- 09 366-390
513	PD01841	PHOSPHORYLASE KINASE	PD01841A 21.71 1.000e-
	1	ALPHA MUSCL.	40 110-160 PD01841B
			14.35 1.000e-40 181-
			222 PD01841D 17.87
			1.000e-40 243-295
			PD01841F 13.36 1.000e- 40 333-382 PD01841G
			24.26 1.000e-40 386-
			440 PD01841L 18.42
			1.000e-40 968-1010
			PD01841I 23.00 4.545e-
			37 762-804 PD01841E
			18.60 3.750e-36 295- 333 PD01841J 14.94
	.		6.023e-35 851-888
			PD01841H 21.30 2.909e-
			33 490-527 PD01841K
		1	14.81 7.088e-33 924-
			954 PD01841C 13.78 9.386e-23 222-243
		1	PD01841M 10.82 8.594e-
			21 1054-1073 PD01841I
			23.00 2.667e-13 549-
51			591
514	PR00153	CYCLOPHILIN PEPTIDYL-	PR00153C 11.01 7.188e-
		PROLYL CIS-TRANS ISOMERASE SIGNATURE	13 95-111 PR00153E 9.10 4.150e-12 122-138
515	BL00740	MAM domain proteins.	BL00740A 13.87 7.188e-
			12 410-423
516	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 6.087e-
517	BL00242		12 1018-1052
DI /	BL00242	Integrins alpha chain proteins.	BL00242C 16.86 8.320e- 09 12-42
523	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 3.750e-
			39 20-68 DM00031B
			15.41 1.000e-25 84-118
525	BL00319	Amyloidogenic	BL00319C 17.12 8.375e-
		glycoprotein	10 61-95
	1	extracellular domain proteins.	
526	PF00789	Domain present in	PF00789B 19.70 3.308e-
		ubiquitin-regulatory	12 322-343 PF00789C
		proteins.	20.98 5.269e-09 367-
530	1		392
528	BL01162	Quinone oxidoreductase /	BL01162C 22.80 1.500e-
		zeta-crystallin proteins.	16 120-164
		Processes.	

SEQ ID NO	ACCESSION	DESCRIPTION	RESULTS*
	NO.	·	
529	PR00910	LUTEOVIRUS ÖRF6 PROTEIN	PR00910A 2.51 3.893e-
532	BL00215	SIGNATURE Mitochondrial energy	09 60-73 BL00215A 15.82 4.000e-
332	2500213	transfer proteins.	17 11-36 BL00215A
			15.82 8.660e-11 123-
			148
533	BL00215	Mitochondrial energy	BL00215A 15.82 4.000e-
		transfer proteins.	17 11-36 BL00215A 15.82 8.660e-11 97-122
534	BL0009B	Thiolases acyl-enzyme	BL00098C 21.65 2.800e-
		intermediate proteins.	38 181-227 BL00098B
			32.59 5.345e-38 86-141
			BL00098D 26.30 8.364e-
			35 245-288 BL00098E 22.12 1.000e-34 314-
			352 BL00098F 10.18
			4.971e-22 365-386
			BL00098A 10.60 6.455e-
535	PR00370	FLAVIN-CONTAINING	11 38-50
555	FR003/0	MONOOXYGENASE (FMO)	PR00370E 11.96 7.429e- 22 321-340 PR00370D
		SIGNATURE	16.33 6.143e-21 185-
			204 PR00370F 17.75
		1	6.559e-21 376-396 PR00370B 10.91 9.591e-
		1	21 27-46 PR00370C
		1	12.72 3.500e-20 140-
			157 PR00370A 3.35
536	DI 00000	61-41	6.442e-17 4-20
536	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.429e- 16 285-302 BL00028
		domain proteins.	16.07 6.294e-14 341-
		}	358 BL00028 16.07
		1	1.346e-11 369-386
			BL00028 16.07 1.692e- 11 397-414 BL00028
			16.07 4.462e-11 453-
			470 BL00028 16.07
			7.23le-11 425-442
			BL00028 16.07 4.300e-
537	BL00762	WHEP-TRS domain	10 313-330 BL00762A 23.43 9.419e-
		proteins.	15 844-881
538	BL00762	WHEP-TRS domain	BL00762A 23.43 9.419e-
£3.0	DI AAGGO	proteins.	15 819-856
539	BL00762	WHEP-TRS domain proteins.	BL00762A 23.43 9.419e- 15 822-859
540	PR00985	LEUCYL-TRNA SYNTHETASE	PR00985A 12.10 9.000e-
		SIGNATURE	10 357-375
541	PD02102	SUBUNIT E V-ATPASE	PD02102A 16.74 1.000e-
		VACUOLAR ATP SYNTHASE HYDROL.	40 3-47 PD02102B
		HIDROD.	18.28 4.375e-34 57-100 PD02102D 21.69 1.923e-
			30 179-218 PD02102C
			26.34 8.929e-26 100- ·
E42	DI GOGGO		146
543	BT00058	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.000e- 10 48-65 BL00028
		Comain processes.	16.07 6.400e-10 193-
			210 BL00028 16.07
			1.000e-09 343-360
	1		BL00028 16.07 6.914e-
545	BL00250	TGF-beta family	09 78-95
	12200230	proteins.	BL00250A 21.24 8.000e- 31 293-329 BL00250B
			27.37 5.286e-24 354-
	PR00319		390
547		BETA G-PROTEIN	PR00319B 11.47 2.714e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		(TRANSDUCIN) SIGNATURE	09 186-201 PR00319A 15.27 7.344e-09 210- 227
548	BL01204	NF-kappa-B/Rel/dorsal domain proteins.	BL01204A 17.74 1.000e- 40 8-56 BL01204D 16.42 1.000e-40 177- 221 BL01204E 13.83 7.652e-30 225-250 BL01204C 13.93 8.714e- 22 141-160 BL01204B 15.41 4.333e-16 102- 116
549	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 8.364e-
551	PF00632	HECT-domain (ubiquitin- transferase).	PF00632C 20.66 3.302e- 23 1569-1601 PF00632B 18.45 3.700e-21 1515- 1543
554	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 1.600e- 14 187-205 BL00290A 20.89 2.059e-14 130- 153
557	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.339e- 09 846-879
559	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111L 11.93 3.762e- 09 7-35
562	PF00658	Poly-adenylate binding protein, unique domain proteins.	PF00658C 16.33 9.455e- 32 118-155
564	BL00141	Rukaryotic and viral aspartyl proteases proteins.	BL00141A 12.10 4.150e- 10 472-488
566	PF00855	PWWP domain proteins.	PF00855 13.75 5.667e- 15 272-289
567	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 4.977e- 13 229-268
569	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.000e- 19 118-149 BL00107B 13.31 5.500e-15 183- 199
570	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.000e- 19 118-149 BL00107B 13.31 5.500e-15 183- 199
572	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 1.857e- 34 454-483 PR00193C 12.60 2.636e-31 223- 251 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e- 22 115-135 PR00193E 19.47 6.559e-19 508- 537
573	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 1.857e- 34 470-499 PR00193C 12.60 2.636e-31 239- 267 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e- 22 115-135 PR00193E 19.47 6.559e-19 524- 553
575	BL00752	XPA protein.	BL00752B 19.17 9.703e- 10 885-929
576	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.000e- 09 276-295
577	BL00116	DNA polymerase family B	BL00116A 12.81 5.737e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		proteins.	13 864-877 BL00116B 11.82 1.529e-12 952- 965
578	BL00195	Glutaredoxin proteins.	BL00195B 15.31 7.158e- 09 121-141
579	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 9.000e- 11 217-231 PR00019B 11.36 1.360e-09 386- 400 PR00019A 11.19 3.333e-09 389-403 PR00019B 11.36 8.920e- 09 363-377
580	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 2.125e- 25 275-296 PR00253B 13.47 7.923e-24 301- 323 PR00253D 16.68 5.846e-23 444-465 PR00253C 13.85 2.241e- 20 335-357
583	PR00343	SELECTIN SUPERFAMILY COMPLEMENT-BINDING REPEAT SIGNATURE	PR00343C 16.85 2.286e- 11 1233-1252 PR00343C 16.85 5.500e-11 333- 352 PR00343C 16.85 5.500e-11 783-802 PR00343C 16.85 4.246e- 10 1491-1510 PR00343C 16.85 8.230e-10 1686- 1705
584	DM01537	kw SKI2W SKI2 NUCLEOLAR HELICASE.	DM01537B 21.63 1.878e- 37 79-126 DM01537B 21.63 9.491e-30 916- 963 DM01537A 15.14 3.186e-11 784-804
586	PF00013	KH domain proteins family of RNA binding proteins.	PF00013 5.78 1.450e-09 124-136
587	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 4.409e- 13 262-296
589	BL00478	LIM domain proteins.	BL00478B 14.79 1.643e- 13 261-276 BL00478B 14.79 7.709e-09 321- 336
590	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e- 15 931-948
591	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e- 15 1062-1079
593	PF00628	PHD-finger.	PF00628 15.84 3.455e- 12 424-439
594	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 2.241e- 16 558-576 PR00205A 14.73 9.308e-13 542- 558 PR00205C 13.65 5.304e-12 594-609 PR00205B 11.39 4.273e- 10 336-354
596	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 4.789e- 18 307-338
598	PD01675	GLYCOPROTEIN MAJOR ENVELOPE PROBABLE U3.	PD01675C 19.89 2.330e- 10 55-89
600	BL00242	Integrins alpha chain proteins.	BL00242E 9.03 9.591e- 27 985-1014 BL00242C 16.86 4.115e-26 286- 316 BL00242D 13.57 4.150e-25 357-382 BL00242B 8.13 7.353e- 12 189-199 BL00242D 13.57 3.455e-11 421- 446 BL00242A 13.80

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			5.000e-11 61-73 BL00242D 13.57 4.986e- 10 291-316
601	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 5.610e- 09 198-213
602	PR00278	PANCREATIC HORMONE SIGNATURE	PR00278A 12.43 4.569e- 10 331-348
603	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479C 12.01 3.250e- 12 170-183
604	BL00315	Dehydrins proteins.	BL00315A 9.35 1.672e- 09 424-452
605	BL00415	Synapsins proteins.	BL00415N 4.29 9.794e- 10 295-339
606	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926F 17.75 1.000e-
608	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e-
609	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e-
612	DM01206	CORONAVIRUS NUCLEOCAPSID . PROTEIN .	DM01206B 10.69 7.411e- 10 877-897 DM01206B 10.69 8.027e-10 861- 881 DM01206B 10.69 9.137e-10 873-893 DM01206B 10:69 1.456e- 09 859-879 DM01206B 10.69 1.797e-09 879- 899 DM01206B 10.69 4.076e-09 865-885 DM01206B 10.69 7.038e- 09 898-918 DM01206B 10.69 7.949e-09 871- 891 DM01206B 10.69 8.291e-09 767-787
615	PD02699	PROTEIN DNA-BINDING BINDING DNA.	PD02699A 8.91 2.023e- 28 129-158 PD02699C 24.84 1.000e-27 317- 364 PD02699B 18.28 1.000e-17 158-182
616	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 4.086e- 22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455'
617	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 4.086e- 22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455
618	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 5.143e- 12 531-551 DM01206B 10.69 2.603e-10 535- 555
621	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700B 16.80 3.160e- 21 561-582
622	ВЪ00239	Receptor tyrosine kinase class II proteins.	BL00239F 28.15 3.222e- 10 647-692 BL00239C 18.75 8.304e-10 543- 566
623	PR00407	EUKARYOTIC MOLYBDOPTERIN DOMAIN SIGNATURE	PR00407K 9.94 8.448e- 09 326-339
624	BL00641	Respiratory-chain NADH dehydrogenase 75 Kd	BL00641C 21.10 1.000e- 40 157-202 BL00641E

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		24.37 1.000e-40 255-
		subunit proteins.	308 BL00641F 33.12
			1.000e-40 571-623
			BL00641A 17.15 1.818e-
			37 48-80 BL00641B
			12.62 5.846e-34 113-
			139 BL00641D 13.23
			9.308e-29 216-240
627	PR00103	CAMP-DEPENDENT PROTEIN	PR00103E 17.80 2.500e-
		KINASE SIGNATURE	18 367-380 PR00103B
			13.39 2.080e-14 297-
		1	312 PR00103A 9.59
			2.957e-14 282-297
			PR00103D 10.83 3.077e-
		ļ	12 346-358 PR00103C
			15.68 1.000e-11 334- 344 PR00103B 13.39
	İ		1.450e-11 175-190
	1		PR00103A 9.59 1.720e-
			10 160-175
630	PR00081	GLUCOSE/RIBITOL	PR000B1A 10.53 6.211e-
330	1200001	DEHYDROGENASE FAMILY	16 4-22
		SIGNATURE	
631	PF00651	BTB (also known as BR-	PF00651 15.00 8.500e-
		C/Ttk) domain proteins.	14 37-50
632	DM01206	CORONAVIRUS NUCLEOCAPSID	DM01206B 10.69 2.233e-
		PROTEIN.	10 1324-1344 DM01206B
			10.69 4.822e-10 1276-
	Ì		1296 DMC1206B 10.69
			7.658e-10 1328-1348
1	}		DM01206B 10.69 8.274e-
			10 1280-1300 DM01206B 10.69 4.532e-09 1320~
			1340 DM01206B 10.69
	1	1	7.266e-09 1326-1346
635	BL00107	Protein kinases ATP-	BL00107A 18.39 7.600e-
033	2200107	binding region proteins.	23 145-176 BL00107B
			13.31 2.636e-13 211-
			227
636	BL00657	Fork head domain	BL00657A 19.39 1.545e-
		proteins.	30 101-143 BL00657B
			22.27 7.750e-26 149-
			192
637	BL00107	Protein kinases ATP-	BL00107B 13.31 1.000e-
		binding region proteins.	10 607-623
643	BL00018	EF-hand calcium-binding	BL00018 7.41 4.913e-09
	DD00655	domain proteins. PHD-finger.	199-212 PF00628 15.84 2.350e-
647	PF00628	PHU-IInger.	13 385-400 PF00628
			15.84 3.455e-12 464-
		1	479
648	BL01129	Hypothetical	BL01129E 13.25 4.000e-
***	1 200112	yab0/yceC/sfhB family	25 332-357 BL01129C
		proteins.	25.56 8.200e-23 236-
1		-	279 BL01129B 12.51
	1		6.118e-13 191-212
649	BL01228	Hypothetical cof family	BL01228D 17.44 3.908e-
		proteins.	10 455-480
650	BL00027	'Homeobox' domain	BL00027 26.43 5.684e-
		proteins.	13 771-814
651	BL50002	Src homology 3 (SH3)	BL50002A 14.19 1.750e-
		domain proteins profile.	12 1026-1045
653	PR00253	GAMMA-AMINOBUTYRIC ACID	PR00253A 9.15 4.000e-
		(GABA) RECEPTOR	24 253-274 PR00253C
]	1	SIGNATURE	13.85 8.800e-24 313-
	1		335 PR00253B 13.47
			3.143e-22 279-301 PR00253D 16.68 7.652e-
		İ	*VOOTOTO TO'00 1'0376-

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			20 422-443
654	PD01719	PRECURSOR GLYCOPROTEIN SIGNAL RE.	PD01719A 12.89 4.452e- 11 969-997 PD01719A 12.89 3.961e-10 128-
			156 PD01719A 12.89 7.395e-10 1276-1304 PD01719A 12.89 1.222e-
			09 1220-1248
657	BL00354	HMG-I and HMG-Y DNA-	BL00354C 6.61 8.397e-
037	220033.	binding domain proteins (Ahook).	09 563-578
658	BL00354	HMG-I and HMG-Y DNA- binding domain proteins (Ahook).	BL00354C 6.61 8.397e- 09 580-595
659	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.174e-
			13 539-572 DM00215
			19.43 4.750e-12 549-
		1	582 DM00215 19.43
	1	1	9.824e-11 551-584
			DM00215 19.43 2.929e-
			10 548-581 DM00215
			19.43 4.054e-10 550-
		<u> </u>	583 DM00215 19.43
			5.339e-10 552-585
		•	DM00215 19.43 7.107e-
	770000	WIT OOD TOOURNAD	10 544-577 PR00688I 13.78 9.518e-
660	PR00688	XYLOSE ISOMERASE	09 224-236
661	BL00027	'Homeobox' domain	BL00027 26.43 5.950e-
99T	BB00027	proteins.	23 249-292
662	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e-
002	FROUSCO	CE BOILEN BEGINGONE	10 596-610
663	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e-
			10 596-610
664	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e-
			10 596-610
666	PR00819	CBXX/CFQX SUPERFAMILY	PR00819B 10.83 8.988e-
	D1.0040	SIGNATURE Elongation factor 1	10 704-720 BL50040C 22.62 2.143e-
667	BL50040	gamma chain profile.	16 135-178
668	PR00019	LEUCINE-RICH REPEAT	PR00019B 11.36 1.360e-
000	TROUGES	SIGNATURE	09 139-153 PR00019A
			11.19 1.667e-09 94-108
			PR00019B 11.36 4.600e-
			09 163-177
670	BL00018	EF-hand calcium-binding	BL00018 7.41 3.250e-10
		domain proteins.	681-694 BL00018 7.41
			6.400e-10 717-730
672	PD00131	ATP-BINDING TRANSPORT	PD00131B 34.97 1.000e-
	1	TRANSMEMBR.	34 356-410 PD00131C
			19.59 1.346e-26 504-
		DESTRUCTION DESCRIPTION	542
673	PR00667	RETINAL PIGMENT EPITHELIUM-RETINAL GPCR	PR00667G 15.33 7.557e-
		SIGNATURE	10 106-123
674	PR00320	G-PROTEIN BETA WD-40	PR00320A 16.74 4.857e-
0/1	1100320	REPEAT SIGNATURE	13 593-608 PR00320B
		ADI MILITARE	12.19 4.115e-12 635-
		-	650 PR00320C 13.01
			8.435e-11 717-732
			PR00320C 13.01 2.800e-
			10 635-650 PR00320C
			13.01 6.400e-10 593-
			608 PR00320B 12.19
			3.250e-09 593-608
675	PR00320	G-PROTEIN BETA WD-40	PR00320A 16.74 4.857e-
		REPEAT SIGNATURE	13 572-587 PR00320B
	1	i	12.19 4.115e-12 614-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			629 PR00320C 13.01 8.435e-11 696-711 PR00320C 13.01 2.800e- 10 614-629 PR00320C 13.01 6.400e-10 572-
757			587 PR00320B 12.19 3.250e-09 572-587
676	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 9.667e- 09 249-263
679	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 3.700e- 16 225-236 PF00642 11.59 7.900e-12 187- 198
680	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 8.754e- 10 286-296
681	BL00019	Actinin-type actin- binding domain proteins.	BL00019D 15.33 4.200e- 19 227-257
682	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700D 12.47 4.000e- 09 99-118
687	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.500e- 10 538-553
689	BL01024	Protein phosphatase 2A regulatory subunit PR55 proteins.	BL01024A 10.26 1.000e- 40 22-69 BL01024B 8.91 1.000e-40 86-127 BL01024C 7.80 1.000e- 40 146-185 BL01024D 13.22 1.000e-40 185- 222 BL01024E 11.96 1.000e-40 222-266 BL01024F 9.42 1.000e- 40 266-317 BL01024G 11.09 1.000e-40 317- 349 BL01024H 13.88 1.000e-40 389-442
691	BL00027	'Homeobox' domain proteins.	BL00027 26.43 8.071e- 31 152-195
692	BL00211	ABC transporters family proteins.	BL00211A 12.23 5.050e- 09 45-57
693	BL00211	ABC transporters family proteins.	BL00211A 12.23 5.050e- 09 45-57
694	BL00211	ABC transporters family proteins.	BL00211A 12.23 5.050e- 09 58-70
696	BL00680	Methionine aminopeptidase subfamily 1 proteins.	BL00680 14.37 5.304e- 17 173-195
697	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 3.418e- 11 242-265
698	DM01930	2 kw FINGER SMCX SMCY YDR096W.	DM01930E 15.41 1.367e- 37 170-215 DM01930F 14.16 8.232e-28 267- 303 DM01930B 19.86 9.163e-10 37-71
700	PR00869	DNA-POLYMERASE FAMILY X SIGNATURE	PR00869A 12.80 1.281e- 16 245-263
701	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 2.174e- 10 77-91 PR00048A 10.52 6.870e-10 133- 147 PR00048A 10.52 8.826e-10 105-119 PR00048A 10.52 5.320e- 09 161-175
702	BL00523	Sulfatases proteins.	BL00523E 19.27 2.565e- 25 326-356 BL00523A 13.36 5.050e-16 38-55 BL00523B 8.64 5.909e- 15 86-98 BL00523C 12.64 5.500e-13 137-

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			148 BL00523D 9.89 1.844e-11 290-302 BL00523G 9.46 5.500e- 10 513-523 BL00523F 10.85 6.351e-09 413- 424
703	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.412e- 12 376-390 PR00048B 6.02 1.000e-10 334-344 PR00048B 6.02 1.474e- 09 364-374
707	PD00787	SYNTHASE BIOSYNTHESIS TRANSFERASE.	PD00787A 14.84 8.941e- 14 66-82
708	PR00761	BINDIN PRECURSOR SIGNATURE	PR00761E 14.32 8.500e- 10 822-841
712	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354Y 10.69 4.977e- 38 425-465 DM01354X 13.86 7.300e-34 376- 415 DM01354V 12.97 4.923e-17 311-358 DM01354W 12.64 5.596e- 10 356-376
713	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 7.545e- 27 450-496 BL00039A 18.44 2.537e-18 147- 186 BL00039C 15.63 2.216e-14 280-304 BL00039B 19.19 1.947e- 13 194-220
715	BL00383	Tyrosine specific protein phosphatases proteins.	BL00383E 10.35 4.981e- 10 150-161
717	PF00777	Sialyltransferase family.	PF00777C 18.60 4.035e- 21 106-161
718	DM00031	IMMUNOGLOBULIN V RÉGION.	DM00031A 16.80 3.750e- 39 20-68 DM00031B 15.41 2.688e-28 84-118 DM00031C 12.79 1.300e- 12 131-142
719	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243B 17.54 1.000e- 40 131-172 BL00243C 16.42 1.000e-40 172- 208 BL00243D 24.07 1.000e-40 222-274 BL00243F 22.63 1.000e- 40 314-358 BL00243I 31.77 6.571e-39 607- 650 BL00243E 16.70 3.077e-35 274-304. BL00243G 21.38 3.625e- 34 358-400 BL00243H 17.53 5.235e-29 567- 593 BL00243A 17.61 3.250e-21 63-84 BL00243H 17.53 7.167e- 16 477-503 BL00243H 17.53 2.304e-11 524- 550 BL00243H 17.53 5.304e-11 606-632 BL00243I 31.77 1.380e- 09 610-653
720	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 8.022e- 09 20-36
722	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE	PR00704D 11.05 5.909e- 34 135-161 PR00704F 13.61 7.000e-26 190- 218 PR00704E 12.55 8.071e-26 165-189

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			PR00704B 17.94 2.241e- 23 75-98 PR00704A 14.68 4.094e-19 30-54 PR00704C 11.88 1.871e- 18 99-116
725	PR00194	TROPOMYOSIN SIGNATURE	PR00194A 7.86 7.652e- 09 169-187
726	PR00194	TROPOMYOSIN SIGNATURE	PR00194A 7.86 7.652e- 09 169-187
727	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 2.125e- 13 277-292 PR00320A 16.74 1.310e-11 277- 292 PR00320C 13.01 4.522e-11 323-338 PR00320A 16.74 6.586e- 11 323-338 PR00320B 12.19 4.343e-10 323- 338 PR00320B 12.19 6.914e-10 277-292
731	PR00195	DYNAMIN SIGNATURE	PR00195A 11.94 8.627e- 16 288-307 PR00195E 9.82 3.912e-11 457-474
733	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 9.082e- 10 787-798
738	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039A 18.44 2.565e- 28 26-65 BL00039D 21.67 2.105e-20 338- 384 BL00039C 15.63 9.100e-13 160-184 BL00039B 19.19 9.617e- 11 73-99
739	BL01289	TSC-22 / dip / bun family proteins.	BL01289A 12.18 8.909e- 31 326-353 BL01289B 10.45 9.571e-17 353- 383
742	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 7.078e- 12 41-81
743	BL00965	Phosphomannose isomerase type I proteins.	BL00965C 23.78 1.000e- 40 256-305 BL00965B 17.77 1.600e-25 126- 153 BL00965A 10.57 6.400e-19 94-113
747	BL00021	Kringle domain proteins.	BL00021D 24.56 4.563e- 25 231-273 BL00021B 13.33 5.345e-21 60-78
748	BL00612	Osteonectin domain proteins.	BL00612B 11.35 2.034e- 11 93-126
749	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 6.880e- 10 135-157
752	BL00795	Involucrin proteins.	BL00795C 17.06 6.000e- 11 384-429 BL00795C 17.06 9.444e-11 370- 415
754	BL00051	Ribosomal protein L39e proteins.	BL00051 20.92 1.935e- 16 4-50
755	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 7.723e- 09 171-184
760	BL01020	SAR1 family proteins.	BL01020C 15.35 9.020e- 12 99-150
762	BL00046	Histone H2A proteins.	BL00046 12.95 1.000e- 40 33-88
763	PD02411	PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	PD02411 21.89 9.137e- 10 206-240
764	BL00027	'Homeobox' domain proteins.	BL00027 26.43 8.800e- 29 417-460
767	BL01208	VWFC domain proteins.	BL01208B 15.83 6.063e- 10 309-324 BL01208B 15.83 8.031e-10 165-

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			180 BL01208B 15.83
	<u> </u>		4.162e-09 85-100
770	BL00031	Nuclear hormones	BL00031A 19.55 9.571e-
		receptors DNA-binding region proteins.	32 ·208-241 BL00031B
		region proceins.	22.25 5.500e-27 242- 274
772	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 1.450e-
		RAS SIGNATURE	18 4-26 PR00449E
			13.50 3.520e-14 142-
	ļ		165 PR00449C 17.27
			3.032e-13 44-67
			PR00449D 10.79 8.579e-
		i	14.34 3.455e-11 27-44
773	BL00523	Sulfatases proteins.	BL00523E 19.27 9.333e-
			23 299-329 BL00523A
			13.36 2.200e-13 47-64
			BL00523B 8.64 2.607e-
			13 91-103 BL00523D
ļ			9.89 7.923e-12 224-236 BL00523C 12.64 4.512e-
			10 141-152 BL00523F
	1		10.85 5.821e-10 373-
			384
775	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 7.686e-
		domain proteins.	09 568-585
776	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 7.686e-
777	BL00028	domain proteins. Zinc finger, C2H2 type,	09 621-638 BL00028 16.07 7.686e-
, , ,		domain proteins.	09 595-612
778	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 8.412e-
		region RNP-1 proteins.	11 322-341 BL00030A
	1		14.39 7.000e-10 220-
770	5500000	di Masani di Biyoonii ma	239
779	PR00079	GLUCOSE-6-PHOSPHATE DEHYDROGENASE SIGNATURE	PR00079B 12.98 2.929e- 26 193-222 PR00079E
		DENIDROGENASE SIGNATURE	16.65 4.150e-23 348-
		1	375 PR00079C 8.68
			6.351e-16 246-264
		•	PR00079D 13.51 7.070e-
			16 264-281 PR00079A
			16.12 6.769e-13 169-
781	BL00215	Mitochondrial energy	BL00215A 15.82 9.250e-
		transfer proteins.	17 10-35 BL00215A
		_	15.82 6.000e-16 221-
•			246 BL00215A 15.82
			7.857e-12 108-133
•			BL00215B 10.44 9.526e-
783	PD00289	PROTEIN SH3 DOMAIN	PD00289 9.97 6.276e-09
		REPEAT PRESYNA.	159-173
785	BL00690	DEAH-box subfamily ATP-	BL00690B 13.38 1.000e-
		dependent helicases	12 147-165 BL00690A
		proteins.	6.87 5.320e-10 114-124
	}		BL00690C 7.51 3.189e-
786	PR00449	TRANSFORMING PROTEIN P21	09 218-228 PR00449C 17.27 8.500e-
		RAS SIGNATURE	16 50-73 PR00449A
			13.20 5.235e-14 8-30
			PR00449E 13.50 2.853e-
			11 150-173 PR00449D
			10.79 1.545e-09 111-
788	DM01206	CORONNUT DITE MICH EOGN DOTE	125
,00	2001206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 8.767e- 10 1-21
790	BL00915	Phosphatidylinositol 3-	BL00915C 22.43 9.182e-
	1	and 4-kinases proteins.	39 725-764 BL00915B
·	·		

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			22.78 5.050e-33 633- 671 BL00915D 27.02 1.529e-21 795-831 BL00915A 10.09 1.000e- 13 395-407
791	PR00208	GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE	PRO0208A 12.59 6.294e- 10 120-138 PR00208A 12.59 6.294e-10 121- 139 PR00208A 12.59 6.294e-10 122-140 PR00208A 12.59 6.294e- 10 123-141 PR00208A 12.59 6.294e-10 124- 142 PR00208A 12.59 6.294e-10 125-143 PR00208A 12.59 6.294e- 10 126-144 PR00208A 12.59 6.294e-10 127- 145 PR00208A 12.59 6.294e-10 128-146 PR00208A 12.59 6.294e- 10 129-147 PR00208A 12.59 7.411e-09 130- 148 PR00208A 12.59 7.658e-09 131-149 PR00208A 12.59 7.904e- 09 132-150 PR00208A 12.59 8.274e-09 118- 136 PR00208A 12.59 8.274e-09 119-137
795	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 5.034e- 16 302-320 PR00205A 14.73 1.257e-11 284- 300 PR00205C 13.65 1.333e-11 337-352
796	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 4.000e- 12 196-247 BL00412D 16.54 5.705e-11 197- 248 BL00412D 16.54 7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252
797	BL00021	Kringle domain proteins.	BL00021B 13.33 6.339e-
	BL01052	Calponin family repeat proteins.	BL01052C 18.51 1.000e- 40 87-127 BL01052A 16.12 1.529e-32 3-35 BL01052B 15.31 1.257e- 25 52-78 BL01052D 10.26 5.737e-25 174- 194
800	BL00348	p53 tumor antigen proteins.	BL00348F 23.19 3.714e- 09 197-240
801	BL00309	Vertebrate galactoside- binding lectin proteins.	BL00309C 18.65 1.621e- 09 62-87
802	PR00245	OLFACTORY RECEPTOR SIGNATURE	PRO0245D 10.47 5.224e- 09 187-199
804	PF00774	Dihydropyridine sensitive L-type calcium channel (Beta subuni.	PF00774A 16.47 8.457e- 10 110-156
808	PR00667	RETINAL PIGMENT EPITHELIUM-RETINAL GPCR SIGNATURE	PR00667C 11.71 9.875e- 09 12-28
810	PD02346	PHOTOSYSTEM II PROTEIN PRECURSOR	PD02346F 12.89 4.340e- 09 317-354

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		PHOTOSYNTHESIS.	
811	BL00685	CBF-A/NF-YB subunit proteins.	BL00685B 14.41 6.779e- 14 54-95 BL00685A 11.22 4.798e-13 5-54
812	PR00080	ALCOHOL DEHYDROGENASE SUPERFAMILY SIGNATURE	PR00080A 9.32 9.419e- 10 93-105
813	BL00357	Histone H2B proteins.	BL00357 7.74 1.988e-17
815	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.923e- 15 158-171 PD00066 13.92 5.200e-14 46-59 PD00066 13.92 7.000e- 14 18-31 PD00066 13.92 7.000e-13 130- 143 PD00066 13.92 7.500e-13 214-227 PD00066 13.92 9.000e- 13 102-115 PD00066 13.92 4.429e-12 186- 199 PD00066 13.92 1.783e-11 74-87
816	BL01195	Peptidyl-tRNA hydrolase proteins.	BL01195C 20.12 3.348e- 20 100-139
820	BLC0520	Interleukin-10 family proteins.	BL00520A 6.21 6.471e- 09 1-14
822	BL00972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972A 11.93 8.113e- 09 224-242
825	PR00876	NEMATODE METALLOTHIONEIN SIGNATURE	PR00876B 7.66 2.268e- 10 101-115
829	PD02855	FLAVOPROTEIN PROTEIN DNA/PANTOTHEN.	PD02855A 18.37 4.732e- 28 88-124 PD02855B 8.36 6.478e-09 132-142
830	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405B 11.83 7.000e- 21 44-62 PR00405C 19.41 1.000e-13 65-87 PR00405A 17.71 7.283e- 13 25-45
831	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 1.000e- 09 47-61 PR00019B 11.36 1.720e-09 136- 150 PR00019B 11.36 3.880e-09 44-58
632	PR00011	TYPE III EGP-LIKE SIGNATURE	PR00011B 13.08 3.438e- 16 164-183 PR00011D 14.03 6.850e-16 164- 183 PR00011A 14.06 8.364e-14 164-183 PR00011C 24.25 5.415e- 12 231-260 PR00011D 14.03 9.852e-11 212- 231
834	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 7.000e- 12 232-246
835	PD0030€	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 4.000e- 10 290-304
836	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 7.000e- 12 216-230
837	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 3.898e- 09 78-111
839	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.	PD02784B 26.46 8.302e- 09 73-116
840	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700B 16.80 5.091e- 22 369-390 PR00700D 12.47 5.765e-21 491- 510 PR00700C 13.17 4.750e-14 449-467 PR00700F 11.18 8.500e-

ACCESSION NO.	DESCRIPTION	RESULTS*
		11 538-549 PR00700E 17.57 3.100e-10 522- 538
PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 5.404e- 13 134-153
PD02785	PROTEIN RIBOSOMAL 60S L22 RNA-BINDING HEP.	PD02785B 14.43 1.000e- 40 58-112 PD02785A 15.23 1.915e-28 8-57
BLC0826	MARCKS family proteins.	BL00826C 7.63 6.738e- 09 203-230
BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 4.429e- 10 15-24
	(RING finger), proteins.	BL00518 12.23 1.000e- 08 340-349
	PROTEIN SIGNATURE	PR00308A 5.90 6.506e- 09 12-27
	REGULATION NUCLEAR.	PD02411 21.89 7.000e- 16 246-280
BL00420	Speract receptor repeat proteins domain proteins.	BL00420B 22.67 1.000e- 40 723-778 BL00420B 22.67 1.321e-38 933- 988 BL00420B 22.67 8.457e-28 482-537 BL00420B 22.67 4.500e- 27 587-642 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B 22.67 6.464e-20 377- 432 BL00420B 22.67 2.800e-15 830-885 BL00420C 11.90 1.900e- 13 355-366 BL00420C 11.90 1.900e-12 808- 819 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e- 11 141-152 BL00420C 11.90 5.119e-11 1018- 1029 BL00420C 11.90 7.955e-10 567-578
BL00420	Speract receptor repeat proteins domain proteins.	BL00420B 22.67 1.000e- 40 756-811 BL00420B 22.67 1.321e-38 966- 1021 BL00420B 22.67 8.457e-28 482-537 BL00420B 22.67 4.500e- 27 620-675 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B 22.67 6.464e-20 377- 432 BL00420B 22.67 2.800e-15 863-918 BL00420C 11.90 1.900e- 13 355-366 BL00420C 11.90 1.900e-12 841- 852 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e- 11 141-152 BL00420C 11.90 5.119e-11 1051- 1062 BL00420C 11.90
	PR00109 PD02785 BL00826 BL00518 PR00308 PD02411 BL00420	PRO0109 TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE PD02785 PROTEIN RIBOSOMAL 60S L22 RNA-BINDING HEP. BL00826 MARCKS family proteins. BL00518 Zinc finger, C3HC4 type (RING finger), proteins. PR00308 TYPE I ANTIFREEZE PROTEIN SIGNATURE PD02411 PROTEIN TRANSCRIPTION REGULATION NUCLEAR. BL00420 Speract receptor repeat proteins. BL00420 Speract receptor repeat proteins.

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			7.955e-10 567-578
857	PR00388	3',5'-CYCLIC NUCLEOTIDE CLASS II PHOSPHODIESTERASE SIGNATURE	PR00388A 10.45 2.778e- 09 64-83
859	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 2.929e- 13 37-56 BL00030B 7.03 1.900e-11 167-177 BL00030A 14.39 2.000e- 10 128-147
861	PR00988	URIDINE KINASE SIGNATURE	PR0098BA 6.39 4.250e- 17 23-41 PR0098BC 13.64 8.714e-16 107- 123 PR0098BF 12.23 7.828e-15 198-212 PR0098BE 8.27 9.769e- 12 176-188 PR0098BD 5.95 8.250e-11 163-174 PR0098BB 11.60 4.512e- 10 60-72
863	BL00215	Mitochondrial energy transfer proteins.	BL00215B 10.44 8.071e- 12 41-54
864	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE	PR00775E 8.06 1.000e- 24 198-221 PR00775B 3.52 1.837e-23 107-130 PR00775D 8.91 4.484e- 17 171-189 PR00775A 9.90 8.342e-17 86-107 PR00775C 10.68 9.379e- 17 153-171 PR00775G 10.64 6.850e-15 267- 286 PR00775F 12.76 6.769e-14 249-267
866	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 9.460e~ 09 89-121
867	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 5.596e- 29 14-53
868	BL01287	RNA 3'-terminal phosphate cyclase proteins.	BL01287A 17.95 2.688e- 26 16-48
869	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.464e- 10 304-337
872	BL00046	Histone H2A proteins.	BL00046 12.95 1.000e- 40 30-85
874	BL00188	Biotin-requiring enzymes attachment site proteins.	BL00188 30.29 9.036e- 32 665-711
876	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e- 09 298-315
877	PD02102	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL.	PD02102A 16.74 4.176e- 10 97-141
879	BL01189	Ribosomal protein S12e proteins.	BL01189A 14.27 1.000e- 40 35-71 BL01189B 13.49 1.000e-40 71-125
882	BL00284	Serpins proteins.	BL00284C 28.56 6.400e- 25 62-104 BL00284B 17.99 6.182e-12 35-56
889	BL00216	Sugar transport proteins.	BL00216B 27.64 4.375e- 21 35-85
896	PR00391	PHOSPHATIDYLINOSITOL TRANSFER PROTEIN SIGNATURE	PR00391E 12.50 7.785e- 15 211-231 PR00391B 8.39 1.000e-13 83-104 PR00391D 12.21 9.328e- 13 191-207 PR00391A 7.83 5.390e-11 16-36
897	PR00327	ICE NUCLEATION PROTEIN	PR00327C 6.37 5.247e-

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		SIGNATURE	09 313-328
898	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 7.800e- 26 386-432 BL00039A 18.44 6.674e-16 113- 152 BL00039B 19.19 1.947e-13 153-179 BL00039C 15.63 9.460e- 11 236-260
901	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e- 16 254-267 PD00066 13.92 8.200e-16 282- 295 PD00066 13.92 8.200e-16 310-323 PD00066 13.92 8.200e- 16 366-379 PD00066 13.92 8.200e-16 394- 407 PD00066 13.92 8.200e-14 338-351
902	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 9.321e- 11 6-50
903	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 9.160e- 09 97-111
904	PR00381	KINESIN LIGHT CHAIN SIGNATURE	PRO0381E 8.75 6.586e- 25 335-356 PR00381B 18.17 2.667e-24 204- 224 PR00381A 9.55 2.800e-24 107-125 PR00381C 12.48 4.522e- 24 226-245 PR00381D 13.94 1.084e-22 291- 309 PR00381F 9.13 3.288e-22 370-392 PR00381F 9.13 7.181e- 13 286-308 PR00381E 8.75 4.066e-11 251-272 PR00381E 8.75 7.033e- 11 293-314 PR00381E 8.75 8.364e-10 377-398 PR00381D 13.94 5.230e- 09 333-351 PR00381C 12.48 7.120e-09 310- 329
906	PR00345	STATHMIN FAMILY SIGNATURE	PR00345C 4.54 8.557e- 09 525-549
907	PR00345	STATHMIN FAMILY SIGNATURE	PR00345C 4.54 8.557e- 09 513-537
908	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 9.308e-11 144-155
910	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.800e- 30 48-87
912	BL01104	Ribosomal protein L13e proteins.	BL01104C 15.14 6.000e- 09 364-392
922	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 3.842e-09 500-511
923	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 2.500e- 09 323-338 PR00320C 13.01 5.500e-09 187- 202
924	PD02181	PROTOCHLOROPHYLLIDE REDUCTASE PHOTOSYNT.	PD02181D 12.85 8.609e- 09 36-64
926	BL00678	Actinin-type actin- binding domain proteins. Trp-Asp (WD) repeat	BL00019C 14.66 7.453e- 25 108-144 BL00019B 13.34 6.510e-11 61-84 BL00019D 15.33 9.338e- 11 205-235 BL00019A 12.56 2.373e-10 34-45 BL00678 9.67 9.308e-11
		1 -ap Top (nb) tapade	1

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		proteins proteins.	273-284 BL00678 9.67 1.600e-10 314-325
			BL00678 9.67 7.600e-10 360-371 BL00678 9.67 8.579e-09 206-217
929	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 1.857e- 10 137-146
930	BL01085	Ribulose-phosphate 3-	BL01085D 16.55 4.600e-
		epimerase family proteins.	24 134-165 BL01085B 10.15 5.680e-22 30-52 BL01085E 18.87 8.676e- 20 172-202 BL01085C 21.81 2.038e-14 66-97
931	BL01085	Ribulose-phosphate 3- epimerase family proteins.	BL01085D 16.55 4.600e- 24 152-183 BL01085B 10.15 5.680e-22 30-52 BL01085E 18.87 8.676e- 20 190-220 BL01085C 21.81 2.038e-14 66-97
933	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301A 10.24 6.400e- 09 160-171
936	PF00168	C2 domain proteins.	PF00168C 27.49 4.000e- 12 336-362
937	BL00415	Synapsins proteins.	BL00415N 4.29 9.519e-
940	PR00862	PROLYL OLIGOPEPTIDASE SERINE PROTEASE (S9A) SIGNATURE	PR00862D 16.17 4.086e- 09 63-84
945	BL01230	RNA methyltransferase trmA family proteins.	BL01230B 11.62 2.373e-
948	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 7.429e- 18 52-68 BL00479A
949	BL00678	Trp-Asp (WD) repeat proteins proteins.	19.86 2.200e-13 26-49 BL00678 9.67 1.474e-09 100-111
954	PD01311	PROTEIN OXIDOREDUCTASE NAD INTERGENIC RE.	PD01311A 30.23 5.909e-
955	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 3.250e-
956	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 3.250e- 12 47-60
957	BL00379	CDP-alcohol phosphatidyltransferases proteins.	BL00379 24.64 1.610e- 15 111-148
959	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 1.884e- 10 31-75
960	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 3.438e- 14 110-154
962	BL00061	Short-chain dehydrogenases/reductase s family proteins.	BL00061B 25.79 6.586e- 13 198-236
963	PR00502	MUTT DOMAIN SIGNATURE	PR00502A 15.06 8.200e- 11 210-225
966	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 7.035e-
967	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 1.286e- 12 104-124 DM01206B 10.69 5.299e-11 23-43 DM01206B 10.69 8.274e- 10 73-93 DM01206B 10.69 3.962e-09 108- 128 DM01206B 10.69 5.671e-09 38-58
969	PF01008	Initiation factor 2 subunit.	375-50 9F01008B 25.59 4.724e- 31 417-460 PF01008C 12.25 5.333e-18 506- 526 PF01008A 20.14 5.875e-15 369-390

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970	BL01277	Ribonuclease PH proteins.	BL01277C 10.18 7.648e- 10 112-143 BL01277A 17.39 9.806e-10 40-78
975	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 3.605e- 12 130-145 BL01159 13.85 4.122e-10 171- 186
977	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791C 20.98 2.235e- 09 55-94
978	BL01167	Ribosomal protein L17 proteins.	BL01167B 20.66 8.258e- 19 88-127
979	BL00478	LIM domain proteins.	BL00478B 14.79 9.357e- 13 33-48 BL00478B 14.79 7.250e-12 98-113
980	PR00312	CALSEQUESTRIN SIGNATURE	PR00312E 8.32 3.423e- 36 169-199 PR00312I 15.78 5.286e-35 332- 361 PR00312F 15.06 5.865e-35 199-229 PR00312H 13.31 8.313e- 35 263-291 PR00312J 13.73 5.688e-34 363- 392 PR00312D 9.43 2.636e-33 128-158 PR00312C 15.14 8.839e- 33 92-122 PR00312B 15.08 8.941e-33 62-92 PR00312G 11.11 6.657e- 32 230-258 PR00312A 11.70 6.914e-27 35-59
981	PF00992	Troponin.	PF00992A 16.67 8.816e- 09 414-449
982	PR00299	ALPHA CRYSTALLIN SIGNATURE	PR00299F 13.20 2.367e- 09 127-149
983	BL01150	Respiratory-chain NADH dehydrogenase 20 Kd subunit proteins.	BL01150B 17.16 1.000e- 40 156-202 BL01150A 14.10 8.200e-39 100- 138
986	BL00795	Involucrin proteins.	BL00795C 17.06 7.211e- 14 4-49 BL00795C 17.06 1.778e-11 1-46 BL00795C 17.06 3.407e- 10 14-59 BL00795C 17.06 7.802e-10 2-47 BL00795C 17.06 8.640e- 10 19-64 BL00795C 17.06 7.400e-09 11-56 BL00795C 17.06 7.800e- 09 3-48
987	BL00939	Ribosomal protein Lle proteins.	BL00939F 17.27 5.393e- 09 810-840
988	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e- 11 525-541
989	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e- 11 497-513
994	BL00027	'Homeobox' domain proteins.	BL00027 26.43 2.500e- 25 146-189
997	BL01304	ubiH/COQ6 monooxygenase family proteins.	BL01304A 8.05 3.893e- 11 65-79
998	DM01767	5 TRANSMITTER DOMAIN.	DM01767B 10.07 7.868e- 09 22-39
1000	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926C 16.07 1.750e- 24 73-94 PR00926D 10.53 3.250e-23 126- 145 PR00926F 17.75 6.211e-23 217-240 PR00926E 11.70 6.625e-

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			20 174-193 PR00926B 16.07 2.125e-18 24-39 PR00926A 10.41 1.000e- 15 11-25 PR00926F 17.75 5.565e-09 120- 143
1005	BL00406	Actins proteins.	BL00406B 5.47 1.000e- 40 88-143 BL00406C 6.75 1.000e-40 147-202 BL00406D 12.58 3.700e- 40 270-325 BL00406E 8.44 7.375e-38 327-377 BL00406A 9.95 3.348e- 29 11-46
1006	BL00406	Actins proteins.	BL00406B 5.47 1.000e- 40 88-143 BL00406C 6.75 1.000e-40 147-202 BL00406E 8.44 1.000e- 35 248-298 BL00406A 9.95 3.348e-29 11-46
1007	PR00304	TAILLESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE	PR00304D 11.04 8.714e- 22 384-407 PR00304C 8.69 4.667e-20 98-118 PR00304B 11.60 7.577e- 19 68-87 PR00304A 9.20 3.382e-16 46-63 PR00304E 7.79 6.870e- 13 418-431
1009	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.929e- 32 9-48
1011	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.929e- 32 68-107
1012	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.143e- 10 64-73
1016	PD01168	SYNTHETASE LIGASE PROTEIN ALANYL.	PD01168H 12.08 1.000e- 11 174-194
1018	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930B 33.72 1.391e- 32 261-302 PD00930A 25.62 9.550e-22 157- 183
1022	BL00175	Phosphoglycerate mutase family phosphohistidine proteins.	BL00175A 15.42 5.179e- 12 6-26 BL00175C 23.75 8.062e-10 79-111
1025	PR00305	14-3-3 PROTEIN ZETA SIGNATURE	PR00305D 16.34 1.439e- 10 158-185
1026	BL00353	HMG1/2 proteins.	BL00353B 11.47 2.436e- 18 238-288 BL00353C 14.83 8.844e-11 288- 335
1028	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 1.310e- 33 43-91
1033	PF00580	UvrD/REP helicase.	PF00580A 13.37 4.720e- 09 111-133
1034	PR00413	HALOACID DEHALOGENASE/EPOXIDE HYDROLASE FAMILY SIGNATURE	PR00413E 15.78 3.429e- 09 154-171
1037	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.657e- 09 5-44
1038	PD01796	PROTEIN TRANSMEMBRANE COBALT ZINC CADMIU.	PD01796 15.01 4.259e- 11 55-82
1039	BL00299	Ubiquitin domain proteins.	BL00299 28.84 9.036e- 09 17-69
1040	PR00970	ARGININE ADP- RIBOSYLTRANSFERASE	PR00970A 17.73 6.143e- 20 56-78 PR00970D

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		SIGNATURE	9.96 2.154e-18 154-171 PR00970F 12.30 1.000e- 16 224-241 PR00970G 9.97 9.229e-15 242-258 PR00970B 16.37 1.290e- 13 86-105 PR00970C 11.05 1.643e-11 115- 130 PR00970E 11.23 9.820e-11 202-218
1042	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 2.200e-10 243-254
1043	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 6.786e- 13 114-128 PR00048A 10.52 1.000e-09 172- 186
1045	BL00615	C-type lectin domain proteins.	BL00615A 16.68 1.720e- 11 218-236 BL00615B 12.25 1.857e-10 317- 331
1046	BL01092	Adenylate cyclases class-I proteins.	BL01092N 13.54 8.924e- 10 3-40
1047	BL01216	ATP-citrate lyase / succinyl-CoA ligases family proteins.	BL01216D 21.75 4.316e- 28 314-344 BL01216A 13.91 1.000e-10 97-112
1049	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 7.618e- 12 102-136
1050	BL01073	Ribosomal protein L24e proteins.	BL01073 24.30 1.000e- 40 12-62
1054	BL00571	Amidases proteins.	BL00571 25.69 5.875e- 31 160-212
1055	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 5.235e- 11 98-117 BL00030B 7.03 4.316e-09 137-147
1058	BL00223	Annexins repeat proteins domain proteins.	BL00223C 24.79 8.754e- 23 262-317 BL00223A 15.59 9.478e-14 46-80 BL00223A 15.59 5.557e- 11 118-152
1060	BL00027	'Homeobox' domain proteins.	BL00027 26.43 3.455e- 35 158-201
1064	BL00455	Putative AMP-binding domain proteins.	BL00455 13.31 6.211e- 13 280-296
1065	PR00019 .	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101
1066	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 4.600e- 16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e- 14 172-191 PR00326D 19.09 1.257e-13 217- 236
1071	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870B 18.83 B.518e- 11 164-197
1072	PF00856	SET domain proteins.	PF00856A 26.14 5.976e- 09 350-387
1075	BL01009	Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins.	BL01009D 14.19 4.300e- 20 127-148 BL01009A 13.75 6.586e-13 57-75 BL01009E 13.50 1.439e- 11 159-175
1077	PR00724	CARBOXYPEPTIDASE C SERINE PROTEASE (S10) FAMILY SIGNATURE	PR00724A 10.91 1.000e- 08 366-379
1078	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 1.000e- 12 170-195 BL00215A 15.82 7.529e-10 79-104
1079	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 4.316e-09

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	1.00.	proteins proteins.	298-309
1081	BL00326	Tropomyosins proteins.	BL00326A 14.01 7.398e-
	5200520	Table in the second sec	10 23-57
1094	BL00460	Glutathione peroxidases	BL00460A 28.67 3.204e-
		selenocysteine proteins.	18 57-92 BL00460B
			9.73 6.400e-13 100-118
			BL00460D 16.89 9.143e-
			12 162-182 BL00460C
			14.35 5.500e-09 133-
			156
1095	PD02811	PROTEIN PEPTIDE	PD02811A 20.67 3.017e-
		REDUCTASE MG448 PILB	22 67-105 PD02811B
		FIMBRIA TRAN.	17.07 2.263e-21 118-
			151 PD02811C 13.25
			5.696e-13 154-167
1096	PD02811	PROTEIN PEPTIDE	PD02811A 20.67 3.017e- 22 60-98 PD02811B
		REDUCTASE MG448 PILB FIMBRIA TRAN.	17.07 2.263e-21 111-
		FIMBRIA TRAN.	144 PD02811C 13.25
			5.696e-13 147-160
1097	BL00479	Phorbol esters /	BL00479B 12.57 6.143e-
	200413	diacylglycerol binding	09 200-216
		domain proteins.	1
1105	PF00881	Nitroreductase family.	PF00881A 27.15 9.229e-
			13 111-147
1109	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 3.077e-
		RAS SIGNATURE	10 15-37 PR00449E
			13.50 1.857e-09 185-
	1		208 PR00449D 10.79
			8.364e-09 131-145
1115	PR00405	HIV REV INTERACTING	PR00405B 11.83 5.737e-
		PROTEIN SIGNATURE	20 42-60 PR00405A
			17.71 2.703e-17 23-43
			PR00405C 19.41 6.902e-
			10 63-85
1116	BL00355	HMG14 and HMG17	BL00355 5.97 2.528e-25 20-51
1117	BL00355	proteins. HMG14 and HMG17	BL00355 5.97 2.528e-25
111/	BE00333	proteins.	20-51
1120	BL00107	Protein kinases ATP-	BL00107B 13.31 4.857e-
1120	5500107	binding region proteins.	10 290-306
1123	PR00412	EPOXIDE HYDROLASE	PR00412F 18.76 9.526e-
		SIGNATURE	12 301-324
1125	PR00186	HEMERYTHRIN SIGNATURE	PR00186A 13.62 2.800e-
			09 87-101
1129	BL00170	Cyclophilin-type	BL00170C 18.49 3.077e-
		peptidyl-prolyl cis-	33 84-129 BL00170B
		trans isomerase	1 00 00 6 000 00 00 00
			20.97 6.838e-25 37-77
		signatur.	BL00170A 17.08 3.455e-
		signatur.	BL00170A 17.08 3.455e- 15 10-37
1131	BL00636		BL00170A 17.08 3.455e- 15 10-37 BL00636A 8.07 5.304e-
1131	BL00636	signatur.	BL00170A 17.08 3.455e- 15 10-37 BL00636A 8.07 5.304e- 15 29-46 BL00636B
		signatur. Nt-dnaJ domain proteins.	BL00170A 17.08 3.455e- 15 10-37 BL00636A 8.07 5.304e- 15 29-46 BL00636B 15.11 1.360e-14 59-80
1131	BL00636	Signatur. Nt-dnaJ domain proteins. Trp-Asp (WD) repeat	BL00170A 17.08 3.455e- 15 10-37 BL00636A 8.07 5.304e- 15 29-46 BL00636B 15.11 1.360e-14 59-80 BL00678 9.67 6.211e-09
1132	BL00678	signatur. Nt-dnaJ domain proteins. Trp-Asp (WD) repeat proteins proteins.	BL00170A 17.08 3.455e- 15 10-37 BL00636A 8.07 5.304e- 15 29-46 BL00636B 15.11 1.360e-14 59-80 BL00678 9.67 6.211e-09 29-40
		signatur. Nt-dnaJ domain proteins. Trp-Asp (WD) repeat proteins proteins. Trp-Asp (WD) repeat	BL00170A 17.08 3.455e- 15 10-37 BL00636A 8.07 5.304e- 15 29-46 BL00636B 15.11 1.360e-14 59-80 BL00678 9.67 6.211e-09 29-40 BL00678 9.67 6.211e-09
1132	BL00678	signatur. Nt-dnaJ domain proteins. Trp-Asp (WD) repeat proteins proteins. Trp-Asp (WD) repeat proteins.	BL00170A 17.08 3.455e- 15 10-37 BL00636A 8.07 5.304e- 15 29-46 BL00636B 15.11 1.360e-14 59-80 BL00678 9.67 6.211e-09 29-40 BL00678 9.67 6.211e-09 29-40
1132	BL00678	signatur. Nt-dnaJ domain proteins. Trp-Asp (WD) repeat proteins proteins. Trp-Asp (WD) repeat proteins proteins. Clathrin adaptor	BL00170A 17.08 3.455e- 15 10-37 BL00636A 8.07 5.304e- 15 29-46 BL00636B 15.11 1.360e-14 59-80 BL00678 9.67 6.211e-09 29-40 BL00678 9.67 6.211e-09 29-40 BL00990C 18.78 4.176e-
1132	BL00678	signatur. Nt-dnaJ domain proteins. Trp-Asp (WD) repeat proteins proteins. Trp-Asp (WD) repeat proteins. Clathrin adaptor complexes medium chain	BL00170A 17.08 3.455e- 15 10-37 BL00636A 8.07 5.304e- 15 29-46 BL00636B 15.11 1.360e-14 59-80 BL00678 9.67 6.211e-09 29-40 BL00678 9.67 6.211e-09 29-40 BL00990C 18.78 4.176e- 38 235-269 BL00990A
1132	BL00678	signatur. Nt-dnaJ domain proteins. Trp-Asp (WD) repeat proteins proteins. Trp-Asp (WD) repeat proteins proteins. Clathrin adaptor	BL00170A 17.08 3.455e- 15 10-37 BL00636A 8.07 5.304e- 15 29-46 BL00636B 15.11 1.360e-14 59-80 BL00678 9.67 6.211e-09 29-40 BL00678 9.67 6.211e-09 29-40 BL00990C 18.78 4.176e- 38 235-269 BL00990A 21.44 4.316e-36 94-132
1132	BL00678	signatur. Nt-dnaJ domain proteins. Trp-Asp (WD) repeat proteins proteins. Trp-Asp (WD) repeat proteins. Clathrin adaptor complexes medium chain	BL00170A 17.08 3.455e- 15 10-37 BL00636A 8.07 5.304e- 15 29-46 BL00636B 15.11 1.360e-14 59-80 BL00678 9.67 6.211e-09 29-40 BL00678 9.67 6.211e-09 29-40 BL00990C 18.78 4.176e- 38 235-269 BL00990A 21.44 4.316e-36 94-132 BL00990B 20.15 2.125e-
1132	BL00678	signatur. Nt-dnaJ domain proteins. Trp-Asp (WD) repeat proteins proteins. Trp-Asp (WD) repeat proteins. Clathrin adaptor complexes medium chain	BL00170A 17.08 3.455e- 15 10-37 BL00636A 8.07 5.304e- 15 29-46 BL00636B 15.11 1.360e-14 59-80 BL00678 9.67 6.211e-09 29-40 BL00678 9.67 6.211e-09 29-40 BL00990C 18.78 4.176e- 38 235-269 BL00990A 21.44 4.316e-36 94-132 BL00990B 20.15 2.125e- 27 157-187 BL00990D
1132	BL00678	signatur. Nt-dnaJ domain proteins. Trp-Asp (WD) repeat proteins proteins. Trp-Asp (WD) repeat proteins. Clathrin adaptor complexes medium chain	BL00170A 17.08 3.455e- 15 10-37 BL00636A 8.07 5.304e- 15 29-46 BL00636B 15.11 1.360e-14 59-80 BL00678 9.67 6.211e-09 29-40 BL00678 9.67 6.211e-09 29-40 BL00990C 18.78 4.176e- 38 235-269 BL00990A 21.44 4.316e-36 94-132 BL00990B 20.15 2.125e- 27 157-187 BL00990D 16.13 5.320e-18 403-
1132 1133 1136	BL00678 BL00990	signatur. Nt-dnaJ domain proteins. Trp-Asp (WD) repeat proteins proteins. Trp-Asp (WD) repeat proteins proteins. Clathrin adaptor complexes medium chain proteins.	BL00170A 17.08 3.455e- 15 10-37 BL00636A 8.07 5.304e- 15 29-46 BL00636B 15.11 1.360e-14 59-80 BL00678 9.67 6.211e-09 29-40 BL00678 9.67 6.211e-09 29-40 BL00990C 18.78 4.176e- 38 235-269 BL00990A 21.44 4.316e-36 94-132 BL00990B 20.15 2.125e- 27 157-187 BL00990D 16.13 5.320e-18 403- 422
1132	BL00678	signatur. Nt-dnaJ domain proteins. Trp-Asp (WD) repeat proteins proteins. Trp-Asp (WD) repeat proteins. Clathrin adaptor complexes medium chain proteins.	BL00170A 17.08 3.455e- 15 10-37 BL00636A 8.07 5.304e- 15 29-46 BL00636B 15.11 1.360e-14 59-80 BL00678 9.67 6.211e-09 29-40 BL00678 9.67 6.211e-09 29-40 BL00990C 18.78 4.176e- 38 235-269 BL00990A 21.44 4.316e-36 94-132 BL00990B 20.15 2.125e- 27 157-187 BL00990D 16.13 5.320e-18 403- 422 PR00314B 15.68 8.000e-
1132 1133 1136	BL00678 BL00990	signatur. Nt-dnaJ domain proteins. Trp-Asp (WD) repeat proteins proteins. Trp-Asp (WD) repeat proteins proteins. Clathrin adaptor complexes medium chain proteins.	BL00170A 17.08 3.455e- 15 10-37 BL00636A 8.07 5.304e- 15 29-46 BL00636B 15.11 1.360e-14 59-80 BL00678 9.67 6.211e-09 29-40 BL00678 9.67 6.211e-09 29-40 BL00990C 18.78 4.176e- 38 235-269 BL00990A 21.44 4.316e-36 94-132 BL00990B 20.15 2.125e- 27 157-187 BL00990D 16.13 5.320e-18 403- 422

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			32 159-188 PR00314A
			14.53 1.281e-22 13-34
1139	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 6.364e- 13 13-57
1141	BL00107	Protein kinases ATP-	BL00107A 18.39 4.000e-
		binding region proteins.	19 451-482 BL00107B
		•	13.31 3.077e-12 519-
			535
1148	PR00685	TRANSCRIPTION INITIATION	PR00685A 13.62 4.676e-
1155	PD01652	FACTOR IIB SIGNATURE RECEPTOR CELL NK	PD01652B 8.50 9.396e
1133	PD01832	GLYCOPROTEIN IMMUNOGLOB.	10 522-574 PD01652B
,		CDICOTROLDIN ILLIONOSCOD.	8.50 9.463e-10 740-792
1157	PD02894	HYDROLASE N4- PRECURSOR	PD02894A 21.96 7.873e-
		PROTEIN SIGNAL BE.	28 81-127 PD02894B
	1		13.93 1.188e-27 178-
			211
1159	BL00623	GMC oxidoreductases	BL00623E 15.00 3.531e-
		proteins.	20 391-414 BL00623C
	-		10.86 4.240e-20 155-
1161	DD01933	DNA DROTETH POLYMERACE	176
1161	PD01937	DNA PROTEIN POLYMERASE ENDONUCLEASE DNA	PD01937A 6.68 3.475e-
1162	PD01937	DNA PROTEIN POLYMERASE	PD01937A 6.68 3.475e-
1102	1201337	ENDONUCLEASE DNA	09 221-232
1163	PR00624	HISTONE H5 SIGNATURE	PR00624D 11.94 7.455e-
			10 214-239 PR00624D
			11.94 1.961e-09 312-
			337
1167	BL00226	Intermediate filaments	BL00226B 23.86 7.384e-
		proteins.	09 302-350
1177	BL01032	Protein phosphatase 2C	BL01032G 8.33 1.422e-
1178	PR00320	proteins. G-PROTEIN BETA WD-40	10 34-48 PR00320A 16.74 1.794e-
1176	PR00320	REPEAT SIGNATURE	10 205-220 PR00320C
		NOT BELL GEORGE	13.01 7.840e-10 205-
			220 PR00320B 12.19 .
			8.457e-10 35-50
			PR00320A 16.74 7.146e-
			09 35-50 PR00320B
	DD00454	Toma nowath atamaguna	12.19 9.100e-09 79-94
1180	PR00454	ETS DOMAIN SIGNATURE	PR00454D 10.89 4.150e-
1181	BL00291	Prion protein.	BL00291A 4.49 8.962e-
1101	BBooksi	Prior process.	11 152-187
1184	BL00720	Guanine-nucleotide	BL00720B 16.57 4.103e-
		dissociation stimulators	18 1089-1113
		CDC25 family sign.	
1185	BL00215	Mitochondrial energy	BL00215A 15.82 4.553e-
		transfer proteins.	13 204-229 BL00215A
			15.82 1.429e-12 11-36
			BL00215A 15.82 9.809e-
1187	BL00983	Ly-6 / u-PAR domain	11 104-129 BL00983C 12.69 2.761e-
,	BE00303	proteins.	10 77-93
1188	BL00878	Orn/DAP/Arg	BL00878B 10.95 6.000e-
		decarboxylases family 2	16 189-204 BL00878C
		pyridoxal-P attachment	17.74 8.435e-15 225-
		si.	245 BL00878F 19.67
			3.625e-13 379-402
	1	1	BL00878D 16.56 1.621e-
1101	700000	DOGOTA	09 270-289
1191	PD02939	PROTEIN GLUTATHIONE	PD02939B 10.10 2.723e-
		SYNTHETASE SY.	12 203-220 PD02939C 20.01 1.000e-11 224-
			252
1193	PR00345	STATHMIN FAMILY	PR00345B 7.12 2.800e-
ļ		SIGNATURE	28 72-101 PR00345E
			

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		8.54 7.652e-28 149-174
			PR00345C 4.54 9.100e-
			28 101-125 PR00345D
			10.97 1.964e-24 125-
			149 PR00345A 13.46
			5.645e-16 43-62
1194	PR00345	STATHMIN FAMILY	PR00345B 7.12 2.800e-
	1	SIGNATURE	28 108-137 PR00345E
			8.54 7.652e-28 185-210
			PR00345C 4.54 9.100e-
			28 137-161 PR00345D
			10.97 1.964e-24 161-
			185 PR00345A 13.46
			5.645e-16 79-98
1195	PF00995	Sec1 family.	PF00995B 17.37 1.120e-
			13 224-264
1196	BL00982	Bacterial-type phytoene	BL00982A 18.41 6.738e-
		dehydrogenase proteins.	11 15-47
1197	BL01298	Dihydrodipicolinate	BL01298A 13.90 5.959e-
		reductase proteins.	09 51-73
1203	BL00061	Short-chain	BL00061B 25.79 1.000e-
		dehydrogenases/reductase	14 152-190
		s family proteins.	
1204	PR00118	BETA-LACTAMASE CLASS A	PR00118F 16.42 9.386e-
		SIGNATURE	09 213-229
1206	BL01183	ubiE/COQ5	BL01183B 21.31 1.429e-
		methyltransferase family	37 184-229 BL01183D
		proteins.	27.71 8.535e-27 264-
	}		307 BL01183A 13.25
			3.250e-23 51-73
			BL01183C 10.77 5.295e-
			09 246-258
1208	BL00979	G-protein coupled	BL00979L 20.63 2.485e-
		receptors family 3	09 105-146
		proteins.	
1209	PFC0023	Ank repeat proteins.	PF00023A 16.03 4.857e-
	1		11 49-65 PF00023B
			14.20 1.818e-09 45-55
1212	PR00048	C2H2-TYPE ZINC FINGER	PR00048A 10.52 7.750e-
	1	SIGNATURE	14 227-241 PR00048A
			10.52 4.316e-11 199-
1			213
1213	PR00450	RECOVERIN FAMILY	PR00450C 12.22 1.720e-
		SIGNATURE	10 20-42 PR00450C
	1	1	12.22 3.506e-09 56-78
i			PR00450D 16.58 6.769e-
}			09 44-64
1216	BL00412	Neuromodulin (GAP-43)	BL00412D 16.54 5.598e-
ł		proteins.	10 179-230
1219	PR00456	RIBOSOMAL PROTEIN P2	PR00456E 3.06 5.348e-
		SIGNATURE	11 249-264
1222	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 7.231e-
		METAL-BINDI.	15 295-308 PD00066
	Ì		13.92 7.231e-15 406-
			419 PD00066 13.92
			2.286e-12 378-391
			PD00066 13.92 7.857e-
			12 434-447 PD00066
1			13.92 3.348e-11 350-
J	1		363
	DICORCO	G-protein gamma subunit	BL50058 27.23 1.000e-
1223	BL50058	1	40 13-61
1223	BUSUUSA	profile.	
1223	BL00412	Profile. Neuromodulin (GAP-43)	BL00412D 16.54 8.439e-
			BL00412D 16.54 8.439e- 09 279-330
		Neuromodulin (GAP-43)	BL00412D 16.54 8.439e- 09 279-330 BL00437A 18.82 1.000e-
1226	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 8.439e- 09 279-330 BL00437A 18.82 1.000e- 40 49-101 BL00437B
1226	BL00412	Neuromodulin (GAP-43) proteins. Catalase proximal heme-	BL00412D 16.54 8.439e- 09 279-330 BL00437A 18.82 1.000e-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		1.000e-40 190-239
			BL00437D 25.72 1.000e-
			40 248-301 BL00437E
			23.95 1.000e-40 327-
			379
1230	BL01160	Kinesin light chain	BL01160B 19.54 8.297e-
		repeat proteins.	10 6-60
1231	PR00735	GLYCOSYL HYDROLASE	PR00735A 11.19 6.857e-
		FAMILY 8 SIGNATURE	09 391-405
1232	PR00497	NEUTROPHIL CYTOSOL	PR00497A 6.92 5.553e-
		FACTOR P40 SIGNATURE	10 158-176
1233	PR00497	NEUTROPHIL CYTOSOL	PR00497A 6.92 5.553e-
		FACTOR P40 SIGNATURE	10 158-176 BL00866B 36.29 2.776e-
1235	BL00866	Carbamoyl-phosphate	09 75-121
		synthase subdomain proteins.	09 /5-121
1000	BL00027	'Homeobox' domain	BL00027 26.43 1.818e-
1237	BL00027	proteins.	21 36-79
1243	PR00403	WW DOMAIN SIGNATURE	PR00403B 12.19 1.184e-
1243	PRODEOS	WW BOIRIEN GIGINITONS	11 10-25
1246	PD01168	SYNTHETASE LIGASE	PD01168L 9.47 2.837e-
2230	1 202200	PROTEIN ALANYL.	10 31-46 PD01168L
			9.47 4.490e-10 174-189
			PD01168L 9.47 7.612e-
			10 183-198
1249	BL00018	EF-hand calcium-binding	BL00018 7.41 2.800e-10
		domain proteins.	183-196
1254	BL00183	Ubiquitin-conjugating	BL00183 28.97 2.440e-
		enzymes proteins.	36 96-144
1255	BL01115	GTP-binding nuclear	BL01115A 10.22 5.670e-
		protein ran proteins.	11 8-52 BL00373C 10.35 3.348e-
1256	BL00373	Phosphoribosylglycinamid e formyltransferase	12 143-156
	[proteins.	12 143-130
1258	PR00011	TYPE III EGF-LIKE	PR00011B 13.08 3.217e-
1256	PROUUTI	SIGNATURE	10 174-193
1259	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 8.286e-
1237		(RING finger), proteins.	10 31-40
1261	PR00070	DIHYDROFOLATE REDUCTASE	PR00070D 11.63 1.000e-
		SIGNATURE	15 112-127 PR00070C
İ		ł	13.09 9.500e-15 51-63
		Ì	PR00070A 12.92 5.500e-
			12 16-27
			DT 004602 00 00 6 430-
1262	BL00462	Gamma-	BL00462A 20.89 6.438e-
1262	BL00462	glutamyltranspeptidase	24 140-183 BL00462B
1262	BL00462		I .
1262	BL00462	glutamyltranspeptidase	24 140-183 BL00462B 17.88 5.500e-20 230-
		glutamyltranspeptidase proteins.	24 140-183 BL00462B 17.88 5.500e-20 230- 267 BL00462C 27.41
1263	BL00462	glutamyltranspeptidase	24 140-183 BL00462B 17.88 5.500e-20 230- 267 BL00462C 27.41 2.023e-11 292-347
		glutamyltranspeptidase proteins. Myc-type, 'helix-loop-	24 140-183 BL00462B 17.88 5.500e-20 230- 267 BL00462C 27.41 2.023e-11 292-347 BL00038B 16.97 9.455e-
		glutamyltranspeptidase proteins. Myc-type, 'helix-loop-helix' dimerization	24 140-183 BL00462B 17.88 5.500e-20 230- 267 BL00462C 27.41 2.023e-11 292-347 BL00038B 16.97 9.455e-
1263	BL00038	glutamyltranspeptidase proteins. Myc-type, 'helix-loop-helix' dimerization domain proteins. GTP-binding nuclear protein ran proteins.	24 140-183 BL00462B 17.88 5.500e-20 230- 267 BL00462C 27.41 2.023e-11 292-347 BL00038B 16.97 9.455e- 11 62-83 BL01115A 10.22 5.670e- 12 17-61
1263	BL00038	glutamyltranspeptidase proteins. Myc-type, 'helix-loop-helix' dimerization domain proteins. GTP-binding nuclear	24 140-183 BL00462B 17.88 5.500e-20 230- 267 BL00462C 27.41 2.023e-11 292-347 BL00038B 16.97 9.455e- 11 62-83 BL01115A 10.22 5.670e- 12 17-61 PR00837C 17.21 2.714e-
1263	BL00038	glutamyltranspeptidase proteins. Myc-type, 'helix-loop-helix' dimerization domain proteins. GTP-binding nuclear protein ran proteins.	24 140-183 BL00462B 17.88 5.500e-20 230- 267 BL00462C 27.41 2.023e-11 292-347 BL00038B 16.97 9.455e- 11 62-83 BL01115A 10.22 5.670e- 12 17-61 PR00837C 17.21 2.714e- 18 165-182 PR00837A
1263	BL00038	glutamyltranspeptidase proteins. Myc-type, 'helix-loop-helix' dimerization domain proteins. GTP-binding nuclear protein ran proteins. ALLERGEN VS/TPX-1 FAMILY	24 140-183 BL00462B 17.88 5.500e-20 230- 267 BL00462C 27.41 2.023e-11 292-347 BL00038B 16.97 9.455e- 11 62-83 BL01115A 10.22 5.670e- 12 17-61 PR00837C 17.21 2.714e- 18 165-182 PR00837A 14.77 4.512e-12 86-105
1263	BL00038	glutamyltranspeptidase proteins. Myc-type, 'helix-loop-helix' dimerization domain proteins. GTP-binding nuclear protein ran proteins. ALLERGEN VS/TPX-1 FAMILY	24 140-183 BL00462B 17.88 5.500e-20 230- 267 BL00462C 27.41 2.023e-11 292-347 BL00038B 16.97 9.455e- 11 62-83 BL01115A 10.22 5.670e- 12 17-61 PR00837C 17.21 2.714e- 18 165-182 PR00837A 14.77 4.512e-12 86-105 PR00837D 11.12 7.577e-
1263 1264 1266	BL00038 BL01115 PR00837	glutamyltranspeptidase proteins. Myc-type, 'helix-loop-helix' dimerization domain proteins. GTP-binding nuclear protein ran proteins. ALLERGEN V5/TPX-1 FAMILY SIGNATURE	24 140-183 BL00462B 17.88 5.500e-20 230- 267 BL00462C 27.41 2.023e-11 292-347 BL00038B 16.97 9.455e- 11 62-83 BL01115A 10.22 5.670e- 12 17-61 PR00837C 17.21 2.714e- 18 165-182 PR00837A 14.77 4.512e-12 86-105 PR00837D 11.12 7.577e- 12 201-215
1263	BL00038	glutamyltranspeptidase proteins. Myc-type, 'helix-loop-helix' dimerization domain proteins. GTP-binding nuclear protein ran proteins. ALLERGEN VS/TPX-1 FAMILY SIGNATURE TRANSFORMING PROTEIN P21	24 140-183 BL00462B 17.88 5.500e-20 230- 267 BL00462C 27.41 2.023e-11 292-347 BL00038B 16.97 9.455e- 11 62-83 BL01115A 10.22 5.670e- 12 17-61 PR00837C 17.21 2.714e- 18 165-182 PR00837A 14.77 4.512e-12 86-105 PR00837D 11.12 7.577e- 12 201-215 PR00449C 17.27 9.308e-
1263 1264 1266	BL00038 BL01115 PR00837	glutamyltranspeptidase proteins. Myc-type, 'helix-loop-helix' dimerization domain proteins. GTP-binding nuclear protein ran proteins. ALLERGEN V5/TPX-1 FAMILY SIGNATURE	24 140-183 BL00462B 17.88 5.500e-20 230- 267 BL00462C 27.41 2.023e-11 292-347 BL00038B 16.97 9.455e- 11 62-83 BL01115A 10.22 5.670e- 12 17-61 PR00837C 17.21 2.714e- 18 165-182 PR00837A 14.77 4.512e-12 86-105 PR00837D 11.12 7.577e- 12 201-215 PR00449C 17.27 9.308e- 22 40-63 PR00449B
1263 1264 1266	BL00038 BL01115 PR00837	glutamyltranspeptidase proteins. Myc-type, 'helix-loop-helix' dimerization domain proteins. GTP-binding nuclear protein ran proteins. ALLERGEN VS/TPX-1 FAMILY SIGNATURE TRANSFORMING PROTEIN P21	24 140-183 BL00462B 17.88 5.500e-20 230- 267 BL00462C 27.41 2.023e-11 292-347 BL00038B 16.97 9.455e- 11 62-83 BL01115A 10.22 5.670e- 12 17-61 PR00837C 17.21 2.714e- 18 165-182 PR00837A 14.77 4.512e-12 86-105 PR00837D 11.12 7.577e- 12 201-215 PR00449C 17.27 9.308e- 22 40-63 PR00449B 13.50 1.000e-16 137-
1263 1264 1266	BL00038 BL01115 PR00837	glutamyltranspeptidase proteins. Myc-type, 'helix-loop-helix' dimerization domain proteins. GTP-binding nuclear protein ran proteins. ALLERGEN VS/TPX-1 FAMILY SIGNATURE TRANSFORMING PROTEIN P21	24 140-183 BL00462B 17.88 5.500e-20 230- 267 BL00462C 27.41 2.023e-11 292-347 BL00038B 16.97 9.455e- 11 62-83 BL01115A 10.22 5.670e- 12 17-61 PR00837C 17.21 2.714e- 18 165-182 PR00837A 14.77 4.512e-12 86-105 PR00837D 11.12 7.577e- 12 201-215 PR00449C 17.27 9.308e- 22 40-63 PR00449B 13.50 1.000e-16 137- 160 PR00449D 10.79
1263 1264 1266	BL00038 BL01115 PR00837 PR00449	glutamyltranspeptidase proteins. Myc-type, 'helix-loophelix' dimerization domain proteins. GTP-binding nuclear protein ran proteins. ALLERGEN VS/TPX-1 FAMILY SIGNATURE TRANSFORMING PROTEIN P21 RAS SIGNATURE	24 140-183 BL00462B 17.88 5.500e-20 230- 267 BL00462C 27.41 2.023e-11 292-347 BL00038B 16.97 9.455e- 11 62-83 BL01115A 10.22 5.670e- 12 17-61 PR00837C 17.21 2.714e- 18 165-182 PR00837A 14.77 4.512e-12 86-105 PR00837D 11.12 7.577e- 12 201-215 PR00449C 17.27 9.308e- 22 40-63 PR00449B 13.50 1.000e-16 137- 160 PR00449D 10.79 3.520e-11 102-116
1263 1264 1266	BL00038 BL01115 PR00837	glutamyltranspeptidase proteins. Myc-type, 'helix-loophelix' dimerization domain proteins. GTP-binding nuclear protein ran proteins. ALLERGEN V5/TPX-1 FAMILY SIGNATURE TRANSFORMING PROTEIN P21 RAS SIGNATURE	24 140-183 BL00462B 17.88 5.500e-20 230- 267 BL00462C 27.41 2.023e-11 292-347 BL00038B 16.97 9.455e- 11 62-83 BL01115A 10.22 5.670e- 12 17-61 PR00837C 17.21 2.714e- 18 165-182 PR00837A 14.77 4.512e-12 86-105 PR00837D 11.12 7.577e- 12 201-215 PR00449C 17.27 9.308e- 22 40-63 PR00449B 13.50 1.000e-16 137- 160 PR00449D 10.79 3.520e-11 102-116 BL00276A 8.87 1.500e-
1264 1266 1269	BL00038 BL01115 PR00837 PR00449	glutamyltranspeptidase proteins. Myc-type, 'helix-loop-helix' dimerization domain proteins. GTP-binding nuclear protein ran proteins. ALLERGEN VS/TPX-1 FAMILY SIGNATURE TRANSFORMING PROTEIN P21 RAS SIGNATURE Channel forming colicins proteins.	24 140-183 BL00462B 17.88 5.500e-20 230- 267 BL00462C 27.41 2.023e-11 292-347 BL00038B 16.97 9.455e- 11 62-83 BL01115A 10.22 5.670e- 12 17-61 PR00837C 17.21 2.714e- 18 165-182 PR00837A 14.77 4.512e-12 86-105 PR00837D 11.12 7.577e- 12 201-215 PR00449C 17.27 9.308e- 22 40-63 PR00449B 13.50 1.000e-16 137- 160 PR00449D 10.79 3.520e-11 102-116 BL00276A 8.87 1.500e- 09 17-29
1263 1264 1266	BL00038 BL01115 PR00837 PR00449	glutamyltranspeptidase proteins. Myc-type, 'helix-loophelix' dimerization domain proteins. GTP-binding nuclear protein ran proteins. ALLERGEN V5/TPX-1 FAMILY SIGNATURE TRANSFORMING PROTEIN P21 RAS SIGNATURE	24 140-183 BL00462B 17.88 5.500e-20 230- 267 BL00462C 27.41 2.023e-11 292-347 BL00038B 16.97 9.455e- 11 62-83 BL01115A 10.22 5.670e- 12 17-61 PR00837C 17.21 2.714e- 18 165-182 PR00837A 14.77 4.512e-12 86-105 PR00837D 11.12 7.577e- 12 201-215 PR00449C 17.27 9.308e- 22 40-63 PR00449B 13.50 1.000e-16 137- 160 PR00449D 10.79 3.520e-11 102-116 BL00276A 8.87 1.500e-

SEQ ID NO		DESCRIPTION	RESULTS*
	NO.		
		SIGNATURE	12 119-135 PR00412C 11.30 1.857e-11 165- 179 PR00412A 13.23
1277	PF00756	Putative esterase.	3.400e-11 100-119 PF00756C 14.12 9.538e-
1279	BL00134	Serine proteases,	10 127-157 BL00134A 11.96 9.325e-
	2200231	trypsin family, histidine proteins.	13 128-145
1280	BL01220	Phosphatidylethanolamine -binding protein family proteins.	BL01220C 14.75 9.348e- 15 248-276
1285	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 2.286e- 10 33-42
1287	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 7.182e- 11 288-343
1292	PR00802	SERUM ALBUMIN FAMILY SIGNATURE	PR00802B 16.51 1.610e-
1297	PR00716	M-PHASE INDUCER PHOSPHATASE SIGNATURE	PR00716C 17.65 5.696e-
1298	BL00478	LIM domain proteins.	BL00478B 14.79 6.478e- 14 268-283
1301	BL00127	Pancreatic ribonuclease family proteins.	BL00127C 31.49 3.571e- 28 82-126 BL00127B 26.57 8.800e-28 23-68
1302	PR00637	TYPE 3 BOMBESIN RECEPTOR SIGNATURE	PR00637E 11.27 4.250e- 09 290-306
1307	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 5.500e- 17 13-38 BL00215A 15.82 1.000e-16 226- 251 BL00215A 15.82
1308	PR00898	VASOPRESSIN V2 RECEPTOR SIGNATURE	2.658e-13 107-132 PR00898H 11.34 4.682e- 09 552-572
1309	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301B 5.49 2.731e- 09 390-401
1310	BL00983	Ly-6 / u-PAR domain proteins.	BL00983C 12.69 9.654e- 13 73-89 BL00983B 8.19 3.132e-09 12-22
1313	BL00194	Thioredoxin family proteins.	BL00194 12.16 1.900e- 11 15-28
1314	BL00594	Aromatic amino acids permeases proteins.	BL00594A 16.75 8.969e-
1316	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134A 11.96 9.325e- 13 128-145
1320	BL00783	Ribosomal protein L13 proteins.	BL00783C 22.43 6.559e- 24 87-117 BL00783A 14.55 1.600e-19 8-33 BL00783B 12.76 3.500e- 12 74-86
1327	PF00514	Armadillo/beta-catenin- like repeat proteins.	PF00514A 31.30 7.268e- 11 82-120
1329	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 6.294e- 11 129-148 BL00030B 7.03 4.789e-09 168-178
1331	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	PR00497A 6.92 7.239e- 09 25-43
1332	PR00161	NICKEL-DEPENDENT HYDROGENASE/B-TYPE CYTOCHROME SIGNATURE	PR00161C 9.51 4.930e- 09 317-337
1333	PD01066	PROTRIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 6.769e- 33 10-49
1336	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700D 12.47 2.200e- 09 262-281
1337	PR00700	PROTEIN TYROSINE	PR00700D 12.47 2.200e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		PHOSPHATASE SIGNATURE	09 211-230
1340	PR00860	VERTEBRATE METALLOTHIONEIN SIGNATURE	PR00860A 5.46 5.034e- 13 5-18
1341	BL00893	mutT domain proteins.	BL00893 18.99 6.750e- 16 46-71
1343	BL01282	BIR repeat proteins.	BL01282B 30.49 5.974e- 21 383-422
1344	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 8.313e- 09 417-427
1345	BL00923	Aspartate and glutamate racemases proteins.	BL00923B 11.41 5.935e- 10 135-146
1348	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 7.231e- 13 44-57
1350	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 3.571e- 32 416-445 PR00193C 12.60 6.318e-31 179- 207 PR00193B 11.69 3.571e-24 133-159 PR00193E 19.47 9.069e- 22 470-499 PR00193A 15.41 1.783e-20 77-97
1352	PR00447	NATURAL RESISTANCE- ASSOCIATED MACROPHAGE PROTEIN SIGNATURE	PR00447E 9.73 1.554e- 15 299-319 PR00447D 13.54 3.408e-15 200- 224 PR00447A 12.73 6.357e-11 97-124 PR00447G 6.69 9.877e- 10 353-373
1353	BL00303	S-100/ICaBP type calcium	BL00303A 21.77 6.667e-
r		binding protein.	26 45-82 BL00303B 26.15 1.000e-24 93-130
1355	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 5.950e- 29 375-421 BL00039A 18.44 7.136e-29 99-138 BL00039C 15.63 4.000e- 18 225-249 BL00039B 19.19 3.182e-14 141- 167
1357	PF00615	Regulator of G protein signalling domain proteins.	PF00615B 16.25 2.216e- 12 84-101 PF00615C 10.06 8.412e-12 162- 176
1360	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.234e- 29 10-49
1361	PR00925	NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY SIGNATURE	PR00925A 5.47 5.091e- 18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D 6.56 1.857e-10 76-87
1362	BL01272	Glucokinase regulatory protein family proteins.	BL01272B 19.61 6.870e- 30 136-171 BL01272C 11.68 3.314e-25 249- 274 BL01272A 6.49 1.231e-18 99-117
1363	BL01272	Glucokinase regulatory protein family proteins.	BL01272B 19.61 6.870e- 30 113-148 BL01272C 11.68 3.314e-25 226- 251 BL01272A 6.49 1.231e-18 76-94
1364	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.304e- 09 167-177
1368	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 1.592e- 09 76-96
1370	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 1.794e-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
SEQ ID NO:	NO.	DESCRIPTION	, Addodie
	1		10 1-19
1371	BL00242	Integrins alpha chain	BL00242B 8.13 8.615e-
	i	proteins.	09 469-479
1372	PR00625	DNAJ PROTEIN FAMILY	PR00625B 13.48 7.353e-
		SIGNATURE	19 46-67 PR00625A
			12.84 1.391e-16 14-34
1373	BL00434	HSF-type DNA-binding	BL00434C 23.85 3.778e- 09 90-130
1111	PR00962	domain proteins. LETHAL(2) GIANT LARVAE	PR00962C 8.00 6.337e-
1374	PR00962	PROTEIN SIGNATURE	09 505-526
1375	PD02475	MUCIN EPITHELIAL TUMOR-	PD02475A 23.18 8.552e-
1373	1002475	ASSOCIATE.	10 1111-1150
1376	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 9.571e-
		ZINC-FINGER METAL-	32 24-63
		BINDING NU.	
1380	BL00194	Thioredoxin family	BL00194 12.16 8.333e-
		proteins.	12 48-61
1381	DM01970	0 kw ZK632.12 YDR313C	DM01970B 8.60 1.458e-
		ENDOSOMAL III.	15 1123-1136
1383	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 7.600e-10 243-254
1384	BL00678	proteins proteins. Trp-Asp (WD) repeat	BL00678 9.67 7.600e-10
1384	מ/ פטטעמ	proteins proteins.	271-282
1385	BL00303	S-100/ICaBP type calcium	BL00303B 26.15 6.203e-
2303	1 550000	binding protein.	10 95-132
1386	BL01160	Kinesin light chain	BL01160B 19.54 5.042e-
		repeat proteins.	09 1574-1628
1387	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 1.000e-
		(RING finger), proteins.	11 52-61
1389	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 3.600e-
		ZINC-FINGER METAL-	30 10-49
	7701066	BINDING NU.	PD01066 19.43 3.512e-
1390	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-	31 32-71
	ļ	BINDING NU.	31 32-71
1392	PR00308	TYPE I ANTIFREEZE	PR00308C 3.83 9.723e-
13,72	1 Koosoo	PROTEIN SIGNATURE	10 127-137
1393	PR00380	KINESIN HEAVY CHAIN	PR00380A 14.18 9.625e-
		SIGNATURE	25 88-110 PR00380D
			9.93 2.406e-20 304-326
			PR00380B 12.64 4.414e-
			16 208-226 PR00380C 13:18 6.538e-16 243-
		1	262
1394	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 3.400e-
2373	1200000	METAL-BINDI.	14 462-475 PD00066
	1		13.92 8.800e-14 348-
			361 PD00066 13.92
			9.571e-12 405-418 ·
	1		PD00066 13.92 6.087e-
			11 490-503 PD00066
			13.92 8.043e-11 320- 333
1398	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 6.786e-
1376	FD01000	ZINC-FINGER METAL-	32 10-49
	10-	BINDING NU.	
1400	DM01206	CORONAVIRUS NUCLEOCAPSID	DM01206B 10.69 7.038e-
		PROTEIN.	09 270-290
1406	PD00930	PROTEIN GTPASE DOMAIN	PD00930A 25.62 7.324e-
		ACTIVATION.	15 363-389
1407	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 7.500e-
		region RNP-1 proteins.	10 457-476
1408	PR00019	LEUCINE-RICH REPEAT	PR00019A 11.19 9.550e-
1		SIGNATURE	11 179-193 PR00019A 11.19 8.826e-10 228-
		.	242 PR00019B 11.36
]			1.360e-09 199-213
1			PR00019B 11.36 4.960e-
L			

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			09 176-190
1409	PR00510	NEBULIN SIGNATURE	PROC510A 9.09 4.150e- 12 182-202 PRO0510B 12.96 8.767e-12 210- 230 PRO0510F 9.88 8.172e-10 58-75 PRO0510D 9.21 2.367e- 09 251-267
1410	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.696e- 09 31-44
1412	BL00358	Ribosomal protein L5 proteins.	BL00358B 22.76 1.000e- 40 57-103 BL00358C 13.75 6.087e-14 122- 136 BL00358D 14.26 5.500e-13 143-158 BL00358A 13.06 1.931e- 11 33-44
1414	BL00282	Kazal serine protease inhibitors family proteins.	BL00282 16.88 7.338e- 10 511-534
1415	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 4.300e- 29 40-77
1417	PR00681	RIBOSOMAL PROTEIN SI SIGNATURE	PR00681G 12.54 2.149e- 09 38-60
1418	DM00973	3 kw RESISTANCE BENOMYL YLL028W CYCLOHEXIMIDE.	DM00973A 21.17 1.462e- 09 171-208
1419	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 1.571e- 09 428-443
1420	PD01941	TRANSMEMBRANE COTRANSPORTER SYMP.	PD01941A 14.81 1.000e- 40 142-196 PD01941B 15.02 7.049e-30 400- 447 PD01941E 15.92 2.475e-20 817-864 PD01941C 19.96 3.118e- 19 488-543 PD01941D 27.18 9.614e-18 641- 690 PD01941F 28.52 5.382e-15 1038-1093
1422	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 8.043e- 12 199-217
1423	PR00209	ALPHA/BETA GLIADIN FAMILY SIGNATURE	PR00209B 4.88 6.318e- 11 1009-1028
1424	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258
1425	PF00628	PHD-finger.	PF00628 15.84 3.045e- 12 330-345
1426	PF00628	PHD-finger.	PF00628 15.84 3.045e- 12 377-392
1427	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405B 11.83 5.114e- 16 281-299 PR00405A 17.71 4.306e-14 262- 282
1428	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 5.219e- 34 147-193
1429	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 8.920e- 10 577-592
1430	PR00378	INOSITOL PHOSPHATASE SIGNATURE	PR00378D 16.86 7.563e- 12 295-314 PR00378B 13.80 8.650e-10 166- 186
1431	PR00928	GRAVES DISEASE CARRIER	PR00928B 13.53 3.769e-

PROTEIN SIGNATURE 10 103-124	SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1433 BL0113 Ciq domain proteins		1.0.	PROTEIN SIGNATURE	10 103-124
15 14-5	1433	BL01113		1
13.18 7.000e-12 82-102 13.4			Tag assumed process.	
BETA G-PROTEIN FRO0319 BETA G-PROTEIN (TRANSUCIN) SIGNATURE INSTITUTE				
TRANSDUCIN SIGNATURE 10 115-150	1434	PR00319	BETA G-PROTEIN	
1438 BL00290 Immunglobulins and major histocompatibility complex proteins BL00290E 13.17 2.500e- 09.250-268 BL00290N 20.89 4.000e-09.188- 21.000e-09.188- 21.000e-09.188- 21.000e-09.188- 21.000e-09.188- 21.000e-09.188- 21.000e-09.188- 21.000e-09.188- 21.000e-09.188- 21.000e-09.188- 21.000e-09.188- 21.000e-09.188- 21.000e-09.188- 21.000e-09.188- 22.000e-09.188-			(TRANSDUCIN) SIGNATURE	
1438 BL00290 Immunglobulins and major histocompatibility complex proteins BL00290E 13.17 2.500e- 09.250-268 BL00290N 20.89 4.000e-09.188- 21.000e-09.188- 21.000e-09.188- 21.000e-09.188- 21.000e-09.188- 21.000e-09.188- 21.000e-09.188- 21.000e-09.188- 21.000e-09.188- 21.000e-09.188- 21.000e-09.188- 21.000e-09.188- 21.000e-09.188- 21.000e-09.188- 22.000e-09.188-	1436	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 1.000e-
major histocompatibility 250-268 BL00290A 20.89 4.000e-09 188-21 21.89 4.000e-09 188-21 21.89 4.000e-09 188-21 21.89 4.000e-09 188-21 21.89 4.000e-09 188-21 21.89 4.000e-09 38-52 21.89 4.000e-09 38-52 21.89 4.000e-09 38-52 21.89 4.000e-09 38-52 21.89 4.000e-09 38-52 21.89 4.000e-09 38-102 2	\setminus		region RNP-1 proteins.	
major histocompatibility 250-268 BL00290A 20.89 4.000e-09 188-21 21.89 4.000e-09 188-21 21.89 4.000e-09 188-21 21.89 4.000e-09 188-21 21.89 4.000e-09 188-21 21.89 4.000e-09 38-52 21.89 4.000e-09 38-52 21.89 4.000e-09 38-52 21.89 4.000e-09 38-52 21.89 4.000e-09 38-52 21.89 4.000e-09 38-102 2	1438	BL00290	Immunoglobulins and	BL00290B 13.17 2.500e-
1440 PR00806 VINCULIN SIGNATURE PR00806B 4.28 4.960e- 1441 PR00806 VINCULIN SIGNATURE PR00806B 4.28 4.960e- 09 38-52 PR00806B 4.28 4.960e- 09 38-52 PR00806B 4.28 4.960e- 09 88-102 9.48 1.000e- 00 114-138 PR00806B 4.28 4.960e- 09 88-102 9.48 1.000e- 00 114-138 PR00806B 4.28 4.960e- 00 114-138 PR00806B 4.28 4.960e- 00 114-138 PR00806B 4.28 4.960e- 00 114-138 PR00806B 4.28 4.960e- 00 114-138 PR0084B 1.30 PR0084B 1.30 PR0084B 1.30 1.000e-40 144- 1.85			major histocompatibility	09 250-268 BL00290A
1440 PR00806 VINCULIN SIGNATURE PR00806B 4.28 4.960e-09 38-52 PR00806F 4.28 4.960e-09 38-52 PR00806B 4.28 4.960e-09 88-102 PR00806B 4.28 4.960e-09 88-102 PR00806B 4.28 4.960e-09 88-102 PR00806B 4.28 4.960e-09 88-102 PR00806B 4.28 4.960e-09 88-102 PR00806B 4.28 4.960e-09 88-102 PR00806B 4.28 4.960e-09 88-102 PR00806B 4.28 4.960e-09 88-102 PR00806B 4.28 4.960e-09 88-102 PR0081AD 17.1 1.000e-09 88-102 PR0081AD 17.1 1.000e-40 81.1 1.000e-40 104-105 PR0081AD 17.87 1.000e-40 104-105 PR0081AD 17.87 1.000e-40 104-105 PR0081AD 17.87 1.000e-40 108-31 125 PR0081AD 13.00 1.000e-40 494-536 PR0081AD 13.00 1.000e-40 494-536 PR0081AD 13.00 1.000e-40 494-536 PR0081AD 13.00 1.000e-40 494-536 PR0081AD 13.00 1.000e-40 494-536 PR0081AD 13.00 1.000e-40 494-536 PR0081AD 13.00 1.000e-40 494-536 PR0081AD 13.00 1.000e-40 494-536 PR0081AD 13.00 1.000e-40 494-536 PR0081AD 13.00 1.000e-40 494-536 PR0081AD 13.78 1.000e-35 185-206 PR0081AD 13.78 1.000e-35 185-206 PR0081AD 13.78 1.000e-25 185-206 PR0081AD 13.78 1.250e-20 1175-1194 PR00816B 13.84 8.875e-20 1175-1194 PR00816B 13.84 8.875e-20 1175-1194 PR00816B 13.84 8.875e-20 1175-1194 PR00816B 13.84 8.875e-20 1175-1194 PR00816B 13.84 8.875e-20 1175-1194 PR00816B 13.03 8.085e-20 1175-1194 PR00816B 13.03 8.085e-20 1175-1194 PR00816B 13.03 8.085e-20 1175-1194 PR00816B 13.03 8.085e-20 1175-1194 PR00816B 13.03 8.085e-20 1175-1195 PR00816B 13.03 8.085e-20 1175-1195 PR00816B 13.03 8.085e-20 1175-1195 PR00816B 13.03 8.085e-20 1175-1195 PR00816B 13.03 8.085e-20 1175-1195 PR00816B 13.03 8.085e-20 1175-1195 PR00816B 13.03 8.085e-20 1175-1195 PR00816B 13.03 8.085e-20 1175-1195 PR00816B 13.03 8.085e-20 1175-1195 PR00816B 13.03 8.085e-20 1175-1195 PR00816B 13.03 8.085e-20 1175-1195 PR00816B 13.03 8.085e-20 1175-1195 PR00816B 13.03 8.085e-20 1175-1195 PR00816B 13.03 8.085e-20 1175-1195 PR00816B 13.03 8.085e-20 1175-1195 PR00816B 13.03 8.085e-20 1175-1195 PR00816B 13.03 8.085e-20 1175-1195 P			complex proteins.	20.89 4.000e-09 188-
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proteins. 17 169-182 BL00545A 10.20 2.071e-15 73-89 BL00545B 13.10 3.942e- 09 140-153 1466 PR00097 ANTHRANILATE SYNTHASE PR00097C 9.42 9.069e- COMPONENT II SIGNATURE 09 233-245 1472 BL01129 Hypothetical BL01129E 13.25 5.250e- yabO/yceC/sfhB family 22 170-195 BL01129C proteins. 25.56 9.526e-18 63-106 1473 BL00790 Receptor tyrosine kinase BL00790I 20.01 2.821e- class V proteins. 09 2114-2145 1475 PF00686 Starch binding domain PF00686A 13.45 9.100e-				
10.20 2.071e-15 73-89 BL00545B 13.10 3.942e- 09 140-153 1466 PR00097 ANTHRANILATE SYNTHASE COMPONENT II SIGNATURE PR00097C 9.42 9.069e- COMPONENT II SIGNAT	1460	BL00545		
BL00545E 13.10 3.942e- 09 140-153 1466 PR00097 ANTHRANILATE SYNTHASE PR00097C 9.42 9.069e- COMPONENT II SIGNATURE 09 233-245 1472 BL01129 Hypothetical BL01129E 13.25 5.250e- yabO/yceC/sfhB family 22 170-195 BL01129C proteins. 25.56 9.526e-18 63-106 1473 BL00790 Receptor tyrosine kinase BL00790I 20.01 2.821e- class V proteins. 09 2114-2145 1475 PF00686 Starch binding domain PF00686A 13.45 9.100e-			proteins.	
1466 PR00097 ANTHRANILATE SYNTHASE PR00097C 9.42 9.069e- COMPONENT II SIGNATURE 09 233-245 1472 BL01129 Hypothetical BL01129E 13.25 5.250e- yabO/yceC/sfhB family 22 170-195 BL01129C Proteins. 25.56 9.526e-18 63-106 1473 BL00790 Receptor tyrosine kinase BL00790I 20.01 2.821e- class V proteins. 09 2114-2145 1475 PF00686 Starch binding domain PF00686A 13.45 9.100e-				1
1466 PR00097 ANTHRANILATE SYNTHASE PR00097C 9.42 9.069e- COMPONENT II SIGNATURE 09 233-245				
COMPONENT II SIGNATURE	1466	DECOSO.		
1472 BL01129 Hypothetical yab0/yceC/sfhB family proteins. BL01129E 13.25 5.250e-yab0/yceC/sfhB family 22 170-195 BL01129C 25.56 9.526e-18 63-106 1473 BL00790 Receptor tyrosine kinase class V proteins. BL00790I 20.01 2.821e-09 2114-2145 1475 PF00686 Starch binding domain PF00686A 13.45 9.100e-	1400	PR00097		
yabO/yceC/sfhB family 22 170-195 BL01129C proteins. 25.56 9.526e-18 63-106 25.56 9.526	1472	Dr 01120		l
proteins. 25.56 9.526e-18 63-106 1473 BL00790 Receptor tyrosine kinase BL00790I 20.01 2.821e- class V proteins. 09 2114-2145 1475 PF00686 Starch binding domain PF00686A 13.45 9.100e-	11/4	PUUTITA	1	
1473 BL00790 Receptor tyrosine kinase BL00790I 20.01 2.821e- class V proteins. 09 2114-2145 1475 PF00686 Starch binding domain PF00686A 13.45 9.100e-				
class V proteins. 09 2114-2145 1475 PF00686 Starch binding domain PF00686A 13.45 9.100e-	1473	BY.00790		1
1475 PF00686 Starch binding domain PF00686A 13.45 9.100e-	14/3	2000130	1 -	
110000A 13:43 9:100e	1475	PE00686		
P-0001118. US 261-211				
		<u> </u>		0.5 201-211

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1477	PF00566	Probable rabGAP domain proteins.	PF00566A 12.64 7.333e- 10 466-476
1478	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030B 7.03 9.400e- 10 43-53
1479	DM00406	GLIADIN.	DM00406 7.73 8.541e-10 292-305
1480	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 2.385e- 15 69-87 BL00290A 20.89 5.091e-11 12-35
1481	PR00150	PHOSPHOENOLPYRUVATE CARBOXYLASE SIGNATURE	PR00150F 10.45 9.039e- 09 21-51
1482	PF00780	Domain found in NIK1- like kinases, mouse citron and yeast ROM.	PF00780I 14.69 4.825e- 09 107-137
1483	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 1.153e- 09 108-162
1485	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 5.909e- 25 17-56
1486	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.529e- 09 34-50
1488	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 9.586e- 10 116-162
1490	BL00166	Enoyl-CoA hydratase/isomerase proteins.	BL00166D 22.87 2.607e- 24 190-226 BL00166C 18.93 5.500e-14 140- 167 BL00166B 16.92 9.357e-11 93-115
1491	BL00452	Guanylate cyclases proteins.	BL00452D 28.59 3.700e- 31 63-106 BL00452E 11.92 3.045e-13 115- 131
1492	PR00019	LEUCINE-RICH REPEAT	PR00019A 11.19 3.667e- 09 532-546
1497	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.000e- 11 384-400 BL00107A 18.39 5.345e-11 322- 353
1500	PF00876	Ogre family.	PF00876E 7.99 1.947e-
1502	BL00027	'Homeobox' domain	BL00027 26.43 4.789e- 24 112-155
1503	BL00027	'Homeobox' domain proteins.	BL00027 26.43 4.789e-
1505	BL01177	Anaphylatoxin domain proteins.	BL01177E 20.64 5.800e- 24 448-475 BL01177C 17.39 5.333e-19 402- 421 BL01177B 13.61 7.840e-16 155-171 BL01177D 17.50 1.900e- 15 427-445
1506	BL00972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972D 22.55 5.500e- 14 311-336 BL00972A 11.93 7.429e-14 48-66 BL00972E 20.72 8.759e- 10 341-363
1512	BL00523	Sulfatases proteins.	BL00523B 19.27 4.536e- 22 76-106 BL00523D 9.89 1.563e-11 40-52 BL00523F 10.85 4.162e- 09 159-170 BL00523G 9.46 5.333e-09 256-266
1516	BL00914	Syntaxin / epimorphin family proteins.	BL00914 24.91 7.045e- 14 168-218
1518	BL00600	Aminotransferases class- III pyridoxal-phosphate attachment si.	BL00600A 17.98 6.143e- 19 98-122 BL00600E 16.43 1.771e-17 302-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			331 BL00600G 12.43 9.625e-17 377-396 BL00600B 19.60 5.091e- 15 160-186 BL00600C 16.18 6.040e-12 190- 206 BL00600F 8.77 1.000e-11 343-356 BL00600D 8.71 1.000e- 10 281-295
1523	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930B 33.72 9.600e- 18 41-82
1528	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320B 12.19 4.774e- 11 192-207 PR00320B 12.19 8.839e-11 272- 287 PR00320B 12.19 9.743e-10 106-121 PR00320A 16.74 1.878e- 09 192-207 PR00320A 16.74 2.317e-09 106- 121 PR00320A 16.74 8.683e-09 272-287 PR00320C 13.01 8.800e- 09 106-121
1538	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 4.508e-
1539	PF00781	Diacylglycerol kinase catalytic domain proteins (presumed).	PF00781D 11.11 7.593e- 10 103-127
1540	PR00965	OCULAR ALBINISM TYPE 1 PROTEIN SIGNATURE	PR00965H 10.73 1.231e- 29 312-334 PR00965E 12.93 5.846e-29 172- 195 PR00965F 5.98 1.123e-28 209-231 PR00965C 15.04 1.000e- 27 131-151 PR00965D 5.84 1.000e-27 150-170 PR00965G 8.52 2.440e- 27 258-279 PR00965B 4.80 8.650e-26 88-109 PR00965A 12.52 1.000e- 25 35-55 PR00965I 3.91 6.442e-25 385-406
1541	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 9.719e- 17 163-207
1543	PD02699	PROTEIN DNA-BINDING BINDING DNA.	PD02699C 24.84 1.000e- 40 599-646 PD02699A 8.91 2.286e-34 219-248 PD02699B 18.28 6.143e- 21 485-509
1544	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.857e- 10 182-197 PR00049D 0.00 7.102e-09 67-82
1547	BL00951	ER lumen protein retaining receptor proteins.	BL00951C 19.35 1.000e- 40 93-142 BL00951D 13.94 8.714e-40 142- 177 BL00951A 15.10 1.000e-38 2-38 . BL00951B 14.23 6.250e- 33 38-69
1548	BL00536	Ubiquitin-activating enzyme proteins.	BL00536F 13.65 8.920e- 30 279-318 BL00536D 22.91 5.737e-24 21-65 BL00536B 16.94 4.696e- 18 248-279
1549	PR00139	ASPARAGINASE/GLUTAMINASE FAMILY SIGNATURE	PR00139C 11.72 9.679e- 09 550-569
1553	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 5.119e- 09 58-73

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1556	BL00061	Short-chain	BL00061B 25.79 6.276e-
		dehydrogenases/reductase s family proteins.	13 67-105
1557	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e- 12 107-132
1558	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e- 12 107-132
1559	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e- 12 107-132
1562	BL00522	DNA polymerase family X proteins.	BL00522C 11.90 6.600e- 18 412-436 BL00522B 27.30 1.738e-16 364- 410 BL00522A 25.52 6.000e-16 279-326 BL00522E 19.63 6.123e- 14 502-532 BL00522F 14.90 2.385e-13 551- 575
1563	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 1.947e- 11 46-59
1564	BL00299	Ubiquitin domain proteins.	BL00299 28.84 2.823e- 10 324-376
1566	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 8.594e- 17 184-228 BL01013C 9.97 4.906e-12 14-24
1567	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 3.400e-10 378-389 BL00678 9.67 5.800e-10 418-429 BL00678 9.67 8.800e-10 295-306
1570	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 5.235e- 17 297-313 BL00479A 19.86 6.625e-15 271- 294 BL00479A 19.86 2.667e-14 147-170 BL00479B 12.57 6.294e- 12 173-189
1576	PR00665	SIGNATURE .	PR00665G 12.36 4.673e- 24 364-384 PR00665D 9.93 1.200e-22 138-155 PR00665F 11.73 4.000e- 22 337-354 PR00665C 5.89 1.000e-20 65-80 PR00665B 5.29 4.337e- 19 24-39 PR00665E 5.60 2.929e-15 246-260 PR00665A 5.99 5.622e- 15 11-25
1577	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 9.308e- 10 127-137
1579	BL00524	Somatomedin B domain proteins.	BL00524A 9.65 6.776e- 14 52-73
1580	PD02894	HYDROLASE N4 - PRECURSOR PROTEIN SIGNAL BE.	PD02894B 13.93 6.959e- 16 182-215 PD02894A 21.96 2.125e-10 57-103
1581	BL00411	Kinesin motor domain proteins.	BL00411C 15.04 5.292e- 12 32-54 BL00411H 15.66 4.441e-11 245- 276
1582	PR00604	CLASS IA AND IB CYTOCHROME C SIGNATURE	PR00604A 11.13 2.440e-
1584	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 1.000e- 10 225-238
1585	DM01551	kw OSTEOINDUCTIVE YOPM MEMBRANE OUTER.	DM01551C 14.62 9.455e- 11 125-145
1586	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354S 11.61 7.750e- 09 474-495

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1587	PR00072	MALIC ENZYME SIGNATURE	PR00072B 13.77 7.955e- 33 180-210 PR00072A 12.75 6.040e-25 120- 145 PR00072C 11.42 2.286e-24 216-239 PR00072D 10.77 3.400e- 22 276-295 PR00072E 10.54 1.360e-19 301- 318 PR00072G 10.45 5.304e-19 433-450 PR00072F 8.87 5.935e- 15 332-349
1589	BL00191	Cytochrome b5 family, heme-binding domain proteins.	BL00191H 15.64 1.537e- 22 61-113 BL00191K 17.38 9.027e-12 398- 442
1590	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 7.716e- 13 211-224 DM01970B 8.60 2.157e-12 94-107
1591	DM00517	5 kw NUCLEAR 60.7 NUP1 CHROMOSOME.	DM00517B 10.96 6.625e- 16 1175-1193 DM00517A 8.21 1.000e-11 1015- 1026
1592	BL00037	Myb DNA-binding domain proteins repeat proteins proteins.	BL00037B 15.92 3.250e- 27 116-142 BL00037A 16.68 2.500e-24 83-107 BL00037A 16.68 3.250e- 12 31-55 BL00037B 15.92 3.526e-11 64-90 BL00037C 16.86 9.654e- 10 146-164
1595	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.514e- 09 110-127
1598	PF00628	PHD-finger.	PF00628 15.84 3.250e- 11 1667-1682
1599	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014D 12.04 5.500e- 09 980-995
1600	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.571e- 10 30-39
1602	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.402e- 10 136-187
1605	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 3.571e-
1607	BL00252	Interferon alpha, beta and delta family proteins.	BL00252A 18.49 6.657e- 23 20-57 BL00252B 19.78 9.125e-16 58-109
1610	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 1.000e- 08 61-94
1611	BL00904	Protein prenyltransferases alpha subunit repeat proteins proteins.	BL00904C 8.98 7.353e- 10 91-125 BL00904D 1.47 6.018e-09 127-168
1612	PF00168	C2 domain proteins.	PF00168C 27.49 3.250e- 09 365-391
1613	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 6.051e- 09 932-983 BL00412D 16.54 7.153e-09 933- 984
1614	BL00559	Eukaryotic molybdopterin oxidoreductases proteins.	BL00559I 13.63 3.531e- 25 54-83 BL00559K 13.17 2.957e-18 197- 224 BL00559J 19.63 6.870e-16 124-176 BL00559L 13.60 9.000e- 16 266-284
1615	PD01427	TRANSFERASE METHYLTRANSFERASE BI.	PD01427B 22.45 3.025e- 22 500-541 PD01427A 19.94 8.773e-18 439-

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			472
1616	BL00115	Eukaryotic RNA	BL00115Z 3.12 7.485e-
		polymerase II	09 152-201 BL00115Z
		heptapeptide repeat	3.12 9.603e-09 145-194
1617	BL00303	S-100/ICaBP type calcium	BL00303B 26.15 7.750e-
		binding protein.	32 51-88 BL00303A
		3 .	21.77 1.947e-31 4-41
1618	BL01254	Fetuin family proteins.	BL01254F 10.02 8.754e-
1010	BBOTEST	recuir family process.	09 137-147
1619	PD01888	PEPTIDE REDUCTASE	PD01888B 25.10 1.000e-
		PROTEIN METHI.	40 47-97 PD01888C
	}		21.56 7.000e-30 125-
			155 PD01888A 12.84
			8.800e-15 7-23
1621	PR00239	MOLLUSCAN RHODOPSIN C-	PR00239E 1.58 3.455e-
2002	1.00000	TERMINAL TAIL SIGNATURE	09 692-704 PR00239E
			1.58 4.580e-09 697-709
			PR00239E 1.58 4.580e-
			09 702-714 PR00239E
			1.58 5.193e-09 703-715
1622	PR00860	VERTEBRATE	PR00860B 7.04 1.900e-
1022	IROUGOU	METALLOTHIONEIN	18 27-41 PRO0860C
	1	SIGNATURE	9.61 1.474e-14 41-51
		SIGNATORE	PR00860A 5.46 1.720e-
			14 5-18
1624	PR00784	MITOCHONDRIAL BROWN FAT	PR00784D 15.86 8.027e-
1024	PROUTOR	UNCOUPLING PROTEIN	11 77-95
		SIGNATURE	11 //-95
1626	BL00325	Actin-depolymerizing	BL00325B 21.66 1.000e-
1020	БД00325	proteins.	40 93-139 BL00325A
		process.	24.83 6.786e-23 61-93
1631	BL00064	L-lactate dehydrogenase	BL00064B 23.57 1.000e-
1031	B100004	proteins.	40 82-130 BL00064C
		proceins.	17.28 1.000e-40 137-
		İ	182 BL00064E 27.20
			1.000e-40 223-275
			BL00064F 25.14 7.882e-
			36 286-331 BL00064A
			21.16 1.000e-33 22-60
			BL00064D 14.19 6.500e-
			31 182-212
1632	PR00063	RIBOSOMAL PROTEIN L27	PR00063B 15.24 9.700e-
1032	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	SIGNATURE	11 59-84 PR00063A
		BIOWATOKE	11.71 1.614e-09 34-59
1634	PR00239	MOLLUSCAN RHODOPSIN C-	PR00239D 0.00 1.105e-
1034	1800233	TERMINAL TAIL SIGNATURE	11 36-49 PR00239C
			3.51 2.538e-09 37-45
1636	BL01210	Caveolins proteins.	BL01210B 13.92 9.531e-
			10 133-183
1637	BL00982	Bacterial-type phytoene	BL00982A 18.41 5.388e-
		dehydrogenase proteins.	11 11-43
1639	BL01183	ubiE/COQ5	BL01183B 21.31 8.144e-
		methyltransferase family	12 132-177
		proteins.	
1640	PR00015	GRAM-POSITIVE COCCUS	PR00015B 9.84 8.468e-
-		SURFACE PROTEIN ANCHOR	10 128-149
		SIGNATURE	
1641	PR00320	G-PROTEIN BETA WD-40	PR00320B 12.19 5.935e-
		REPEAT SIGNATURE	11 364-379 PR00320A
		The state of the s	16.74 7.828e-11 364-
		•	379 PR00320C 13.01
			2.800e-10 279-294
			PR00320C 13.01 2.800e-
			10 364-379 PR00320B
]		12.19 5.114e-10 279-
			294 PR00320A 16.74
			1.659e-09 279-294

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			PR00320A 16.74 2.098e- 09 229-244
1642	PF00023	Ank repeat proteins.	PF00023A 16.03 6.464e; 09 114-130
1643	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 1.806e- 11 74-94
1644	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 2.200e-10
		proteins proteins.	109-120 BL00678 9.67 5.737e-09 528-539
1645	BL01108	Ribosomal protein L24 proteins.	BL01108A 20.33 7.366e- 17 56-89
1646	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 9.270e- 21 103-125 PR00380D 9.93 6.308e-18 386-408 PR00380C 13.18 7.923e- 16 332-351 PR00380B 12.64 6.657e-15 292- 310
1647	DM01242	3 THREONINETRNA LIGASE.	DM01242C 17.15 9.791e- 37 340-381 DM01242E 23.00 5.071e-31 463- 505 DM01242D 23.29 3.925e-30 420-463 DM01242B 23.57 8.054e- 18 265-314 DM01242F 10.61 7.618e-14 526- 540
1649	PD00126	PROTEIN REPEAT DOMAIN TPR NUCLEA.	PD00126A 22.53 5.500e- 10 13-34
1651	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.720e- 11 431-485
1652	BL00933	FGGY family of carbohydrate kinases proteins.	BL00933A 17.50 4.673e- 12 11-35 BL00933E 13.80 9.217e-09 456- 472
1653	BL00795	Involucrin proteins.	BL00795C 17.06 2.988e- 10 70-115
1654	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e- 17 302-334
1655	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e- 17 282-314
1656	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 1.391e- 16 607-630
1657	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 7.938e- 11 114-136
1658	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 8.889e-
1659	BL00972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972D 22.55 4.140e- 12 376-401 BL00972E 20.72 5.629e-09 446- 468
1660	BL00406	Actins proteins.	BL00406D 12.58 8.767e- 15 188-243
1661	PR00105	CYTOSINE-SPECIFIC DNA METHYLTRANSFERASE SIGNATURE	PR00105A 10.36 4.900e- 13 1140-1157 PR00105B 12.32 2.800e-12 1259- 1274 PR00105C 10.86 1.000e-10 1305-1319
1662	BI:00580	Fancreatic trypsin inhibitor (Kunitz) family proteins.	BL00280 24.61 3.172e- 33 3119-3163
1663	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 107-125 PR00319C 13.41 5.714e-20 89-105 PR00319A 15.27 5.286e- 19 51-68 PR00319B 11.47 8.200e-19 70-85

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1664	BL00018	EF-hand calcium-binding	BL00018 7.41 5.050e-10 489-502
1667	555566	domain proteins. PROTEIN ZINC FINGER	
1667	PD01066	ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 8.500e- 38 7-46
1669	BL01153	NOL1/NOP2/sun family	BL01153D 19.69 1.188e-
2.00	2202233	proteins.	17 115-141 BL01153C
		procesns.	13.67 8.977e-15 66-80
			BL01153B 20.52 1.885e-
			10 13-37
1671	PR00678	PI3 KINASE P85	PR00678H 9.13 3.100e-
1671	PR00676	REGULATORY SUBUNIT	10 1146-1169
1672	BL00598	Chromo domain proteins.	BL00598 14.45 8.500e-
1673	PR00326	GTP1/OBG GTP-BINDING	PR00326A 8.75 8.329e-
1073	FR00326	PROTEIN FAMILY SIGNATURE	09 686-707
1674	PR00049	WILM'S TUMOUR PROTEIN	PR00049D 0.00 7.580e-
1074	PROODES	SIGNATURE	11 343-358 PR00049D
		JAMATORE	0.00 1.286e-10 342-357
1676	PR00747	GLYCOSYL HYDROLASE	PR00747H 12.76 8.636e-
10/0	PRUU /4/	FAMILY 47 SIGNATURE	19 427-448 PR00747G
	1	PANILUI 4/ SIGNATURE	19 427-448 PR00747G
			14.50 2.286e-18 368- 393 PR00747C 12.06
	!	i,	7.500e-18 112-131
			PR00747A 14.05 4.600e-
			17 42-63 PR00747D
	İ		15.23 8.759e-17 163-
			183 PR00747E 15.13
		}	8.244e-15 254-272
	1		PR00747B 7.65 5.355e-
	1		13 75-90 PR00747F
	1		13.56 8.714e-10 311-
	1	1	328
1677	PR00747	GLYCOSYL HYDROLASE	PR00747H 12.76 8.636e-
1077	FR00/4/	FAMILY 47 SIGNATURE	19 309-330 PR00747G
		PARILI 47 SIGNATURE	14.50 2.286e-18 250-
			275 PR00747C 12.06
			7.500e-18 112-131
			PR00747A 14.05 4.600e-
		1	17 42-63 PR00747B
		·	7.65 5.355e-13 75-90
		,	PR00747F 13.56 8.714e-
	1	İ	10 193-210
1680	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 4.600e-10
	Ì	proteins proteins.	406-417 BL00678 9.67
		-	6.684e-09 320-331
1681	BL00678	Trp-Asp (WD) repeat	BL0067B 9.67 4.600e-10
		proteins proteins.	329-340 BL00678 9.67
			6.684e-09 243-254
1683	PR00326	GTP1/OBG GTP-BINDING	PR00326A 8.75 1.346e-
		PROTEIN FAMILY SIGNATURE	13 389-410
1685	PR00646	RDC1 ORPHAN RECEPTOR	PR00646H 6.32 4.188e-
		SIGNATURE	09 755-771
1690	BL01160	Kinesin light chain	BL01160B 19.54 6.644e-
		repeat proteins.	09 75-129
1691	PR00456	RIBOSOMAL PROTEIN P2	PR00456E 3.06 7.281e-
		SIGNATURE	10 418-433 PR00456E
			3.06 7.281e-10 419-434
	1	1	PR00456E 3.06 8.125e-
	ļ		10 420-435
1692	PR00456	RIBOSOMAL PROTEIN P2	PR00456E 3.06 7.281e-
		SIGNATURE	10 487-502 PR00456B
		1	3.06 7.281e-10 488-503
			PR00456E 3.06 8.125e-
			10 489-504
1693	+		
7023	BL00674	AAA-protein family	BL00674C 22.50 8.043e-
1633	BL00674	AAA-protein family proteins.	BL00674C 22.60 8.043e- 24 274-317 BL00674B

SEQ ID NO	: ACCESSION NO.	DESCRIPTION	RESULTS*
			4.46 4.000e-23 241-263 BL00674D 23.41 8.560e- 18 338-385 BL00674E 15.24 1.720e-15 414-
1697	PR00409	PHTHALATE DIOXYGENASE REDUCTASE FAMILY SIGNATURE	PR00409F 12.70 4.388e- 10 427-447
1698	PR00466	CYTOCHROME B-245 HEAVY CHAIN SIGNATURE	PR00466C 10.17 3.443e- 13 187-208 PR00466B 5.03 5.500e-11 162-186 PR00466F 9.16 6.159e- 09 498-517
1699	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.217e- 12 283-300 BL00028 16.07 3.769e-11 255- 272 BL00028 16.07 5.154e-11 171-188 BL00028 16.07 5.500e- 11 227-244 BL00028 16.07 1.600e-10 199- 216
1700	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 3.348e- 15 62-102 BL01019B 19.49 4.000e-15 107- 162
1703	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.484e- 12 200-239
1707	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 4.558e- 14 134-153
1710	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.565e- 10 116-130 PR00019B 11.36 4.600e-09 113- 127 PR00019B 11.36 7.120e-09 204-218
1711	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 6.523e- 11 232-247 BL01159 13.85 5.408e-10 613- 628
1712	PF00023	Ank repeat proteins.	PF00023A 16.03 7.000e- 10 187-203
1713	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 9.550e- 11 230-241
1715	BL01115 .	Zinc finger C-x8-C-x5-C- x3-H type (and similar). GTP-binding nuclear	PF00642 11.59 9.550e- 11 230-241 BL01115A 10.22 7.129e-
1718	BL00353	protein ran proteins. HMG1/2 proteins.	09 7-51 BL00353C 14.83 6.018e-
1719	BL00412	Neuromodulin (GAP-43)	10 136-183 BL00353B 11.47 8.866e-09 86-136
1721	BL00038	proteins. Myc-type, 'helix-loop-	BL00412D 16.54 5.408e- 09 432-483 BL0003BB 16.97 8.448e-
		helix' dimerization domain proteins.	12 79-100 BL00038A 13.61 4.000e-11 52-68
1723	PD00567	PROTEIN RNA-BINDING RNA REPEAT HYD.	PD00567C 9.17 8.500e- 09 418-428
1724	BL01279	Protein-L- isoaspartate(D- aspartate) O- methyltransferase signa.	BL01279A 24.27 5.663c- 12 233-281
1728	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 2.059e-11 73-86 BL00018 7.41
1730	BL00594	Aromatic amino acids permeases proteins.	4.176e-11 157-170 BL00594A 16.75 1.089e- 09 17-61

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1731	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.676e- 10 296-350
1732	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.676e- 10 316-370
1733	PF00850	Histone deacetylase family.	PF00850F 15.70 4.349e- 22 246-279 PF00850D 14.76 6.850e-20 177- 201 PF00850E 8.88 8.691e-18 209-235 PF00850G 22.75 4.098e- 14 281-323
1734	BL00354	HMG-I and HMG-Y DNA- binding domain proteins (Ahook).	BL00354C 6.61 5.932e- 09 292-307
1735	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.263e- 10 492-502
1743	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.188e- 11 5-27 PR00449D 10.79 2.241e-10 109- 123 PR00449E 13.50 9.289e-10 144-167
1744	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.188e- 11 5-27 PR00449D 10.79 2.241e-10 109- 123 PR00449E 13.50 9.289e-10 144-167
1745	BL00720	Guanine-nucleotide dissociation stimulators CDC25 family sign.	BL00720B 16.57 8.297e- 15 136-160
1746	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081B 10.38 6.727e- 11 45-57 PR00081E 17.54 3.935e-10 150- 168
1747	BL00439	Acyltransferases ChoActase / COT / CPT family proteins.	BL00439H 18.24 8.435e- 14 65-91 BL00439G 13.40 2.895e-12 3-14
1749	PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE	PR00819B 10.83 7.158e- 11 4-20
1751	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 3.400e- 14 33-46 PD00066 13.92 1.000e-13 89-102 PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117- 130
1753	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 6.516e- 18 33-77
1754	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318
1756	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.750e- 35 10-49
1758	DM00406	GLIADIN.	DM00406 7.73 7.600e-09 653-666
1762	PD02929	ADHESION GLYCOPROTEIN PRECURSOR I.	PD02929A 28.27 4.529e- 09 224-278
1765	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 5.950e- 11 146-167
1775	PF00023	Ank repeat proteins.	PF00023A 16.03 3.077e- 14 523-539
1776	BL00942	glpT family of transporters proteins.	BL00942F 15.07 4.343e- 10 371-389 BL00942B 20.36 8.040e-09 94-137
1777	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.373e- 09 279-312

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1778	BL00084	Copper type II, ascorbate-dependent monooxygenases proteins.	BL00084D 25.11 3.700e- 20 169-224 BL00084B 24.26 8.134e-16 10-58 BL00084C 27.71 8.412e- 11 107-158
1779	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 3.758e- 18 611-655 BL01013A 25.14 2.881e-15 344- 380 BL01013C 9.97 6.308e-13 435-445 BL01013B 11.33 3.717e- 12 409-420
1783	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e- 13 492-515
1784	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e- 13 492-515

^{*} results include in order: accession number subtype; raw score; p-value; postion of signature in amino acid sequence.

TRADOCS:1416223.I(%CRJ01!.DOC)

TABLE 4

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
2	ig	Immunoglobulin domain	2.1e-32	109.5
3	pkinase	Eukaryotic protein kinase domain	1.3e-29	110.7
4	zf-C2H2	Zinc finger, C2H2 type	1.6e-21	84.9
5	fn3	Fibronectin type III domain	0	1097.1
6	fn3	Fibronectin type III domain	0	1035.0
7	fn3	Fibronectin type III domain	0	1090.4
8	fn3	Fibronectin type III domain	0	1097.1
9	TBC	TBC domain	4e-40	146.7
10	p450	Cytochrome P450	9.5e-17	62.0
12	ank	Ank repeat	6e-20	79.7
		Immunoglobulin domain	1.7e-05	22.7
14	ig zf-MYND		1.7e-05	35.4
15		MYND finger	1	1
16	zf-MYND	MYND finger	1.3e-06	35.4
17	zf-C2H2	Zinc finger, C2H2 type	1.7e-99	343.9
18	CAP_GLY	CAP-Gly domain	1.2e-25	98.7
20	IMPDH_C	IMP dehydrogenase / GMP	1.6e-119	410.5
		reductase C terminus		<u> </u>
21	IMPDH_C	IMP dehydrogenase / GMP reductase C terminus	4.3e-102	352.6
22	pkinase	Eukaryotic protein kinase domain	2.4e-79	277.0
23	pkinase	Eukaryotic protein kinase domain	8.4e-74	258.6
25	RNA pol A	RNA polymerase alpha subunit	0	1077.7
26	Clq	Clq domain	1.9e-10	44.4
27	Ribosomal_L2	Ribosomal protein L23	7.8e-32	111.2
28	Ribosomal_L2	Ribosomal protein L23	le-29	104.2
30	zf-A20	A20-like zinc finger	1.5e-10	48.5
31	zf-A20	A20-like zinc finger	1.5e-10	48.5
32	FMN_dh	FMN-dependent dehydrogenase	5.4e-179	608.1
34	PID	Phosphotyrosine interaction domain (PTB/PID)	3.8e-59	209.9
35	Ig	Immunoglobulin domain	1.4e-13	48.8
36	1 <u>ig</u>	Immunoglobulin domain	1.4e-13	48.8
40	kinesin	Kinesin motor domain	6.7e-76	265.6
44	1			
	Ets	Ets-domain	1.4e-56	182.1
45	Ets Ets	Ets-domain Ets-domain	1.4e-56 1.4e-56	182.1
45 46	Ets Ets LRR	Ets-domain Ets-domain Leucine Rich Repeat	1.4e-56 1.4e-56 1.7e-13	182.1 182.1 58.3
45 46 48	Ets Ets LRR zf-C2H2	Ets-domain Ets-domain Leucine Rich Repeat Zinc finger, C2H2 type	1.4e-56 1.4e-56 1.7e-13 2.3e-162	182.1 182.1 58.3 552.8
45 46 48 49	Ets Ets LRR 2f-C2H2 ITAM	Ets-domain Ets-domain Leucine Rich Repeat Zinc finger, C2H2 type Immunoreceptor tyrosine-based activation mot	1.4e-56 1.4e-56 1.7e-13 2.3e-162 1.4e-05	182.1 182.1 58.3 552.8 31.9
45 46 48 49	Ets Ets LRR Zf-C2H2 ITAM	Ets-domain Ets-domain Leucine Rich Repeat Zinc finger, C2H2 type Immunoreceptor tyrosine-based activation mot Ubiquitin carboxyl-terminal hydrolase family	1.4e-56 1.4e-56 1.7e-13 2.3e-162 1.4e-05	182.1 182.1 58.3 552.8 31.9
45 46 48 49 50	Ets Ets LRR 2f-C2H2 ITAM	Ets-domain Ets-domain Leucine Rich Repeat Zinc finger, C2H2 type Immunoreceptor tyrosine-based activation mot Ubiquitin carboxyl-terminal hydrolase family Ubiquitin carboxyl-terminal hydrolase family	1.4e-56 1.4e-56 1.7e-13 2.3e-162 1.4e-05 1.1e-26	182.1 182.1 58.3 552.8 31.9
45 46 48 49 50 51	Ets Ets LRR zf-C2H2 ITAM UCH-2 UCH-2	Ets-domain Ets-domain Leucine Rich Repeat Zinc finger, C2H2 type Immunoreceptor tyrosine-based activation mot Ubiquitin carboxyl-terminal hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family	1.4e-56 1.4e-56 1.7e-13 2.3e-162 1.4e-05	182.1 182.1 58.3 552.8 31.9 102.0
45 46 48 49 50 51 52 53	Ets Ets LRR Zf-C2H2 ITAM UCH-2 UCH-2 ras PRK	Ets-domain Ets-domain Leucine Rich Repeat Zinc finger, C2H2 type Immunoreceptor tyrosine-based activation mot Ubiquitin carboxyl-terminal hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family Phosphoribulokinase	1.4e-56 1.4e-56 1.7e-13 2.3e-162 1.4e-05 1.1e-26 1.1e-26 8.5e-45 2.1e-65	182.1 182.1 58.3 552.8 31.9
45 46 48 49 50 51 52 53	Ets Ets LRR zf-C2H2 ITAM UCH-2 VCH-2 ras PRK myb_DNA- binding	Ets-domain Ets-domain Leucine Rich Repeat Zinc finger, C2H2 type Immunoreceptor tyrosine-based activation mot Ubiquitin carboxyl-terminal hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family	1.4e-56 1.4e-56 1.7e-13 2.3e-162 1.4e-05 1.1e-26 8.5e-45	182.1 182.1 58.3 552.8 31.9 102.0
45 46 48 49 50 51 52 53 54	Ets Ets LRR zf-C2H2 ITAM UCH-2 UCH-2 ras PRK myb_DNA-	Ets-domain Ets-domain Leucine Rich Repeat Zinc finger, C2H2 type Immunoreceptor tyrosine-based activation mot Ubiquitin carboxyl-terminal hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family Phosphoribulokinase	1.4e-56 1.4e-56 1.7e-13 2.3e-162 1.4e-05 1.1e-26 1.1e-26 8.5e-45 2.1e-65	182.1 182.1 58.3 552.8 31.9 102.0 102.0
45 46 48 49 50 51 52 53 54	Ets Ets LRR zf-C2H2 ITAM UCH-2 VCH-2 ras PRK myb_DNA- binding	Ets-domain Ets-domain Leucine Rich Repeat Zinc finger, C2H2 type Immunoreceptor tyrosine-based activation mot Ubiquitin carboxyl-terminal hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family Phosphoribulokinase Myb-like DNA-binding domain	1.4e-56 1.4e-56 1.7e-13 2.3e-162 1.4e-05 1.1e-26 1.1e-26 8.5e-45 2.1e-65 0.096	182.1 182.1 58.3 552.8 31.9 102.0 102.0 162.3 230.7 15.2
45 46 48 49 50 51 52 53 54 55 56	Ets Ets LRR zf-C2H2 ITAM UCH-2 VCH-2 ras PRK myb_DNA- binding voltage_CLC	Ets-domain Ets-domain Leucine Rich Repeat Zinc finger, C2H2 type Immunoreceptor tyrosine-based activation mot Ubiquitin carboxyl-terminal hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family Phosphoribulokinase Myb-like DNA-binding domain Voltage gated chloride channels	1.4e-56 1.4e-56 1.7e-13 2.3e-162 1.4e-05 1.1e-26 1.1e-26 8.5e-45 2.1e-65 0.096 3.3e-186	182.1 182.1 58.3 552.8 31.9 102.0 102.0 162.3 230.7 15.2
45 46 48 49 50 51 52 53 54 55 56 57	Ets Ets LRR zf-C2H2 ITAM UCH-2 VCH-2 ras PRK myb_DNA- binding voltage_CLC sugar_tr	Ets-domain Ets-domain Leucine Rich Repeat Zinc finger, C2H2 type Immunoreceptor tyrosine-based activation mot Ubiquitin carboxyl-terminal hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family Phosphoribulokinase Myb-like DNA-binding domain Voltage gated chloride channels Sugar (and other) transporter	1.4e-56 1.4e-56 1.7e-13 2.3e-162 1.4e-05 1.1e-26 1.1e-26 8.5e-45 2.1e-65 0.096 3.3e-186 0.00015	182.1 182.1 58.3 552.8 31.9 102.0 102.0 162.3 230.7 15.2 631.9 -64.3
45 46 48 49 50 51 52 53 54 55 56 57 58	Ets Ets LRR zf-C2H2 ITAM UCH-2 VCH-2 ras PRK myb_DNA- binding voltage_CLC sugar_tr TBC ank	Ets-domain Ets-domain Leucine Rich Repeat Zinc finger, C2H2 type Immunoreceptor tyrosine-based activation mot Ubiquitin carboxyl-terminal hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family Phosphoribulokinase Myb-like DNA-binding domain Voltage gated chloride channels Sugar (and other) transporter TBC domain Ank repeat	1.4e-56 1.4e-56 1.7e-13 2.3e-162 1.4e-05 1.1e-26 1.1e-26 8.5e-45 2.1e-65 0.096 3.3e-186 0.00015 2.2e-37 5.9e-25	182.1 182.1 58.3 552.8 31.9 102.0 102.0 162.3 230.7 15.2 631.9 -64.3 137.6 96.3
45 46 48 49 50 51 52 53 54 55 56 57 58 59	Ets Ets LRR zf-C2H2 ITAM UCH-2 UCH-2 ras PRK myb_DNA- binding voltage_CLC sugar_tr TBC ank ank PMP22_Claudi	Ets-domain Ets-domain Leucine Rich Repeat Zinc finger, C2H2 type Immunoreceptor tyrosine-based activation mot Ubiquitin carboxyl-terminal hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family Phosphoribulokinase Myb-like DNA-binding domain Voltage gated chloride channels Sugar (and other) transporter TBC domain	1.4e-56 1.4e-56 1.7e-13 2.3e-162 1.4e-05 1.1e-26 8.5e-45 2.1e-65 0.096 3.3e-186 0.00015 2.2e-37	182.1 182.1 58.3 552.8 31.9 102.0 102.0 162.3 230.7 15.2 631.9 -64.3 137.6
45 46 48 49 50 51 52 53 54 55 56 57 58 59 67	Ets Ets LRR zf-C2H2 ITAM UCH-2 UCH-2 ras PRK myb_DNA- binding voltage_CLC sugar_tr TBC ank ank PMP22_Claudi n	Ets-domain Ets-domain Leucine Rich Repeat Zinc finger, C2H2 type Immunoreceptor tyrosine-based activation mot Ubiquitin carboxyl-terminal hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family Phosphoribulokinase Myb-like DNA-binding domain Voltage gated chloride channels Sugar (and other) transporter TBC domain Ank repeat Ank repeat PMP-22/EMP/MP20/Claudin family	1.4e-56 1.4e-56 1.7e-13 2.3e-162 1.4e-05 1.1e-26 1.1e-26 8.5e-45 2.1e-65 0.096 3.3e-186 0.00015 2.2e-37 5.9e-25 5.9e-25 7.9e-49	162.1 182.1 58.3 552.8 31.9 102.0 102.0 102.3 230.7 15.2 631.9 -64.3 137.6 96.3 96.3
45 46 48 49 50 51 52 53 54 55 56 57 58 59 67	Ets Ets LRR zf-C2H2 ITAM UCH-2 UCH-2 ras PRK myb_DNA- binding voltage_CLC sugar_tr TBC ank ank ank PMP22_Claudi n C2	Ets-domain Ets-domain Leucine Rich Repeat Zinc finger, C2H2 type Immunoreceptor tyrosine-based activation mot Ubiquitin carboxyl-terminal hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family Phosphoribulokinase Myb-like DNA-binding domain Voltage gated chloride channels Sugar (and other) transporter TBC domain Ank repeat Ank repeat PMP-22/EMP/MP20/Claudin family C2 domain	1.4e-56 1.4e-56 1.7e-13 2.3e-162 1.4e-05 1.1e-26 1.1e-26 8.5e-45 2.1e-65 0.096 3.3e-186 0.00015 2.2e-37 5.9e-25 5.9e-25 7.9e-49	182.1 182.1 58.3 552.8 31.9 102.0 102.0 102.3 230.7 15.2 631.9 -64.3 137.6 96.3 175.6
45 46 48 49 50 51 52 53 54 55 56 57 58 59 67 68 69	Ets Ets LRR zf-C2H2 ITAM UCH-2 ras PRK myb_DNA- binding voltage_CLC sugar_tr TBC ank ank PMP22_Claudi n C2 C2	Ets-domain Ets-domain Leucine Rich Repeat Zinc finger, C2H2 type Immunoreceptor tyrosine-based activation mot Ubiquitin carboxyl-terminal hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family Phosphoribulokinase Myb-like DNA-binding domain Voltage gated chloride channels Sugar (and other) transporter TBC domain Ank repeat Ank repeat FMP-22/EMP/MP20/Claudin family C2 domain C2 domain	1.4e-56 1.4e-56 1.7e-13 2.3e-162 1.4e-05 1.1e-26 1.1e-26 8.5e-45 2.1e-65 0.096 3.3e-186 0.00015 2.2e-37 5.9e-25 7.9e-49 7.9e-54 2.3e-54	182.1 182.1 58.3 552.8 31.9 102.0 102.0 162.3 230.7 15.2 631.9 -64.3 137.6 96.3 96.3 175.6
44 45 46 48 49 50 51 52 53 54 55 56 57 58 59 67 68 69 70 72	Ets Ets LRR zf-C2H2 ITAM UCH-2 UCH-2 ras PRK myb_DNA- binding voltage_CLC sugar_tr TBC ank ank ank PMP22_Claudi n C2	Ets-domain Ets-domain Leucine Rich Repeat Zinc finger, C2H2 type Immunoreceptor tyrosine-based activation mot Ubiquitin carboxyl-terminal hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family Phosphoribulokinase Myb-like DNA-binding domain Voltage gated chloride channels Sugar (and other) transporter TBC domain Ank repeat Ank repeat PMP-22/EMP/MP20/Claudin family C2 domain	1.4e-56 1.4e-56 1.7e-13 2.3e-162 1.4e-05 1.1e-26 1.1e-26 8.5e-45 2.1e-65 0.096 3.3e-186 0.00015 2.2e-37 5.9e-25 5.9e-25 7.9e-49	182.1 182.1 58.3 552.8 31.9 102.0 102.0 102.3 230.7 15.2 631.9 -64.3 137.6 96.3 175.6

NO:				SCORE
		domain		
74	pkinase	Eukaryotic protein kinase domain	2.8e-38	140.6
76	zf- C4_Topoisom	Topoisomerase DNA binding C4 zinc fing	5.4e-54	192.8
83	Peptidase_S9	Prolyl oligopeptidase family	4.3e-10	36.8
84	fn3	Fibronectin type III domain	4.1e-51	183.2
86	SH2	Src homology domain 2	3.1e-22	67.7
88	ig	Immunoglobulin domain	0.0091	14.0
89	WD40	WD domain, G-beta repeat	2.1e-21	84.6
92 93	laminin_G AMP-binding	Laminin G domain AMP-binding enzyme	6.1e-27 2.4e-13	98.5
95	pkinase	Eukaryotic protein kinase	1.4e-59	211.4
96	pkinase	domain Eukaryotic protein kinase		
96	pkinase	domain	2.6e-51	183.9
97	adh_short	short chain dehydrogenase	2e-61	217.5
98	kinesin	Kinesin motor domain	2.2e-86	300.4
101	IRS	PTB domain (IRS-1 type)	5.4e-36	133.0
102	AAA	ATPases associated with various cellular act	6.8e-05	-5.2
104	pkinase	Eukaryotic protein kinase domain	2.7e-73	256.9
106	ras	Ras family	8.3e-24	92.5
107	FYVE	FYVE zinc finger	5.4e-27	100.7
108	Cyt_reductas	FAD/NAD-binding Cytochrome reductase	7.7e-61	215.5
109	zf-C2H2	Zinc finger, C2H2 type	2.3e-122	420.0
113	pkinase	Eukaryotic protein kinase domain	4e-88	306.2
116	PH	PH domain	3.1e-11	45.2
117	lipocalin	Lipocalin / cytosolic fatty- acid binding pr	2.4e-14	53.5
118	pkinase	Eukaryotic protein kinase domain	4.5e-20	76.3
120	WD40	WD domain, G-beta repeat	2.4e-14	61.1
121	WD40	WD domain, G-beta repeat	2.4e-14	61.1
123	IF5_eIF4_eIF 2	eIF4-gamma/eIF5/eIF2-epsilon	1e-32	122.2
124	ig	Immunoglobulin domain	6.5e-08	30.6
127	mito_carr PP2C	Mitochondrial carrier proteins Protein phosphatase 2C	3e-16	58.6
129	ATP1G1_PLM_M AT8	ATPIGI/PLM/MAT8 family	2.2e-71 3.1e-20	250.6 80.6
130	pfkB	pfkB family carbohydrate kinase	4.5e-42	137.1
133	ACBP	Acyl CoA binding protein	4.6e-22	86.7
134	rrm	RNA recognition motif.	1.2e-31	118.5
135	IQ	IQ calmodulin-binding motif	2.6e-08	41.0
136	ATP1G1_PLM_M AT8	ATP1G1/PLM/MAT8 family	9.3e-22	85.7
139	WH2	Wiskott Aldrich syndrome homology region 2	0.0067	23.1
140	zf-C2H2	Zinc finger, C2H2 type	1.7e-82	287.5
141	Peptidase_S2	Signal peptidase I	5.7e-10	35.7
143	arf	ADP-ribosylation factor family	1.2e-39	145.2
146	KRAB	KRAB box	7.3e-30	112.6
148	DUF6	Integral membrane protein DUF6	0.096	8.0
149	PDEase	3'5'-cyclic nucleotide phosphodiesterase	3.8e-80	231.1
151	S4	S4 domain	1.1e-08	42.3
153	tRNA-synt_ld	tRNA synthetases class I (R)	3.8e-103	356.1
154	Cyt_reductas e	FAD/NAD-binding Cytochrome reductase	7.8e-60	212.2
155	ras	Ras family	3.6e-28	107.0
157	actin	Actin	3.8e-26	87.1

SEO ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:		225000000000000000000000000000000000000	F	SCORE
158	Jacalin	Jacalin-like lectin domain	0.09	-24.9
160	Zn_carbOpept	Zinc carboxypeptidase	5e-138	471.9
165	pkinase	Eukaryotic protein kinase	5.1e-67	236.1
	5 00 100	domain		
167	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.3e-07	27.0
168	Ribosomal_S1 5	Ribosomal protein S15	1.le-06	29.0
169	DEAD	DEAD/DEAH box helicase	le-48	157.0
171	DUF59	Domain of unknown function	0.07	-17.4
		DUF59		-
172	pkinase	Eukaryotic protein kinase domain	3.7e-15	58.6
173	globin	Globin	4.6e-18	67.4
174	WW	WW domain	7.3e-06	32.9
175	ras	Ras family	1e-31	118.8
178	ATPIG1_PLM_M AT8	ATPIG1/PLM/MAT8 family	2.5e-17	71.0
179	zf-C2H2	Zinc finger, C2H2 type	1.5e-99	344.2
180	Clq	Clq domain	8.8e-72	251.9
190	Y_phosphatas	Protein-tyrosine phosphatase	4.9e-287	967.0
191	efhand	EF hand	7.5e-16	66.1
193	pkinase	Eukaryotic protein kinase domain	6.5e-82	285.6
194	bromodomain	Bromodomain	5.8e-31	111.4
195	PALP	Pyridoxal-phosphate dependent	2.5e-64	227.1
195	PALIP	enzyme	2.56-64	227.1
197	DnaJ	DnaJ domain	1.6e-38	141.4
199	RrnaAD	Ribosomal RNA adenine	0.00018	16.9
200	acid phospha	dimethylases Histidine acid phosphatase	2.5e-10	37.2
	t			
201	WH2	Wiskott Aldrich syndrome homology region 2	0.00048	26.9
204	vATP-	ATP synthase (C/AC39) subunit	1.3e-159	543.7
	synt_AC39		1	
205	vATP- synt_AC39	ATP synthase (C/AC39) subunit	1.6e-139	476.9
206	ldl_recept_a	Low-density lipoprotein receptor domain	2.4e-25	97.6
209	ank	Ank repeat	1.4e-19	78.4
210	Rhomboid	Rhomboid family	0.0035	1.2
211	Clq	Clq domain	1.6e-70	247.7
212	UQ con	Ubiquitin-conjugating enzyme	7.4e-74	258.8
213	UQ con	Ubiquitin-conjugating enzyme	le-53	191.9
215	DEAD	DEAD/DRAH box helicase	1.8e-43	140.4
216	PMP22_Claudi	PMP-22/EMP/MP20/Claudin family	4.5e-21	83.4
218	Glycos trans f 2	Glycosyl transferases	4e-21	83.6
219	ig	Immunoglobulin domain	0.092	10.7
222	WD40	WD domain, G-beta repeat	7.4e-23	89.4
224	TPR	TPR Domain	1.2e-08	42.1
225	DnaJ_CXXCXGX	DnaJ central domain (4 repeats)	1.5e-38	141.5
226	DnaJ_CXXCXGX	DnaJ central domain (4 repeats)	1.5e-38	141.5
229	HSP70	Hsp70 protein	2.4e-54	194.0
230	GSHP×	Glutathione peroxidases	3.4e-47	170.2
231	tsp 1	Thrombospondin type 1 domain	0.0075	17.1
233	cyclin	Cyclin	4.6e-144	492.0
		Ras family	4.8e-50	179.7
	ITAS	,		
234	ras	Leucine Rich Repeat	1 20-30	115 3
234 235	LRR	Leucine Rich Repeat	1.2e-30	115.3
234 235 236 237		Leucine Rich Repeat Leucine Rich Repeat PDZ domain (Also known as DHR	1.2e-30 6.7e-29 1.7e-09	115.3 109.4 45.0

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
244	dCMP_cyt_dea	Cytidine and deoxycytidylate deaminase	2.5e-05	31.1
·	m	Immunoglobulin domain	6.7e-08	30.5
45	ig	wnt family of developmental	9.1e-270	742.6
48	wnt	signaling protei Mitochondrial carrier proteins	1.3e-55	193.6
250	mito_carr		1.8e-14	55.7
254	adenylatekin ase	Adenylate kinase		
255	Cation_efflu x	Cation efflux family	2.8e-33	124.0
256	SH3	SH3 domain	3.9e-14	60.4
257	Aa trans	Transmembrane amino acid	2.6e-52	187.2
	_	transporter protein		
258	adenylatekin ase	Adenylate kinase	2.1e-110	380.2
259	HIT	HIT family	8.2e-07	25.3
260	Bacterial_PQ	PQQ enzyme repeat	1.6e-15	65.0
262	proteasome	Proteasome A-type and B-type	6.5e-64	225.7
267	pkinase	Eukaryotic protein kinase domain	6.3e-27	101.0
270	filament	Intermediate filament proteins	3.2e-150	512.5
271	Choline_kina	Choline/ethanolamine kinase	2e-67	237.4
277	Ribosomal S7	Ribosomal protein S7p/S5e	3.3e-20	80.6
279	pkinase	Eukaryotic protein kinase	3.3e-77	269.9
280	WD40	WD domain, G-beta repeat	7.8e-73	255.4
281	WD40	WD domain, G-beta repeat	7.8e-73	255.4
284	zf-DHHC	DHHC zinc finger domain	4.6e-24	93.4
287	Exonuclease	Exonuclease	1.4e-67	238.0
291	SAM	SAM domain (Sterile alpha motif)	0.034	11.2
292	SAM	SAM domain (Sterile alpha motif)	0.034	11.2
294	zf-C2H2	Zinc finger, C2H2 type	1.4e-29	111.7
295	zf-C2H2	Zinc finger, C2H2 type	2.2e-125	430.0
296	mito_carr	Mitochondrial carrier proteins	4.1e-59	205.5
297	HMG_box	HMG (high mobility group) box	6.7e-29	109.4
302	Glycos_trans f 4	Glycosyl transferase	5e-87	302.5
304	tRNA-synt_2	tRNA synthetases class II (D, K and N)	1.1e-84	294.8
305	KRAB	KRAB box	2e-44	161.0
306	rrm	RNA recognition motif.	2.7e-44	160.6
308	7tm_1	7 transmembrane receptor (rhodopsin family)	5.2e-39	126.1
309	DNA_polymera	DNA polymerase X family	2.4e-64	227.2
311	F-box	F-box domain.	9.5e-08	39.2
312	ig	Immunoglobulin domain	6.8e-19	65.9
313	Ets	Ets-domain	8.1e-60	192.3
315	Kelch	Kelch motif	1.3e-106	367.6
317	arf	ADP-ribosylation factor family	3.2e-35	130.4
318	sugar_tr	Sugar (and other) transporter	0.0003	-73.1
320	pkinase	Eukaryotic protein kinase domain	8.1e-83	288.6
322	pkinase	Eukaryotic protein kinase domain	4.9e-81	282.6
324	Xlink	Extracellular link domain	4.5e-143	331.5
326	ARID	ARID DNA binding domain	5.1e-37	136.4
327	HMG box	HMG (high mobility group) box	6.7e-29	109.4
328	cadherin	Cadherin domain	8.1e-81	281.9
331	chromo	'chromo' (CHRromatin Organization MOdifier)	4e-18	66.7
333	Peptidase_M2	Glycoprotease family	1.2e-136	467.4

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
335	vwa	von Willebrand factor type A	2.3e-07	37.9
		domain		ļ. <u></u>
339	ras	Ras family	7.8e-07	-59.1
340	zf-C2H2	Zinc finger, C2H2 type	8.2e-64	225.4
342	zf-C2H2	Zinc finger, C2H2 type	2.4e-85	297.0
343	ig	Immunoglobulin domain	0.0005	18.0
346	pkinase	Eukaryotic protein kinase domain	6.5e-65	229.1
347	pkinase	Eukaryotic protein kinase domain	6.5e-65	229.1
351	EGF	EGF-like domain	8.5e-20	79.2
352	ank	Ank repeat	2.5e-101	350.0
354	TBC	TBC domain	5.1e-15	63.3
	PHD	PHD-finger	3.2e-07	37.4
355		Integral membrane protein DUP6	0.033	15.8
358	DUF6		1	79.4
359	zf-C2H2	Zinc finger, C2H2 type	7.4e-20	
361	ank	Ank repeat	6.6e-34	126.1
362	ArfGap	Putative GTP-ase activating protein for Arf	4.7e-53	189.7
363	efhand	BF hand	5.4e-10	46.6
367	LRR	Leucine Rich Repeat	8.8e-44	158.9
368	laminin G	Laminin G domain	1.5e-33	121.7
369	PP2C	Protein phosphatase 2C	5.3e-20	73.9
372	T.TM	LIM domain containing proteins	9.9e-15	57.1
	KRAB	KRAB box	4.8e-23	90.0
373			2.9e-09	-4.2
376	ion_trans	Ion transport protein	1	704.5
377	Beach	Beige/BEACH domain	4.9e-208	
380	pkinase	Eukaryotic protein kinase domain	1.6e-94	327.5
381	AMP-binding	AMP-binding enzyme	1.4e-07	-140.3
382	HECT	HECT-domain (ubiquitin- transferase).	1.3e-07	-13.5
384	ank	Ank repeat	2.5e-101	350.0
386	iq	Immunoglobulin domain	9.5e-06	23.6
388	zf-C2H2	Zinc finger, C2H2 type	1.7e-42	154.6
389	ig	Immunoglobulin domain	2.8e-15	54.3
390	mito carr	Mitochondrial carrier proteins	3.5e-67	233.2
392	TPR	TPR Domain	6.1e-17	69.7
	SH3	SH3 domain	3.5e-09	43.9
393 394	AAA	ATPases associated with various	4.1e-21	83.6
		cellular act	L	1000
396	spectrin	Spectrin repeat	2.1e-67	237.3
397	zf-C2H2	Zinc finger, C2H2 type	0.0066	23.1
399	fn3	Fibronectin type III domain	4.1e-102	352.6
400	WD40	WD domain, G-beta repeat	0.00049	26.8
401	El dehydrog	Dehydrogenase E1 component	3e-119	409.6
402	£n3	Fibronectin type III domain	0	1719.6
404	LRR	Leucine Rich Repeat	2.1e-10	48.0
405	cadherin	Cadherin domain	8.1e-81	281.9
406	zf-CXXC	CXXC zinc finger	5e-15	63.4
410	RhoGEF	RhoGEF domain	1.1e-23	92.1
		F-box domain.	4.2e-06	33.7
411	F-box SNF2_N	SNF2 and others N-terminal	5.8e-16	61.6
415	CPSase_L_cha	domain Carbamoyl-phosphate synthase	1.5e-172	586.6
	in	(CPSase)	L	+
418	LRR	Leucine Rich Repeat	3.8e-24	93.6
419	DENN	DENN (AEX-3) domain	2e-58	207.5
420	RasGEF	RasGEF domain	8.1e-43	155.7
421	ank	Ank repeat	1.4e-153	523.7
424	G-patch	G-patch domain	le-19	78.9
425	pkinase	Eukarvotic protein kinase	2.2e-31	117.1
		domain		24.6
426	Plexin_repea	Plexin repeat	0.0023	
	Plexin repea		0.0023	24.6

SEQ ID	DEAM NAME	I DESCRIPTION		
NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
429	zf-C3HC4	Zinc finger, C3HC4 type (RING	8.6e-11	39.2
431	DEAD	finger)		
432	SH3	DEAD/DEAH box helicase SH3 domain	1e-66	214.0
433	GTP CDC		3.4e-16	67.2
436	Collagen	Cell division protein	2.le-114	393.5
		Collagen triple helix repeat (20 copies)	4.6e-194	658.1
438	Ricin_B_lect in	Similarity to lectin domain of ricin b	0.0085	10.5
441	Alpha_adapti n_C	Alpha adaptin carboxyl-terminal domai	1.2e-256	866.0
442	Alpha_adapti n_C	Alpha adaptin carboxyl-terminal domai	1.8e-235	795.7
443	PDZ	PDZ domain (Also known as DHR or GLGF).	1.9e-65	230.9
445	LON	ATP-dependent protease La (LON) domain	0.00012	-17.1
446	ig	Immunoglobulin domain	0.00011	20.1
451	sushi	Sushi domain (SCR repeat)	1.4e-18	75.2
452	fn3	Fibronectin type III domain	1.5e-06	35.2
454	pyridoxal_de	Pyridoxal-dependent	8.3e-14	50.3
		decarboxylase conse	1	1
456	kinesin	Kinesin motor domain	4.9e-217	734.4
457	neur_chan	Neurotransmitter-gated ion-	le-175	597.1
		channel		
458	Josephin	Josephin	0.0002	18.7
468	bžIP	bZIP transcription factor	1.7e-07	31.8
470	NTP_transfer ase	Nucleotidyl transferase	6.3e-06	-26.3
471	WD40	WD domain, G-beta repeat	2e-28	107.9
473	LIM	LIM domain containing proteins	0.00021	20.7
477	zf-RanBP	Zn-finger in Ran binding protein and others.	0.028	21.0
479	WD40	WD domain, G-beta repeat	6.5e-18	73.0
480	KRAB	KRAB box	le-31	118.8
481	ArfGap	Putative GTP-ase activating protein for Arf	8.4e-66	232.0
485	SH2	Src homology domain 2	0.011	11.4
486	Clq	Clq domain	4.3e-74	259.6
487	dsrm	Double-stranded RNA binding motif	1.le-47	171.9
489	zf-C2H2	Zinc finger, C2H2 type	4.8e-153	521.9
490	Alpha_adapti n_C	Alpha adaptin carboxyl-terminal domai	3.4e-222	751.6
492	SKI	Shikimate kinase	1.2e-10	48.8
497	ENV_polyprot ein	ENV polyprotein (coat polyprotein)	2.6e-22	77.6
498	abhydrolase_ 2	Phospholipase/Carboxylesterase	0.041	-48.1
500	rrm	RNA recognition motif.	5.4e-34	126.4
501	WW	WW domain .	4.6e-18	73.4
502	ig	Immunoglobulin domain	1.1e-10	39.5
504	abhydrolase	alpha/beta hydrolase fold	0.045	-3.6
505	vwa	von Willebrand factor type A domain	7.1e-62	219.0
508	Na_K_ATPase_ C	Na+/K+ ATPase C-terminus	2.3e-145	496.3
509	Exonuclease	Exonuclease	1.3e-56	201.5
510	Glycos_trans f 1	Glycosyl transferases group 1	2.9e-06	27.0
	Glycos trans	Glycosyl transferases group 1	2.9e-06	27.0
511				1
511	f_1 Glycos_trans f 1	Glycosyl transferases group 1	1.9e-09	38.5
	f_1 Glycos_trans	Glycosyl transferases group 1 Cyclophilin type peptidyl-	1.9e-09	38.5

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
515	EGF	EGF-like domain	1.9e-18	74.7
516	Surp	Surp module	4.3e-38	140.0
			3.3e-06	25.0
523	ig	Immunoglobulin domain		1
526	UBX	UBX domain	1.1e-34	128.6
528	adh_zinc	Zinc-binding dehydrogenases	2.7e-34	127.4
530	SAM	SAM domain (Sterile alpha	0.046	10.0
		motif)	0.0025	
531	adh_short	short chain dehydrogenase	1	-34.1
532	mito_carr	Mitochondrial carrier proteins	2.5e-8I	281.7
533	mito_carr	Mitochondrial carrier proteins	2e-61	213.5
534	thiolase	Thiolase	3.5e-183	622.0
535	FMO-like	Flavin-binding monooxygenase- like	0	1153.7
536	SCAN	SCAN domain	4e-55	196.6
537	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	3.1e-136	466.0
538	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	3.1e-136	466.0
539	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	1.9e-117	403.6
540	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	3.le-136	466.0
541	vATP-synt_E	ATP synthase (E/31 kDa) subunit	5.9e-85	295.7
543	zf-C2H2	Zinc finger, C2H2 type	5.5e-69	242.6
	DUF101	Protein of unknown function	8.5e-38	139.0
544	DOF101	DUF101	8.5e-38	139.0
545	TGFb_propept	TGF-beta propeptide	1.le-67	238.2
547	WD4 0	WD domain, G-beta repeat	2.6e-32	120.8
548	RHD	Rel homology domain (RHD).	1.6e-238	686.2
549	MMR HSR1	GTPase of unknown function	5.4e-67	236.0
551	HECT	HECT-domain (ubiquitin-	4.3e-127	435.6
221	RECI	transferase).	4.36-12/	
554	MHC_II_alpha	Class II histocompatibility antigen, alp	3.5e-74	259.8
555	2f-UBR1	Putative zinc finger in N- recognin	3.3e-16	67.3
556	Kelch	Kelch motif	5.5e-29	109.7
561	AMP-binding	AMP-binding enzyme	2.8e-06	-163.7
562	PABP	Poly-adenylate binding protein, unique domai	4.9e-38	139.8
564	Gag_p30	Gag P30 core shell protein	1.2e-67	238.2
566	PWWP	PWWP domain	8.1e-16	66.0
		SCAN domain	1.	
567	SCAN		7.3e-68	238.9
569	pkinase	Eukaryotic protein kinase domain	1.5e-84	294.3
570	pkinase	Bukaryotic protein kinase domain	1.5e-84	294.3
571	CN_hydrolase	Carbon-nitrogen hydrolase	0.00081	-79.7
572	myosin head	Myosin head (motor domain)	0	1495.2
573	myosin head	Myosin head (motor domain)	0	1490.4
575	Surp	Surp module	1.7e-23	91.5
576		Surp module	1.7e-23	91.5
	Surp		<u> </u>	
577	DNA_pol_B	DNA polymerase family B	0	1138.6
578	PDZ	PDZ domain (Also known as DHR or GLGF).	8.3e-09	42.7
579	LRR	Leucine Rich Repeat	4.9e-21	83.3
580	neur_chan	Neurotransmitter-gated ion- channel	5.9e-177	601.3
583	sushi	Sushi domain (SCR repeat)	0	1673.0
584	DEAD	DBAD/DEAH box helicase	7.3e-36	116.3
	KH-domain	KH domain		
586			2.9e-13	57.5
565		G-patch domain	2.3e-14	61.2
587	G-patch			+
589	LIM	LIM domain containing proteins	2.3e-36	133.4
			2.3e-36 6.6e-32	133.4

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:				SCORE
592	hormone_rec	Ligand-binding domain of	3.5e-22	87.1
593	PHD	nuclear hormone PHD-finger	3.8e-12	53.8
594	cadherin	Cadherin domain	4.2e-99	342.7
596	pkinase	Eukaryotic protein kinase	5e-92	319.2
		domain		
597	WD40	WD domain, G-beta repeat	0.00054	26.7
600	FG-GAP	FG-GAP repeat	4.3e-75	262.9
602	G_Adapt_CT	Gamma-adaptin, C-terminus	1.1e-53	191.8
603	pkinase	Eukaryotic protein kinase domain	2.3e-86	
605	Collagen	Collagen triple helix repeat (20 copies)	8e-42	152.4
606	mito carr	Mitochondrial carrier proteins	6.3e-67	232.3
608	PWWP	PWWP domain	2.6e-28	107.5
609	PWWP	PWWP domain	2.6e-28	107.5
613	CAP_GLY	CAP-Gly domain	0.0046	20.1
615	RFX_DNA_bind ing	RFX DNA-binding domain	5.2e-54	192.9
616	kinesin	Kinesin motor domain	1.1e-81	284.8
617	kinesin	Kinesin motor domain	8.4e-80	278.5
618	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.0098	13.1
620	MATH	MATH domain	7.8e-05	22.2
621	Y_phosphatas	Protein-tyrosine phosphatase	1.4e-32	121.6
	е			
622	pkinase	Eukaryotic protein kinase domain	4.46-40	146.6
623	BNR	BNR repeat	2.1e-11	51.3
624	molybdopteri n	Prokaryotic molybdopterin oxidoreductas	1.4e-12	42.2
625	TPR	TPR Domain	1.1e-17	72.2
627	cNMP_binding	Cyclic nucleotide-binding domain	3.7e-58	206.6
630	adh short	short chain dehydrogenase	5e-17	70.0
631	zf-C2H2	Zinc finger, C2H2 type	2.1e-88	307.1
632	rrm	RNA recognition motif.	4e-05	30.5
635	pkinase	Eukaryotic protein kinase domain	1.6e-104	360.7
636	Fork head	Fork head domain	5.9e-27	103.0
637	pkinase	Eukaryotic protein kinase	3.8e-70	246.5
	F	domain		
642	TPR	TPR Domain	4.8e-08	40.1
643	efhand	EF hand	1.9e-27	104.6
647	SNF2_N	SNF2 and others N-terminal domain	1.2e-101	351.1
648	PseudoU_synt	RNA pseudouridylate synthase	1.9e-55	197.6
650	zf-C2H2	Zinc finger, C2H2 type	0.0087	22.7
651	ank	Ank repeat	1.3e-17	71.9
652	I_LWEQ	I/LWEQ domain	9.5e-101	341.0
653	neur_chan	Neurotransmitter-gated ion- channel	4.1e-171	581.8
654	tsp 1	Thrombospondin type 1 domain	4.1e-47	169.9
659	FH2	Formin Homology 2 Domain	1e-107	371.2
661	pou	Pou domain - N-terminal to homeobox domain	5.3e-45	162.9
662	C2	C2 domain	6.7e-19	76.2
663	C2	C2 domain	6.7e-19	76.2
664	C2	C2 domain	6.7e-19	76.2
667	GST	Glutathione S-transferases.	9.3e-34	114.4
668	LRR	Leucine Rich Repeat	9.3e-31	115.6
670	spectrin	Spectrin repeat	4e-57	203.2
671	I_LWEQ	I/LWEQ domain	9.5e-101	341.0
672	ABC_tran	ABC transporter	5.3e-60	212.8
674	WD40	WD domain, G-beta repeat	4.8e-24	93.3

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:				SCORE
675	WD40	WD domain, G-beta repeat	4.8e-24	93.3
676	LRR	Leucine Rich Repeat	0.0015	25.2
679	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-29	107.7
680	zf-C2H2	Zinc finger, C2H2 type	5.2e-05	30.1
681	CH	Calponin homology (CH) domain	2.4e-17	71.1
682	DSPc	Dual specificity phosphatase, catalytic doma	4.3e-43	156.6
683	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.051	10.8
687	Synapsin	Synapsin	0	1890.8
689	PRSS	Protein phosphatase 2A regulatory subunit PR	0	1038.8
691	homeobox	Homeobox domain	8.5e-30	112.4
696	Peptidase_M2	metallopeptidase family M24	2.6e-59	210.5
697	RhoGEF	RhoGEF domain	9.5e-35	128.9
698	PHD	PHD-finger	0.008	9.3
701	zf-C2H2	Zinc finger, C2H2 type	5.5e-123	422.0
701	Sulfatase	Sulfatase	3e-231	781.6
702	zf-C2H2	Zinc finger, C2H2 type	5.7e-20	79.8
703	Acyl transf	Acyl transferase domain	1.1e-22	88.8
708	WD40	WD domain, G-beta repeat	4.8e-19	76.7
710	Ran BP1	RanBP1 domain.	8.4e-06	-7.3
710	DEAD DEAD	DEAD/DEAH box helicase	9.9e-42	134.9
714	PH	PH domain	1.6e-09	39.0
		Dual specificity phosphatase,	1.5e-37	138.2
715	DSPc	catalytic doma		
717	Sialyltransf	Sialyltransferase family	7.5e-31	115.9
718	ig	Immunoglobulin domain	1e-29	100.8
719	integrin_B	Integrins, beta chain	0	1125.4
720	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.1e-08	32.4
722	Peptidase_C2	Calpain family cysteine protease	3e-145	495.9
723	ig	Immunoglobulin domain	2.2e-05	22.4
724	F-box	F-box domain.	0.007	23.0
725	Nop	Putative snoRNA binding domain	8.1e-58	205.5
726	Nop	Putative snoRNA binding domain	8.1e-58	205.5
727	WD40	WD domain, G-beta repeat	7.5e-26	99.3
730	dsrm	Double-stranded RNA binding motif	0.027	12.1
731	dynamin	Dynamin family	4.2e-16	66.9
733	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.8e-10	41.7
735	CDP- OH_P_transf	CDP-alcohol phosphatidyltransferase	4.2e-26	100.1
738	DEAD	DEAD/DEAH box helicase	8.6e-57	182.5
739	TSC22	TSC-22/dip/bun family	6.5e-32	119.5
742	ras	Ras family	2.2e-100	346.9
743	PMI_typeI	Phosphomannose isomerase type I	1.2e-243	822.9
747	trypsin	Trypsin	6.4e-88	279.4
748	kazal	Kazal-type serine protease inhibitor domain	2.2e-52	187.4
749	efhand	EF hand	6.3e-06	33.1
751	PHD	PHD-finger	4.9e-16	66.7
752	zf-C2H2	Zinc finger, C2H2 type	3.2e-21	83.9
753	Hydrolase	haloacid dehalogenase-like hydrolase	6.1e-11	49.8
754	Ribosomal_L3	Ribosomal L39 protein	0.00018	26.7
755	PH	PH domain	3.6e-14	55.7
758	SCAN	SCAN domain	1.4e-53	191.5
759	PA	PA domain	0.0065	23.1
760	arf	ADP-ribosylation factor family	2.2e-19	77.8
	CIDE-N	CIDE-N domain	2.2e-19	147.6
761	CIDD-W	CLDD-II GOMATH	4.26-40	147.0

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
NO:	 	Core histone H2A/H2B/H3/H4	9.9e-53	188.6
762 763	histone zf-MYND	MYND finger	4.1e-14	60.3
763		Pou domain - N-terminal to	1e-52	188.6
	bon	homeobox domain		
767	vwc	von Willebrand factor type C domain	2.9e-34	127.3
769	efhand	EF hand	4.8e-11	50.1
770	zf-C4	Zinc finger, C4 type (two . domains)	2.4e-53	181.6
772	ras	Ras family	7e-90	312.0
773	Sulfatase	Sulfatase	le-142	487.5
775	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
776	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
777	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
778	rrm	RNA recognition motif.	2.1e-32	121.1
779	GGPD	Glucose-6-phosphate dehydrogenase	1.5e-76	236.6
780	spectrin	Spectrin repeat	3.7e-29	110.3
781	mito_carr	Mitochondrial carrier proteins	4.6e-57	198.5
782	SCAN	SCAN domain	1.3e-24	95.2
783	PDZ	PDZ domain (Also known as DHR or GLGF).	4.1e-07	37.1
785	DEAD	DEAD/DEAH box helicase	6e-06	21.7
786	ras	Ras family	5.3e-39	143.0
787	RNase HII	Ribonuclease HII	2.5e-67	237.1
790	PI3_PI4_kina se	Phosphatidylinositol 3- and 4- kinases	5.4e-108	372.2
795	cadherin	Cadherin domain	2.5e-40	147.4
796	ARID	ARID DNA binding domain	1.6e-20	81.6
797	trypsin	Trypsin	9.9e-20	64.8
799	CH	Calponin homology (CH) domain	3.7e-15	63.8
801	Gal-	Vertebrate galactoside-binding	4.1e-25	88.7
	bind lectin	lectin		
803	WD40	WD domain, G-beta repeat	0.00082	26.1
806	TBC	TBC domain	1.8e-26	101.4
807	TBC	TBC domain	1.8e-26	101.4
808	CN hydrolase	Carbon-nitrogen hydrolase	8.8e-80	278.5
811	CBFD_NFYB_HM	Histone-like transcription factor	6e-14	59.8
812	adh short	short chain dehydrogenase	B.1e-20	79.3
814	IMP4	Domain of unknown function	3.3e-71	250.0
815	zf-C2H2	Zinc finger, C2H2 type	8.2e-66	232.1
816	Pept_tRNA_hy	Peptidyl-tRNA hydrolase	1.6e-37	138.0
817	ARID	ARID DNA binding domain	2.5e-18	74.3
826	IF5_eIF4_eIF	eIF4-gamma/eIF5/eIF2-epsilon	1.6e-32	121.5
830	ArfGap	Putative GTP-ase activating protein for Arf	1.5e-53	191.3
831	LRR	Leucine Rich Repeat	2.1e-26	101.1
832	laminin_EGF	Laminin EGF-like (Domains III	2e-57	204.2
020		and V) RNA recognition motif.	1.3e-22	88.5
839 840	rrm Y phosphatas	Protein-tyrosine phosphatase	2.6e-119	409:8
	e			
841	pkinase	Eukaryotic protein kinase domain	3.4e-100	346.3
844	Ribosomal_L2 2e	Ribosomal L22e protein family	le-64	228.4
846	IBR	IBR domain	9e-15	62.5
849	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.4e-07	26.5
850	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.00016	18.9
851	SET	SET domain	5e-30	113.2
852	SRCR	Scavenger receptor cysteine-	0	1025.4

000 35	155	T		
SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
		rich domain		
853	SRCR	Scavenger receptor cysteine- rich domain	0	1025.4
857	lactamase_B	Metallo-beta-lactamase superfamily	0.012	-6.0
858	COX6A	Cytochrome c oxidase subunit	3.4e-58	206.7
859	rrm	RNA recognition motif.	5.4e-45	162.9
861	PRK	Phosphoribulokinase	5.1e-62	219.4
863	mito_carr	Mitochondrial carrier proteins	2.9e-53	185.5
864	HSP90	Hap90 protein	4.7e-158	538.5
866	ig	Immunoglobulin domain	4e-12	44.1
867	zf-C2H2	Zinc finger, C2H2 type	7e-135	461.5
872	histone	Core histone H2A/H2B/H3/H4	4.9e-41	149.8
874	CPSase L cha	Carbamoyl-phosphate synthase	2.1e-218	
879	in Ribosomal S1	(CPSase) Ribosomal protein S12e		739.0
882	2e		2.1e-98	340.3
	serpin	Serpins (serine protease inhibitors)	2.5e-42	145.7
883	Patatin	Patatin	1.2e-51	182.0
884	RA	Ras association (RalGDS/AF-6) domain	0.044	8.0
887	DUF92	Integral membrane protein DUF92	2.7e-12	54.3
889	sugar_tr	Sugar (and other) transporter	8.2e-63	222.1
893	DUF28	Domain of unknown function DUF28	1.3e-43	158.3
896	IP_trans	Phosphatidylinositol transfer protein	6.5e-98	338.7
898	DEAD	DEAD/DEAH box helicase	1.5e-48	156.5
899	KE2	KE2 family protein	7e-61	215.7
900	KE2	KE2 family protein	4.3e-51	183.2
901	zf-C2H2	Zinc finger, C2H2 type	2.7e-57	203.8
902	ras	Ras family	2.3e-75	263.8
904	TPR	TPR Domain	3.2e-22	87.2
906	GBP	Guanylate-binding protein	8.9e-253	853.1
907	GBP	Guanylate-binding protein	1.1e-239	809.6
908	WD40	WD domain, G-beta repeat	2.6e-26	100.8
909	PH	PH domain	1.3e-09	39.4
910	zf-C2H2	Zinc finger, C2H2 type	2.5e-39	144.1
913	Epimerase	NAD dependent epimerase/dehydratase family	5e-07	-88.5
921	TBC	TBC domain	1.5e-09	30.7
922	WD40	WD domain, G-beta repeat	1.6e-25	98.2
923	WD40	WD domain, G-beta repeat	8.2e-07	36.1
924	Hydrolase	haloacid dehalogenase-like hydrolase	2.9e-05	29.1
925	UQ_con	Ubiquitin-conjugating enzyme	0.00033	-27.6
926	CH	Calponin homology (CH) domain	3.3e~53	190.2
928	WD40	WD domain, G-beta repeat	5.9e-48	172.7
929	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	3.1e-10	37.4
930	Ribul_P_3_ep im	Ribulose-phosphate 3 epimerase family	7.2e-105	361.8
931	Ribul_P_3_ep	Ribulose-phosphate 3 epimerase family	1.2e-96	334.4
936	C2	C2 domain	2 2	
937	NAP_family	Nucleosome assembly protein	2.2e-62 1.1e-22	84.6
		(NAP) alpha/beta hydrolase fold	2	
940	annvaro	ı ¤±PµA/Deta DVOTOlâsê fold	0.011	3.1
940	abhydrolase Tropomyosin			
944	Tropomyosin	Tropomyosins	3.2e-07	25.1
944	Tropomyosin pkinase	Tropomyosins Eukaryotic protein kinase domain	3.2e-07 3.4e-75	25.1 263.2
944	Tropomyosin	Tropomyosins Eukaryotic protein kinase	3.2e-07	25.1

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
951	SAM	SAM domain (Sterile alpha motif)	0.014	14.5
954	GFO IDH MocA	Oxidoreductase family	1.3e-11	52.0
955	BTB	BTB/POZ domain	7e-22	86.1
956	BTB	BTB/POZ domain	7e-22	86.1
957	CDP-	CDP-alcohol	0.053	-22.2
,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	OH P transf	phosphatidyltransferase	0.053	-22.2
959	ras	Ras family	2.4e-97	336.8
960	ras	Ras family	8.4e-43	155.6
961	Acetyltransf	Acetyltransferase (GNAT) family	1.2e-08	42.2
962	adh short	short chain dehydrogenase	2.4e-31	117.6
963	mutT	Bacterial mutT protein	5.6e-06	26.2
969	IF-2B	Initiation factor 2 subunit	8.4e-193	653.9
		family		
970	RNase_PH	3' exoribonuclease family	9e-24	92.4
975	WW	WW domain	5.7e-25	96.4
977	PDZ	PDZ domain (Also known as DHR or GLGF).	3.6e-21	83.7
978	Ribosomal_L1	Ribosomal protein L17	2.4e-20	81.0
979	LIM	LIM domain containing proteins	5.8e-42	152.8
980	Calsequestri n	Calsequestrin	1.7e-297	1001.7
982	HSP20	Hsp20/alpha crystallin family	1.2e-10	43.2
983	oxidored_q6	NADH ubiquinone oxidoreductase,	4.8e-63	222.9
		20 Kd sub	1	1
988	TBC	TBC domain	2.2e-50	180.8
989	TBC	TBC domain	2.2e-50	180.8
993	tRNA_int_end	tRNA intron endonuclease	0.0017	-34.2
994	homeobox	Homeobox domain	4e-18	73.6
997	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	0.012	11.6
1000	mito carr	Mitochondrial carrier proteins	9.7e-123	421.2
1001	RA	Ras association (RalGDS/AF-6)	1.2e-15	65.4
1004	DUF81	Domain of unknown function	0.099	10.2
1005	actin	Actin	1.3e-174	574.3
1006	actin	Actin	3.1e-130	428.6
1007	cpn60_TCP1	TCP-1/cpn60 chaperonin family	3.7e-195	661.8
1008	TPR	TPR Domain	8.1e-44	159.0
1009	zf-C2H2	Zinc finger, C2H2 type	3.6e-61	216.6
1011	zf-C2H2	Zinc finger, C2H2 type	3.6e-61	216.6
1012	zf-C3HC4	Zinc finger, C3HC4 type (RING	4.7e-15	
		finger)		53.1
1016	tRNA-synt_2c	tRNA synthetases class II (A)	2.3e-15	55.2
1018	RhoGAP	RhoGAP domain	1.6e-78	274.3
1022	PGAM	Phosphoglycerate mutase family	3.8e-18	69.7
1026	HMG_box	HMG (high mobility group) box	8.4e-20	79.2
1027	TBC	TBC domain	7.3e-45	162.5
1028	UQ_con	Ubiquitin-conjugating enzyme	1.4e-49	178.1
1032	PDZ	PDZ domain (Also known as DHR or GLGF).	0.028	16.3
1034	Hydrolase	haloacid dehalogenase-like hydrolase	2e-21	84.6
1037	KRAB	KRAB box	4.8e-06	32.4
1038	Cation_efflu x	Cation efflux family	7.1e-42	152.5
1040	ART	NAD:arginine ADP-	4.7e-47	169.1
1042	WDAO	ribosyltransferase		
	WD40	WD domain, G-beta repeat	1.9e-18	74.7
1043	zf-C2H2	Zinc finger, C2H2 type	3.7e-24	93.7
1045	lectin_c	Lectin C-type domain	1.9e-28	108.0
1046	Glucosamine	Glucosamine-6-phosphate	0.00013	-25.1
	iso	isomerase		1

SEQ ID	PFAM NAME	DESCRIPTION		
NO:			p-value	PFAM
1047	ligase-CoA	CoA-ligases	4.5e-80	279.4
1049	ig	Immunoglobulin domain	1.7e-09	35.6
1050	Ribosomal_L2	Ribosomal protein L24e	2e-33	124.5
1054	Amidase	Amidase	4.3e-152	518.7
1055	rrm	RNA recognition motif.	3.8e-26	100.3
1058	annexin			159.2
1059	PMP22 Claudi	PMP-22/EMP/MP20/Claudin family	6.9e-44 0.023	
1060	n			-23.6
1062	homeobox	Homeobox domain	3.2e-31	117.2
	Acyltransfer ase	Acyltransferase	0.00065	10.5
1064	AMP-binding	AMP-binding enzyme	6.6e-100	345.3
1065	LRR	Leucine Rich Repeat	3.3e-14	60.6
1066	GTP1_OBG	GTP1/OBG family	4.8e-41	141.8
1071	ig	Immunoglobulin domain	8.4e-48	159.1
1072	PHD	PHD-finger	6.8e-07	36.3
1074	DENN	DENN (AEX-3) domain	8.3e-33	121.5
1075	SCP	SCP-like extracellular protein	4.7e-41	149.8
1077 .	OLF	Olfactomedin-like domain	2.2e-66	234.0
1078	mito carr	Mitochondrial carrier proteins	1e-42	149.3
1079	WD40	WD domain, G-beta repeat	6.2e-45	162.7
1087	START	START domain	1.5e-48	174.7
1093	DSPC	Dual specificity phosphatase,	3.3e-63	223.4
1.004		catalytic doma		223.4
1094	GSHPx	Glutathione peroxidases	9.6e-41	148.8
1095	DUF25	Domain of unknown function DUF25	2e-75	264.0
1096	DUF25	Domain of unknown function DUF25	6e-75	262.4
1105	Nitroreducta se	Nitroreductase family	1.3e-13	58.6
1106	PTE	Phosphotriesterase family	1.3e-179	610.1
1107	DAGKC	Diacylglycerol kinase catalytic domain	0.00049	19.6
1109	ras	Ras family	1 2 2 2 2	1
1115	ArfGap	Putative GTP-ase activating	1.3e-15 9.7e-47	168.7
1116	1000	protein for Arf		
1116	HMG14_17	HMG14 and HMG17	4.4e-21	83.5
1117	HMG14_17	HMG14 and HMG17	9.9e-12	52.4
1119	FAA_hydrolas e	Fumarylacetoacetate (FAA) hydrolase fam	2e-83	290.6
1120	pkinase	Eukaryotic protein kinase domain	1.4e-94	327.6
1123	abhydrolase	alpha/beta hydrolase fold	9.2e-23	89.0
1129	pro_isomeras e	Cyclophilin type peptidyl- prolyl cis-tr	2.2e-56	197.1
1131	DnaJ	DnaJ domain	1.6e-30	114.9
1132	WD40	WD domain, G-beta repeat	1.3e-19	78.6
1133	WD40	WD domain, G-beta repeat	1.8e-15	64.9
1134	PH	PH domain	0.0015	
1136	Adap_comp_su b	Adaptor complexes medium subunit family	1.2e-256	17.8 866.0
1137	Adap_comp_su b	Adaptor complexes medium	2.5e-209	708.8
1139	ras	subunit family		
1139		Ras family	1.5e-86	301.0
	pkinase	Eukaryotic protein kinase domain	9.4e-74	258.4
1152	Acyltransfer ase	Acyltransferase	1.2e-05	29.9
1153	IRS	PTB domain (IRS-1.type)	5.4e-55	196.1
1155	ig	Immunoglobulin domain	1.3e-31	106.9
1157	Asparaginase	Asparaginase	6.4e-72	252.3
1159	GMC oxred	GMC oxidoreductases		405
1160	zf-AN1	AN1-like Zinc finger	4.7e-142 0.00021	27.9

1236 1 1241 1 1243 1 1247 1 1248 (1249 (1254 1 1255 1 1256 1 1259 1 1261 1	efhand crm DUF6 GCAN 3-gamma catalase PX PPCH Peptidase_M2 O WW UPF0006 Glycos_trans f_2 efhand UQ_con ras formyl_trans f zf-C3HC4 DiHfolate_re d G_glu_transp ept PAS	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases EF hand Ubiquitin-conjugating enzyme Ras family Formyl transferase Zinc finger, C3HC4 type (RING finger) Dihydrofolate reductase Gamma-glutamyltranspeptidase PAS domain	2.1e-40 0.015 1.5e-71 3.6e-36 0 2.2e-15 2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10 4e-11 2.1e-73 2.2e-62 4.9e-30 5.3e-13 2.1e-69 1.8e-110	147.7 21.5 251.1 129.5 1158.9 64.5 64.5 44.0 224.1 17.9 215.8 46.9 50.4 257.3 220.7 108.3 46.4
1236 1 1241 1 1243 1 1247 1 1248 6 1249 6 1254 1 1255 1 1256 1 1261 1	efhand crm DUF6 GCAN 3-gamma catalase PX PK FCH Peptidase_M2 0 WW UPF0006 Glycos_trans f_2 efhand UQ_con ras formyl_trans f zf-C3HC4 DiHfolate_re d G_glu_transp	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases BF hand Ubiquitin-conjugating enzyme Ras family Formyl transferase Zinc finger, C3HC4 type (RING finger) Dihydrofolate reductase	0.015 1.5e-71 3.6e-36 0 2.2e-15 2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10 4e-11 2.1e-73 2.2e-62 4.9e-30 5.3e-13 2.1e-69	21.5 251.1 129.5 1158.9 64.5 64.5 44.0 224.1 17.9 215.8 46.9 50.4 257.3 220.7 108.3 46.4
1236 1 1241 1 1243 1 1247 1 1248 (1249 1 1254 1 1255 1 1256 1 1259 1 1261 1	efhand rrm DUF6 SCAN 3-gamma catalase PX PX PCH Peptidase_M2 O WW UPF0006 Slycos_trans f_2 efhand UQ_con ras fformyl_trans ff zf-C3HC4 DiHfolate_re	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain PY domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases BF hand Ubiquitin-conjugating enzyme Ras family Formyl transferase Zinc finger, C3HC4 type (RING finger)	0.015 1.5e-71 3.6e-36 0 2.2e-15 2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10 4e-11 2.1e-73 2.2e-62 4.9e-30 5.3e-13	21.5 251.1 129.5 1158.9 64.5 64.5 44.0 224.1 17.9 215.8 46.9 50.4 257.3 220.7 108.3
1236 1 1241 1 1243 1 1247 1 1248 (1249 1 1254 1 1255 1 1256 1	efhand frm DUF6 SCAN 3-gamma catalase PX FCH Peptidase_M2 0 WW UPF0006 Glycos_trans f_2 efhand UQ_con ras formyl_trans f	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases EF hand Ubiquitin-conjugating enzyme Ras family Formyl transferase Zinc finger, C3HC4 type (RING	0.015 1.5e-71 3.6e-36 0 2.2e-15 2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10 4e-11 2.1e-73 2.2e-62 4.9e-30	21.5 251.1 129.5 1158.9 64.5 64.5 44.0 224.1 17.9 215.8 46.9 50.4 257.3 220.7 108.3
1236 1 1241 1 1243 1 1247 1 1248 (1249 (1254 1 1255 1256 1	efhand crm DUF6 SCAN 3-gamma -atalase PX PX PCH Peptidase_M2 0 WW UPF0006 Glycos_trans f_2 efhand UQ_con ras formyl_trans	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases BF hand Ubiquitin-conjugating enzyme Ras family	0.015 1.5e-71 3.6e-36 0 2.2e-15 2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10 4e-11 2.1e-73 2.2e-62	21.5 251.1 129.5 1158.9 64.5 64.5 44.0 224.1 17.9 215.8 46.9 50.4 257.3 220.7
1236 1 1241 1 1243 1 1247 1 1248 (1249 (1254 1 1255 1	efhand crm DUF6 SCAN 3-gamma catalase PX PX PCH Peptidase_M2 0 WW UPF0006 Glycos_trans f_2 efhand UQ_con ras	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases BF hand Ubiquitin-conjugating enzyme Ras family	0.015 1.5e-71 3.6e-36 0 2.2e-15 2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10 4e-11 2.1e-73 2.2e-62	21.5 251.1 129.5 1158.9 64.5 64.5 44.0 224.1 17.9 215.8 46.9 50.4 257.3 220.7
1236 1 1241 1 1243 1 1247 1 1248 (1249 (efhand crm DUF6 GCAN 3-gamma catalase PX FCH Peptidase_M2 0 WW UPF0006 Glycos_trans f_2 efhand UQ_con	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases BF hand Ubiquitin-conjugating enzyme	0.015 1.5e-71 3.6e-36 0 2.2e-15 2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10 4e-11 2.1e-73	21.5 251.1 129.5 1158.9 64.5 44.0 224.1 17.9 215.8 46.9
1236 1 1241 1 1243 1 1247 1 1248 (efhand crm DUF6 SCAN 3-gamma catalase PX PPX FCH Peptidase_M2 0 WW UPF0006 Slycos_trans f_2 efhand	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases BF hand	0.015 1.5e-71 3.6e-36 0 2.2e-15 2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10	21.5 251.1 129.5 1158.9 64.5 64.5 44.0 224.1 17.9 215.8
1236 1 1241 1 1243 1 1247 1 1248 (efhand rrm DUF6 SCAN 3-gamma catalase PX PX PCH Peptidase_M2 0 WW UPF0006 Glycos_trans f_2	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases	0.015 1.5e-71 3.6e-36 0 2.2e-15 2.2e-15 3.3e-09 2e-63 0.044 6.3e-61	21.5 251.1 129.5 1158.9 64.5 64.5 44.0 224.1 17.9 215.8
1236 1 1241 1 1243 1 1247 1	efhand CTM DUF6 SCAN J-gamma Catalase PX PFCH Peptidase_M2 O WW UPF0006	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006	0.015 1.5e-71 3.6e-36 0 2.2e-15 2.2e-15 3.3e-09 2e-63 0.044 6.3e-61	21.5 251.1 129.5 1158.9 64.5 64.5 44.0 224.1 17.9 215.8
1236 1 1241 1 1243 1	sfhand crm DUF6 SCAN 3-gamma -atalase PX PX FCH Peptidase_M2 0	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain	0.015 1.5e-71 3.6e-36 0 2.2e-15 2.2e-15 3.3e-09 2e-63	21.5 251.1 129.5 1158.9 64.5 64.5 44.0 224.1
1236	efhand crm DUF6 SCAN 3-gamma catalase PX PCH Peptidase_M2 0	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40	0.015 1.5e-71 3.6e-36 0 2.2e-15 2.2e-15 3.3e-09 2e-63	21.5 251.1 129.5 1158.9 64.5 64.5 44.0 224.1
1236 1	efhand rrm DUF6 SCAN 3-gamma catalase PX PX PK	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain Fes/CIP4 homology domain	0.015 1.5e-71 3.6e-36 0 2.2e-15 2.2e-15 3.3e-09	21.5 251.1 129.5 1158.9 64.5 64.5
	efhand TIM DUF6 GCAN J-gamma Catalase PX	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain Fes/CIP4 homology domain	0.015 1.5e-71 3.6e-36 0 2.2e-15 2.2e-15	21.5 251.1 129.5 1158.9 64.5 64.5
1233	efhand crm DUF6 GCAN J-gamma catalase	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain	0.015 1.5e-71 3.6e-36 0 2.2e-15	21.5 251.1 129.5 1158.9 64.5 64.5
	efhand rrm DUF6 SCAN J-ganma catalase	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase	0.015 1.5e-71 3.6e-36 0 2.2e-15	21.5 251.1 129.5 1158.9 64.5
	efhand crm DUF6 SCAN J-gamma	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain	0.015 1.5e-71 3.6e-36	21.5 251.1 129.5
	efhand rrm DUF6 SCAN	RNA recognition motif. Integral membrane protein DUF6 SCAN domain	0.015 1.5e-71	21.5 251.1
	efhand rrm DUF6	RNA recognition motif. Integral membrane protein DUF6	0.015	21.5
	efhand rrm	RNA recognition motif.		
	fhand		2.1e-40	147.7
	LI-CARA	EF hand	3.2e-07	37.4
	synt_AC39 zf-C2H2	Zinc finger, C2H2 type	5.5e-17	69.9
	ATP-	ATP synthase (C/AC39) subunit	2.5e-128	439.7
	ink	Ank repeat	3.9e-15 2.5e-128	439.7
	7tm_3	7 transmembrane receptor	7.2e-09 3.9e-15	63.7
1	can	family		29.0
	Dbie_methylt	ubiE/COQ5 methyltransferase	1.3e-121	417.4
	dh_short	short chain dehydrogenase	8.3e-45	162.3
	7	domain	0.25	1
1202 F	8 tetra	K+ channel tetramerisation	0.022	-16.8
1197	lyco_transf	Glycosyl transferase family 8	1.2e-09	45.5
1730 p	olt_Legox	oxidoreducta	3.16-32	111.0
	oyr_redox	Pyridine nucleotide-disulphide	3.1e-32	111.8
	Sec1	Sec1 family	3.2e-183	622.1
	Stathmin	Stathmin family	1.8e-90	314.0
, ,	tathmin	Stathmin family	1.8e-90	314.0
	orn_DAP_Arg_ leC	Pyridoxal-dependent decarboxylase	0.2e-128	430.6
	IPAR_LY6	u-PAR/Ly-6 domain Pyridoxal-dependent	0.0042 6.2e-128	430.6
	ito_carr	Mitochondrial carrier proteins	1.5e-62 0.0042	15.6
	asGEF	RasGEF domain	1.7e-88 1.5e-62	307.4
	CL1_MTCP1	TCL1/MTCP1 family	9.5e-56	198.6
		(20 copies)		
1181 0	ollagen	Collagen triple helix repeat	0.00016	24.7
1180 E	ts	Ets-domain	1.8e-09	33.3
	D40	WD domain, G-beta repeat	4.7e-35	129.9
	PP2C	Protein phosphatase 2C	5.3e-31	112.5
	AP	SAP domain	3.9e-10	47.1
1170 a	bhydrolase	alpha/beta hydrolase fold	0.098	-7.5
1100	An	motif)	0.04	10.5
	AM	SAM domain (Sterile alpha	0.04	10.5
	RS RS	PTB domain (IRS-1 type)	2.6e-43	157.3
	ED	Death effector domain PTB domain (IRS-1 type)	3.9e-05 2.6e-43	157.3
	e			
	inker histo	linker histone H1 and H5 family	3.8e-14	60.4
EQ ID P	FAM NAME	DESCRIPTION	p-value	PFAM SCORE

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:	1000	000 111		SCORE
1265	SCP	SCP-like extracellular protein K+ channel tetramerisation	6e-29	108.0
	K_tetra	domain	2.8e-27	104.0
1269	ras	Ras family	1.3e-85	297.9
1275	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.2e-10	37.0
1276	abhydrolase	alpha/beta hydrolase fold	5.4e-23	89.8
1277	abhydrolase	alpha/beta hydrolase fold	5.6e-21	B3.1
1279	trypsin	Trypsin	4.4e-41	132.0
1280	PBP	Phosphatidylethanolamine- binding protein	1.3e-13	58.7
1285	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.6e-14	49.6
1287	ank	Ank repeat	1.7e-52	187.8
1294	fn3	Fibronectin type III domain	0.026	20.9
1295	GBP	Guanylate-binding protein	0.00026	-70.0
1296	PMP22_Claudi n	PMP-22/EMP/MP20/Claudin family	6.9e-41	149.3
1297	Rhodanese	Rhodanese-like domain	3.2e-14	60.7
1298	LIM	LIM domain containing proteins	5.8e-21	79.1
1301	rnaseA	Pancreatic ribonucleases	4.9e-43	145.2
1307	mito_carr	Mitochondrial carrier proteins	2.1e-53	186.0
1308	WD40	WD domain, G-beta repeat	1.6e-17	71.6
1310	UPAR_LY6	u-PAR/Ly-6 domain	7.1e-20	75.5
1313	thiored	Thioredoxin	3.6e-05	21.6
1314	Aa_trans	Transmembrane amino acid transporter protein	1.5e-67	237.9
1316	trypsin	Trypsin	4.4e-41	132.0
1320	Ribosomal_L1	Ribosomal protein L13	3.9e-62	219.8
1327	Armadillo_se	Armadillo/beta-catenin-like repeats	0.0054	23.4
1328	KRAB	KRAB box	0.052	-5.6
1329	rrm	RNA recognition motif.	2.1e-40	147.7
1330	Bcl-2	Apoptosis regulator proteins, Bcl-2 family	0.014	-1.6
1331	PX	PX domain	2.1e-10	48.0
1333	KRAB	KRAB box	1.8e-36	134.6
1334	UPP_syntheta se	Putative undecaprenyl diphosphate synt	2.3e-89	310.3
1335	UPP_syntheta	Putative undecaprenyl diphosphate synt	1.8e-59	211.0
1336	DSPc	Dual specificity phosphatase, catalytic doma	1.2e-31	118.6
1337	DSPc	Dual specificity phosphatase, catalytic doma	2.3e-12	54.5
1338	TPR	TPR Domain	0.00021	28.1
1340	metalthio	Metallothionein	0.013	20.3
1341	mutT	Bacterial mutT protein	5.8e-09	36.5
1343	Band_41	FERM domain (Band 4.1 family)	1.3e-38	122.5
1344	Kelch	Kelch motif	1.4e-44	161.5
1345	Antifreeze	Antifreeze protein	1.2e-10	48.8
1347	3Beta_HSD	3-beta hydroxysteroid dehydrogenase/isomera	0.086	-177.2
1348	BTB	BTB/POZ domain	5.3e-28	106.5
1349	DUF6	Integral membrane protein DUF6	0.033	15.8
1350	myosin_head	Myosin head (motor domain)	0	1088.7
1352	Nramp	Natural resistance-associated macrophage pro	1.2e-202	686.6
1353	S_100	S-100/ICaBP type calcium binding domain	5.3e-23	89.9
1355	DEAD	DRAD/DEAH box helicase	3.6e-65	209.0
1356	C2	C2 domain	2.4e-15	64.4
1357	RBD	Raf-like Ras-binding domain	4.2e-57	203.1
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1360	zf-C2H2	Zinc finger, C2H2 type	7.4e-141	481.4

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:	SIS	STS domain	3.8e-30	113.6
1362	SIS	SIS domain	1.3e-28	108.5
		Immunoglobulin domain	0.00026	19.0
1364	ig	K+ channel tetramerisation	1.1e-16	68.9
1368	K_tetra	domain	2.2e-113	390.1
1371	Collagen	Collagen triple helix repeat (20 copies)		
1372	DnaJ	DnaJ domain	6.6e-36	132.7
1376	KRAB	KRAB box	2.1e-38	141.0
1378	ELM2	ELM2 domain	2e-23	91.3
1380	thiored	Thioredoxin	1.2e-23	82.8
1381	ank	Ank repeat	2.3e-83	290.4
1382	BTB	BTB/POZ domain	3e-11	50.8
1383	WD40	WD domain, G-beta repeat	1.6e-19	78.3
1384	WD40	WD domain, G-beta repeat	6.3e-24	92.9
1387	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.1e-09	35.6
1389	zf-C2H2	Zinc finger, C2H2 type	5.5e-50	179.5
1390	zf-C2H2	Zinc finger, C2H2 type	2.5e-85	296.9
1390	kinesin	Kinesin motor domain	7.8e-188	637.4
	zf-C2H2	Zinc finger, C2H2 type	1.2e-49	178.4
1394		KRAB box	5.1e-22	86.6
1398	KRAB	bZIP transcription factor	0.035	13.1
1402	bZIP		0.003	-101.5
1405	sugar_tr	Sugar (and other) transporter	8.9e-47	168.8
1406	RhoGAP	RhoGAP domain		132.1
1407	rrm	RNA recognition motif.	le-35	
1408	LRR	Leucine Rich Repeat	2.1e-13	58.0
1409	Nebulin_repe at	Nebulin repeat	6e-54	192.6
1410	ank	Ank repeat	1.6e-17	71.6
1412	Ribosomal_L5 C	ribosomal LSP family C-terminus	8.2e-58	205.5
1415	trypsin	Trypsin	4.7e-85	.270.4
1416	aminotran 1	Aminotransferases class-I	4.4e-05	-91.2
1417	S1	S1 RNA binding domain	1.6e-07	33.1
1419	WD40	WD domain, G-beta repeat	2.2e-09	44.6
1422	cadherin	Cadherin domain	8.3e-42	152.3
1424	SH3	SH3 domain	2.5e-80	280.3
1425	PHD	PHD-finger	3.2e-17	70.6
1426	PHD	PHD-finger	3.2e-17	70.6
1427	ArfGap	Putative GTP-ase activating protein for Arf	1e-37	138.8
1428	helicase_C	Helicases conserved C-terminal	1e-26	102.2
1429	WD40	WD domain, G-beta repeat	3.9e-07	37.2
1430	inositol P	Inositol monophosphatase family	2.5e-10	40.2
1431	mito carr	Mitochondrial carrier proteins	4.3e-83	287.7
1433	Clq	Clq domain	2.9e-16	66.2
1434	WD40	WD domain, G-beta repeat	1.6e-13	58.3
1435	Inos-1-	Myo-inositol-1-phosphate synthase	7e-228	770.4
1426	P_synth	RNA recognition motif.	1.4e-34	128.3
1436	rrm	Immunoglobulin domain	1.3e-12	45.6
1438	ig	Gamma-adaptin, C-terminus	3.4e-67	236.7
1440	G_Adapt_CT	Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus	3.4e-67	236.7
1441	G_Adapt_CT		0.00013	28.7
1443	Kelch	Kelch motif		84.7
1446	ARID	ARID DNA binding domain	1.8e-21	
1447	zf-C2H2	Zinc finger, C2H2 type	9.4e-28	105.6
1448	AMP-binding	AMP-binding enzyme	2.6e-07	-145.1
1451	rrm	RNA recognition motif.	6.5e-21	82.9
1454	ig	Immunoglobulin domain	5.6e-44	146.7
1455	Sialyltransf	Sialyltransferase family	5.4e-21	83.2
1460	Aldose_epim	Aldose 1-epimerase	1.9e-35	131.2
1461	C2	C2 domain	4e-18	73.6
		1	13 3 - 10	77.3
1470	TIG	IPT/TIG domain	3.1e-19	177.3

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
	h 2	ļ	 	SCORE
1474	DENN	DENN (AEX-3) domain	1.3e-44	161.6
1475	Cation efflu	Cation efflux family	4.6e-49	176.4
	x		1100 .5	1 270.1
1477	TBC	TBC domain	8e-47	169.0
1478	rrm	RNA recognition motif.	2e-21	84.6
1480	ig	Immunoglobulin domain	5.5e-06	24.3
1484	Telo_bind_al	Telomere-binding protein alpha	0.028	-225.9
	pha	subuni		1
1485	zf-C2H2	Zinc finger, C2H2 type	1.8e-68	240.9
1486	pkinase	Eukaryotic protein kinase domain	9.5e-13	49.9
1488	helicase_C	Helicases conserved C-terminal domain	1.4e-15	65.2
1489	DUF89	Protein of unknown function DUF89	0.079	-132.4
1490	ECH	Enoyl-CoA hydratase/isomerase family	5.2e-41	149.7
1491	guanylate_cy c	Adenylate and Guanylate cyclase catalyt	5.9e-46	166.1
1492	LRR	Leucine Rich Repeat	3.4e-19	77.2
1495	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.1e-10	36.3
1497	pkinase	Eukaryotic protein kinase domain	1e-22	85.8
1500	SH3	SH3 domain	9.3e-05	27.2
1502	homeobox	Homeobox domain	0.084	13.8
1503	homeobox	Homeobox domain	0.084	13.8
1505	EGF	EGF-like domain	2.7e-23	90.8
1506	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	2.7e-21	84.2
1508	Peptidase_M2 0	Peptidase family M20/M25/M40	2.8e-28	101.8
1511	PX	PX domain	1.9e-11	51.5
1512	Sulfatase	Sulfatase	2.8e-35	130.7
1516	Syntaxin	Syntaxin	0.011	-62.3
1518	aminotran_3	Aminotransferases class-III pyridoxal-pho	9.7e-106	305.6
1520	ig	Immunoglobulin domain	0.075	11.0
1521	RA	Ras association (RalGDS/AF-6) domain	0.013	13.3
1523	RhoGAP	RhoGAP domain	2.5e-05	18.7
1528	WD40	WD domain, G-beta repeat	5.4e-24	93.1
1535	IMS	impB/mucB/samB family	7.8e-95	328.5
1538 1539	FYVE DAGKC	FYVE zinc finger Diacylglycerol kinase catalytic	3.2e-27	101.5
1540	Ocular alb	domain	6e-07	36.5
1653	SAP	Ocular albinism type 1 protein SAP domain	0	1184.7
1654	Amino_oxidas	Flavin containing amine oxidase	3.2e-43	33.2 157.0
1655	Amino_oxidas	Flavin containing amine oxidase	3.2e-43	157.0
1656	RhoGEF	RhoGEF domain	1.4e-24	95.1
1657	MMR HSR1	GTPase of unknown function	0.0011	-45.5
1659	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	2.5e-11	51.1
1660	actin	Actin	6.6e-21	69.9
1661	BAH	BAH domain	1.7e-82	287.5
1662	vwa	von Willebrand factor type A	0	1909.4
	WD40	WD domain, G-beta repeat	1.4e-67	237.9
1663			1 1.4e-b/	1 43 (. 7
1663 1667				
1663 1667 1669	zf-C2H2 Nol1_Nop2_Su	Zinc finger, C2H2 type NOL1/NOP2/sun family	1.3e-93 1.3e-23	324.4 84.3

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1672	chromo	'chromo' (CHRromatin Organization MOdifier)	2.1e-18	67.7
1674	zf-CCCH	Zinc finger C-x8-C-x3-H	0.0025	17.6
1676	Glyco_hydro_	type Glycosyl hydrolase family 47	1.8e-187	636.2
1677	Glyco_hydro_	Glycosyl hydrolase family 47	4.5e-74	259.5
1680	WD40	WD domain, G-beta repeat	1.le-27	105.5
1681	WD40	WD domain, G-beta repeat	1.1e-27	105.5
1683	MMR HSR1	GTPase of unknown function	1.8e-78	274.1
1691	rrm	RNA recognition motif.	1.8e-37	137.9
1692	rrm	RNA recognition motif.	1.8e-37	137.9
1693	AAA	ATPases associated with various cellular act	1.3e-81	284.5
1697	Ferric_reduc	Ferric reductase like transmembrane com	8.4e-82	285.2
1698	Ferric_reduc	Ferric reductase like transmembrane com	3.5e-53	190.1
1699	zf-C2H2	Zinc finger, C2H2 type	4.4e-34	126.6
1700	arf	ADP-ribosylation factor family	9e-19	75.8
1702	GTP_EFTU	Elongation factor Tu family	0.014	11.4
1703	SCAN	SCAN domain	1.8e-54	194.4
1707	pkinase	Eukaryotic protein kinase domain	1.2e-88	307.9
1709	WD40	WD domain, G-beta repeat	0.0035	24.0
1710	LRR	Leucine Rich Repeat	1.2e-30	115.3
1711	WW	WW domain	7.6e-12	52.8
1712	ank	Ank repeat	4.2e-34	126.7
1713	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-09	38.3
1714	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-09	38.3
1715	ras	Ras family	4.4e-41	149.9
1718	HMG_box	HMG (high mobility group) box	8.3e-21	82.6
1719	TBC	TBC domain	1.1e-45	165.2
1721	HLH	Helix-loop-helix DNA-binding domain	9.2e-10	45.9
1723	dsrm	Double-stranded RNA binding motif	2.9e-05	30.9
1724	RrnaAD	Ribosomal RNA adenine dimethylases	0.045	9.2
1725	CIDE-N	CIDE-N domain	5.9e-40	146.2
1726	HAT	HAT (Half-A-TPR) repeats	2.9e-44	160.5
1728	efhand	EF hand	5.1e-20	79.9
1733	Hist_deacety 1	Histone deacetylase family	1.7e-104	360.6
1735	LRR	Leucine Rich Repeat	4.6e-34	126.6
1739	PI-PLC-X	Phosphatidylinositol-specific phospholipase	0.0023	
1743	ras	Ras family Ras family	3.7e-10 3.7e-10	-21.3
1744	ras RasGEF	Ras Tamily RasGEF domain	3.7e-10 3.2e-49	176.9
1745 1746	adh short	short chain dehydrogenase	7.1e-08	34.6
1751	zf-C2H2	Zinc finger, C2H2 type	9e-39	142.2
1754	fn3	Fibronectin type III domain	5.5e-101	348.9
1756	zf-C2H2	Zinc finger, C2H2 type	6.3e-93	322.1
1758	rrm	RNA recognition motif.	0.017	21.2
1760	Nop	Putative snoRNA binding domain	6.1e-95	328.8
1761	Nop	Putative snoRNA binding domain	6.1e-95	328.8
1765	MMR HSR1	GTPase of unknown function	6.4e-41	149.4
1769	CN hydrolase	Carbon-nitrogen hydrolase	3e-06	-43.9
1775	ank	Ank repeat	4.1e-07	37.1
1779	Oxysterol BP	Oxysterol-binding protein	4.7e-56	199.6
1783	RhoGEF	RhoGEF domain	1.6e-23	91.6

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1785	rrm	RNA recognition motif.	6.4e-14	59.7

TRADOCS:1416227.1(%CRN01!.DOC)

TABLE 5

SEQ ID NO:	POSITION OF	MaxS (MAXIMUM	MeanS (MEAN
SEQ ID NO.	SIGNAL IN AMINO	SCORE)	SCORE)
	ACID SEQUENCE		
1	1-21	0.991	0.955
2	1-31	0.995	0.944
3	1-33	0.949	0.736
4	1-19	0.970	0.951
5	1-26	0.971	0.863
6	1-26	0.971	0.863
7	1-26	0.971	0.863
8	1-26	0.971	0.863
9	1-46	0.982	0.901
10	1-21	0.991	0.955
11	1-23	0.989	0.899
12	1-25	0.955	0.803
13	1-18	0.932	0.625
14	1-18	0.938	0.876
15	1-25	0.941	0.811
16	1-17	0.972	0.939
17	1-27	0.964	0.777
18	1-16	0.914	0.657
19	1-19	0.953	0.840
20	1-20	0.935	0.701
21	1-22	0.974	0.850
22	1-33	0.961	0.895
23	1-19	0.991	0.959
24	1-31	0.995	0.944
25	1-22	0.976	0.935
26	1-27	0.996	0.928
27	1-24	0.953	0.739
28	1-21	0.906	0.688
29	1-31	0.986	0.841
30	1-28	0.980	0.893
31	1-19	0.993	0.976
32	1-22	0.998	0.909
35	1-33	0.949	0.736
36	1-33	0.949	0.736
46	1-19	0.970	0.951
67	1-25	0.968	0.848
71	1-18	0.949	0.845
72	1-30	0.991	0.919
75	1-29	0.958	0.854
88	1-20	0.986	0.945
94	1-33	0.994	0.943
97	1-46	0.964	0.595
103	1-49	0.983	0.570
108	1-26	0.978	0.885
111	1-23	0.989	0.899
126	1-25	0.955	0.803
129	1-19	0.963	0.918
138	1-29	0.971	0.844
143	1-18	0.914	0.628
148	1-20	0.969	0.904
156	1-25	0.941	0.811
158	1-22	0.979	0.927
160	1-17	0.972	0.939
161	1-48	0.903	0.571
162	1-25	0.937	0.729
168	1-16	0.939	0.826
171	1-27	0.964	0.777
178	1-21	0.945	0.825
180	1-27	0.981	0.941
187	1-28	0.982	0.936
190	1-19	0.953	0.840
196	1-22	0.975	0.916
197	1-22	0.963	0.936
			1

SEQ ID NO:	POSITION OF SIGNAL IN AMINO	Maxs (MAXIMUM SCORE)	MeanS (MEAN SCORE)
	ACID SEQUENCE	2001.27	
199	1-20	0.935	0.701
200	1-23	0.977	0.773
206	1-30	0.984	0.890
207	1-19	0.990	0.924
208	1-22	0.974	0.850
210	1-40	0.940	0.670
211	1-28	0.971	0.849
216	1-24	0.986	0.956
218	1-33	0.961	0.895
219	1-19	0.970	0.871
221	1-19	0.904	0.553
230	1-19	0.991	0.555
231	1-26	0.953	0.800
232	1-25	0.988	0.826
239	1-23	0.969	0.828
240	1-17	0.982	0.955
241	1-17	0.982	0.955
245	1-17	0.970	0.722
248	1-30	0.976	0.722
249	1-23	0.968	0.940
252	1-18	0.971	0.923
261	1-24	0.883	0.587
265	1-18	0.939	0.868
272	1-24	0.953	0.739
283	1-21	0.906	0.688
284	1-29	0.997	0.854
290	1-31	0.986	0.841
302	1-28	0.980	0.893
304	1-16	0.907	0.635
312	1-19	0.993	0.976
313	1-17	0.930	0.753
323	1-22	0.998	0.909
324	1-17	0.982	0.954
328	1-19	0.971	0.865
329	1-22	0.963	0.924
330	1-33	0.978	0.841
331	1-24	0.920	0.712
332	1-24	0.975	0.881
333	1-19	0.984	0.941
334	1-20	0.899	0.567
335	1-27	0.942	0.813
336	1-20	0.952	0.850
337	1-38	0.942	0.653
338	1-27	0.973	0.772
339	1-36	0.979	0.804
340	1-27	0.888	0.597
343	1-19	0.971	0.865
344	1-22	0.994	0.928
345	1-17	0.966	0.687
346	1-19	0.936	0.822
347	1-22	0.963	0.924
349	1-24	0.982	0.966
351	1-21	0.918	0.815
352	1-31	0.988	0.912
354	1-31	0.974	0.839
355	1-29	0.932	0.632
356	1-15	0.994	0.969
357	1-33	0.935	0.726
360	1-27	0.938	0.827
361	1-25	0.954	0.674
362	1-22	0.929	0.788
363	1-21	0.881	0.715
364 365	1-33	0.978	0.841
	1-33	0.978	0.841

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	Maxs (MAXIMUM SCORE)	MeanS (MEAN SCORE)
366	1-21	0.916	0.820
367	1-19	0.936	0.822
368	1-29	0.972	0.874
370	1-24	0.920	0.712
371	1-24	0.961	0.773
372	1-27	0.919	0.768
373	1-19	0.986	0.945
375	1-32	0.994	0.932
376	1-34	0.987	0.810
377	1-17	0.995	0.950
378	1-49	0.971	0.749
380	1-20	0.968	0.874
	1-20	0.928	0.782
381		0.986	0.934
382	1-19	0.965	0.829
383	1-28		0.551
384	1-39	0.970	
386	1-24	0.975	0.881
388	1-30	0.989	0.868
389	1-19	0.984	0.941
390	1-26	0.971	0.782
392	1-20	0.981	0.900
393	1-16	0.968	0.890
394	1-23	0.937	0.701
397	1-22	0.985	0.854
399	1-46	0.977	0.698
401	1-20	0.899	0.567
402	1-22	0.967	0.931
403	1-27	0.992	0.934
404	1-19	0.991	0.973
405	1-23	0.994	0.921
407	1-35	0.987	0.658
408	1-39	0.976	0.551
409	1-33	0.897	0.570
	1-25	0.990	0.962
410	1-38	0.977	0.827
411			0.768
412	1-20	0.944	0.965
413	1-20	0.988	
414	1-46	0.993	0.638
415	1-23	0.981	0.940
417	1-29	0.941	0.672
418	1-20	0.952	0.850
419	1-19	0.986	0.967
420	1-29	0.965	0.861
421	1-22	0.889	0.785
422	1-48	0.982	0.862
424	1-19	0.979	0.933
428	1-38	0.942	0.653
430	1-18	0.947	0.595
432	1-33	0.957	0.789
433	1-26	0.979	0.904
434	1-27	0.962	0.777
435	1-24	0.998	0.977
436	1-27	0.973	0.772
	1-15	0.966	0.940
443		0.979	0.804
448	1-36	0.979	0.609
453	1-41		0.609
455	1-33	0.943	
457	1-27	0.888	0.597
462	1-16	0.925	0.681
486	1-27	0.972	0.845
495	1-24	0.917	0.636
498 .	1-26	0.993	0.890
505	1-20	0.976	0.926
507	1-17	0.966	0.687
510	1-23	0.930	0.593

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
511	1-23	0.930	0.593
512	1-23	0.930	0.593
515	1-18	0.978	0.956
523	1-19	0.936	0.822
529	1-22	0.963	0.924
545	1-24	0.982	0.966
550	1-30	0.933	0.713
		0.933	
552	1-21		0.912
554	1-23	0.969	
571	1-21	0.918	0.815
574	1-31	0.988	0.912
580	1-39	0.925	0.556
594	1-31	0.974	0.839
608	1-29	0.932	0.632
609	1-29	0.932	0.632
610	1-21	0.990	0.948
621	1-15	0.994	0.969
623	1-33	0.935	0.726
653	1-27	0.938	0.827
		0.929	0.788
668	1-22		
677	1-16	0.948	0.807
685	1-21	0.881	0.715
699	1-22	0.975	0.816
702	1-31	0.968	0.898
707	1-16	0.880	0.562
713	1-25	0.966	0.743
718	1-19	0.936	0.822
719	1-20	0.961	0.824
729	1-29	0.972	0.874
735	1-46	0.903	0.598
746	1-14	0.916	0.730
	1	0.965	0.736
747	1-22		
748	1-29	0.968	0.785
759	1-24	0.961	0.773
767	1-27	0.919	0.768
768	1-33	0.900	0.585
773	1-42	0.959	0.702
779	1-19	0.986	0.945
797	1-19	0.944	0.759
798	1-19	0.900	0.568
820	1-17	0.995	0.950
827	1-49	0.971	0.749
848	1-20	0.968	0.874
864	1-20	0.928	0.782
	1-20	0.926	0.782
866			0.886
873	1-23	0.948	
881	1-28	0.965	0.829
887	1-39	0.970	0.551
927	1-30	0.989	0.868
934	1-48	0.988	0.777
939	1-39	0.994	0.889
944	1-26	0.971	0.782
950	1-29	0.957	0.845
963	1-20	0.981	0.900
964	1-20	0.886	0.558
973	1-16	0.968	0.890
980	1-34	0.961	0.749
	_1		
981	1-20	0.953	0.822
984	1-12	0.938	0.780
		0.985	0.854
1015	1-22		l
	1-22	0.977	0.698
1015		0.977	0.698 0.842
1015 1040	1-46		
1015 1040 1052	1-46	0.969	0.842

SEQ ID NO:	POSITION OF	MaxS (MAXIMUM	MeanS (MEAN
	SIGNAL IN AMINO	SCORE)	SCORE)
	ACID SEQUENCE		
1075	1-27	0.992	0.934
1080	1-19	0.931	0.829
1092	1-19	0.991	0.973
1094	1-46	0.992	0.653
1095	1-30	0.974	0.929
1105	1-23	0.994	0.921
1123	1-35	0.987	0.658
1138	1-32	0.954	0.613
1140	1-38	0.989	0.789
1142	1-33	0.897	0.570
1152	1-25	0.990	0.962
1170	1-38	0.977	0.827
1176	1-20	0.944	0.768
1187	1-20	0.988	0.965
1189	1-35	0.967	0.839
1192	1-46	0.993	0.638
1193	1-16	0.925	0.710
1197	1-29	0.985	0.853
1208	1-23	0.981	0.940
1225	1-29	0.941	0.672
1245	1-19	0.986	0.967
1258	1-29	0.965	0.861
1265	1-22	0.889	0.785
1266	1-20	0.944	0.809
1276	1-48	0.982	0.862
1292	1-19	0.979	0.933
1296	1-21	0.984	0.944
1297	1-19	0.984	0.953
1332	1-38	0.942	0.653
1358	1-18	0.947	0.595
1371	1-33	0.957	0.789
1380	1-26	0.979	0.904
1397	1-27	0.962	0.777
1399	1-23	0.997	0.960
1404	1-24	0.998	0.977
1410	1-15	0.946	0.845
1414	1-24	0.913	0.588
1415	1-19	0.982	0.929
1416	1-12	0.931	0.891
1418	1-30	0.933	0.563
1420	1-20	0.881	0.561
1421	1-19	0.990	0.968
1423	1-17	0.968	0.863
1424	1-21	0.885	0.591
1425	1-24	0.913	0.588
1426	1-24	0.913	0.588
1428	1-25	0.967	0.899
1430	1-34	0.977	0.819
1431	1-28	0.979	0.813
1432	1-36	0.957	0.923
1433	1-32	0.921	0.613
1434	1-39	0.983	0.753
1435	1-25	0.910	0.631
1436	1-42	0.988	
1437	1-22		0.868
1442		0.998	0.980
1448	1-20	0.918	0.753
	1-12	0.931	0.891
1462	1-18	0.968	0.888
1490	1-20	0.881	0.561
1518	1-17	0.968	0.863
1525	1-21	0.885	0.591
1547	1-28	0.974	0.891
	1-25	0.967	0.899
1561			
1561 1580 1593	1-23	0.923	0.824

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1596	1-16	0.929	0.709
1601	1-36	0.957	0.613
1606	1-22	0.979	0.831
1607	1-20	0.974	0.770
1608	1-32	0.921	0.753
1614	1-33	0.969	0.829
1616	1-20	0.959	0.869
1625	1-39	0.983	0.621
1632	1-25	0.910	0.631
1636	1-33	0.897	0.591
1639	1-42	0.988	0.868
1645	1-20	0.927	0.568
1647	1-17	0.923	0.742
1648	1-22	0.998	0.980

TRADOCS:1416234.1(%CR%01!.DOC)

TABLE 6

TABLE 6					
SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number_	NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		sequence	priority	
	eedneuce			application	
1	1787	3573	5359	784CIP2_1	1103
2	1788	3574	5360	784CIP2_2	2673
3	1789	3575	5361	784CIP2_3	4117
4	1790	3576	5362	784CIP2_4	5556
5	1791	3577	5363	784CIP2_5	5562
6	1792	3578	5364	784CIP2_6	5562
7	1793	3579	5365	784CIP2_7	5562
8	1794	3580	5366	784CIP2_8	5562
9	1795	3581	5367	784CIP2_9	5563
10	1796	3582	5368	784CIP2_10	5564
11	1797	3583	5369	784CIP2_11	5565
12	1798	3584	5370	784CIP2_12	5689
13	1799	3585	5371	784CIP2_13	5729
14	1800	3586	5372	784CIP2_14	5745
15	1801	3587	5373	784CIP2_15	5777
16	1802	3588	5374	784CIP2_16	5777
17	1803	3589	5375	784CIP2_17	5789
18	1804	3590	5376	784CIP2_18	5792
19	1805	3591	5377	784CIP2_19	5804
20	1806	3592	5378	784CIP2_20	5805
21	1807	3593	5379	784CIP2_21	5805
22	1808	3594	5380	784C1P2_22	5844
23	1809	3595	5381	784CIP2_23	5844
24	1810	3596	5382	784CIP2_24	5850
25	1811	3597	5383	784CIP2_25	5867
26	1812	3598	5384	784CIP2_26	5973
27	1813	3599	5385	784CIP2_27	5995
28	1814	3600	5386	784CIP2_28	5995
29	1815	3601	5387	784CIP2_29	6005
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31	1817	3603	5389	784CIP2_31	6007
32	1818	3604	5390	784CIP2_32	6009
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35	1821	3607	5393	784CIP2_35	6016
36	1822	3608	5394	784CIP2_36	6016
37	1823	3609	5395	784CIP2_37	6018
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39	1825	3611	5397	784CIP2_39	6018
40	1826	3612	5398	784CIP2_40	6023
41	1827	3613	5399	784CIP2_41	6070
42	1828	3614	5400	784CIP2_42	6081
43	1829	3615	5401	784CIP2_43	6089
44	1830	3616	5402	784CIP2_44	6118
45	1831	3617	5403	784CIP2_45	6118
46	1832	3618	5404	784CIP2_46	6130
47	1833	3619	5405	784CIP2_47	6177
48	1834	3620	5406	784CIP2_48	6189
49	1835	3621	5407	784CIP2_49	6191
50	1836	3622	5408	784CIP2_50	6204
51	1837	3623	5409	784CIP2_51 ·	6204
52	1838	3624	5410	784CIP2_52	6284
53	1839	3625	5411	784CIP2_53	6367
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56	1842	3628	5414	784CIP2_56	6445
57	1843	3629	5415	784CIP2_57	6457
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62	1848	3634	5420		6472
63	1849	3635	5421	784CIP2_62 784CIP2_63	6499
- 64	1850	3636	5422	784CIP2_63	6499
65	1851	3637	5423	784CIP2_64 784CIP2_65	6505
66	1852	3638	5424	784CIP2_65	6534
67	1853	3639	5425	784CIP2_66	6534 6540
68	1854	3640	5426	784CIP2_67	1
69	1855	3641	5427	784CIP2 69	6550
70	1856	3642	5428	784CIP2_89	6550
71	1857	3643	5429	784CIP2_70	6592
72	1858	3644	5430	784CIP2_71 784CIP2_72	6645
73	1859	3645	5431	784CIP2 73	6763
74	1860	3646	5432	784CIP2_73	6763
75	1861	3647	5433	784CIP2_74	6786
76	1862	3648	5434	784CIP2_75	6824
77	1863	3649	5435	784CIP2_76	6824
78	1864	3650	5436	784CIP2_77	6830
79	1865	3651	5437	784CIP2_78	6832
80	1866	3652	5438	784CIP2 80	6834
81	1867	3653	5439	784CIP2 81	6834
82	1868	3654	5440	784CIP2 82	6835
83	1869	3655	5441	784CIP2 83	6837
84	1870	3656	5442	784CIP2 84	6843
85	1871	3657	5443	784CIP2 85	6859
86	1872	3658	5444	784CIP2 86	6915
87	1873	3659	5445	784CIP2 87	6932
88	1874	3660	5446	784CIP2 88	6957
89	1875	3661	5447	784CIP2 89	6961
90	1876	3662	5448	784CIP2 90	6973
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92	1878	3664	5450	784CIP2 93	7007
93	. 1879	3665	5451	784CIP2 94	7018
94	1880	3666	5452	784CIP2 95	7019
95	1881	3667	5453	784CIP2 96	7020
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100	1886	3672	5458	784CIP2 101	7028
101	1887	3673	5459	784CIP2 102	7029
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103	1889	3675	5461	784CIP2_104	7032
104	1890	3676	5462	784CIP2_105	7033
105	1891	3677	5463	784CIP2_106	7035
106	1892	3678	5464	784CIP2_107	7036
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113	1899	3685	5471	784CIP2_114	7077
114	1900	3686	5472	784CIP2_115	7092
115	1901	3687	5473	784CIP2 116	7094
116	1902	3688	5474	784CIP2 117	7106
117	1903	3689	5475	784CIP2 118	7107
118	1904	3690	5476	784CIP2 119	7111
119	1905	3691	5477	784CIP2 120	7123
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124	1910	3696	5482	784CIP2_125	7169
125	1911	3697	5483	784CIP2_126	7185
126	1912	3698	5484	784CIP2_127	7197
127	1913	3699	5485	784CIP2_128	7219
128	1914	3700	5486	784CIP2_129	7226
129	1915	3701	5487	784CIP2_130	7229
130	1916	3702	5488	784CIP2_131	7234
131	1917	3703	5489	784CIP2_132	7235
132	1918	3704	5490	784CIP2_133	7235
133	1919	3705	5491	784CIP2_134	7238
134	1920	3706	5492	784CIP2_135	7247
135	1921	3707	5493	784CIP2_136	7261
136	1922	3708	5494	784CIP2_137	7262
137	1923	3709	5495	784CIP2_138	7267
	1924	3710	5496	784CIP2_139	7272
139	1925	3711	5497	784CIP2_140	7273
141	1926	3712	5498	784CIP2_141	7282
142	1927	3713	5499	784CIP2_142	7288
143	1928	3714 3715	5500 5501	784CIP2_143	7291
144	1930	3716	5501	784CIP2_144	7293
145	1930	3716	5502	784CIP2_145	7294
146	1932	3718	5504	784CIP2_146	7299 7300
147	1933	3719	5505	784CIP2_147 784CIP2_148	
148	1934	3720	5506	784CIP2_148 784CIP2_149	7312 7313
149	1935	3721	5507	784CIP2 149 784CIP2 150	7313
150	1936	3722	5508	784CIP2_150 784CIP2_151	7318
151	1937	3723	5509	784CIP2_151 784CIP2_152	7321
152	1938	3724	5510	784CIP2 153	7330
153	1939	3725	5511	784CIP2 154	7331
154	1940	3726	5512	784CIP2 155	7333
155	1941	3727	5513	784CIP2 156	7350
156	1942	3728	5514	784CIP2 157	7352
157	1943	3729	5515	784CIP2 158	7384
158	1944	3730	5516	784CIP2 159	7403
159	1945	3731	5517	784CIP2 160	7431
160	1946	3732	5518	784CIP2 161	7441
161	1947	3733	5519	784CIP2 162	7453
162	1948	3734	5520	784CIP2_163	7467
163	1949	3735	5521	784CIP2_164	7471
164	1950	3736	5522	784CIP2_165	7493
165	1951	3737	5523	784CIP2_166	7502
166	1952	3738	5524	784CIP2_167	7511
167	1953	3739	5525	784CIP2_168	7514
168	1954	3740	5526	784CIP2_169	7520
169	1955	3741	5527	784CIP2_170	7541
170	1956	3742	5528	784CIP2_171	7570
171	1957	3743	5529	784CIP2_172	7578
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173	1959	3745	5531	784CIP2_174	7592
174	1960	3746	5532	784CIP2_175	7601
175	1961	3747	5533	784CIP2_176	7602
176	1962	3748	5534	784CIP2_177	7608
177	1963	3749	5535	784CIP2_178	7615
178	1964	3750	5536	784CIP2_179	7617
179	1965	3751	5537	784CIP2_181	7624
180	1966	3752	5538	784CIP2_182	7626
181	1967	3753	5539	784CIP2_183	7640
182	1968	3754	5540	784CIP2_184	7641
103	1969	3755	5541	784CIP2_185	7641

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186	1972	3758	5544	784CIP2_188	7649
188	1973	3759	5545	784CIP2_189	7656
189	1974	3760	5546	784CIP2_190	7657
190	1975 1976	3761	5547	784CIP2_191	7657
191	1976	3762	5548	784CIP2_192	7662
192	1978	3763 3764	5549	784CIP2_193	7668
193	1979	3765	5550	784CIP2_194	7673
194	1980	3766	5551	784CIP2_195	7690
195	1981	3767	5552 5553	784CIP2_196	7700
196	1982	3768	5553	784CIP2 197	7709
197	1983	3769	5554	784CIP2_198	7736
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199	1985	3771	5557	784CIP2_200 784CIP2_201	7744
200	1986	3772	5558		7771
201	1987	3773	5559	784CIP2_202 784CIP2_203	7786
202	1988	3774	5560	784CIP2_203 784CIP2_204	7791
203	1989	3775	5561	784CIP2_204 784CIP2_205	7797
204	1990	3776	5562	784CIP2_205	7806 7812
205	1991	3777	5563	784CIP2 207	7812
206	1992	3778	5564	784CIP2_207	7812
207	1993	3779	5565	784CIP2 209	7822
208	1994	3780	5566	784CIP2 210	7827
209	1995	3781	5567	784CIP2 211	7830
210	1996	3782	5568	784CIP2 212	7835
211	1997	3783	5569	784CIP2 214	7840
212	1998	3784	5570	784CIP2 215	7858
213	1999	3785	5571	784CIP2 216	7858
214	2000	3786	5572	784CIP2_217	7861
215	2001	3787	5573	784CIP2_218	7866
216	2002	3788	5574	784CIP2_219	7868
217	2003	3789	5575	784CIP2_220	7896
218	2004	3790	5576	784CIP2_221	7898
219	2005	3791	5577	784CIP2_222	7900
220	2006	3792	5578	784CIP2_223	7906
222	2007	3793	5579	784CIP2_224	7908
223		3794	5580	784CIP2_225	7909
223	2009	3795 3796	5581	784CIP2_226	7917
225	2010	3796	5582	784CIP2_227	7932
226	2012	3798	5583 5584	784CIP2_228	7940
227	2013	3799		784CIP2_229	7940
228	2014	3800	5585 5586	784CIP2_230	7984
229	2015	3801	5587	784CIP2_231 784CIP2_232	7984
230	2016	3802	5588	784CIP2_232 784CIP2_233	8001
231	2017	3803	5589	784CIP2_233 784CIP2_234	8021
232	2018	3804	5590	784CIP2_234 784CIP2_235	8029 8033
233	2019	3805	5591	784CIP2_235 784CIP2_236	8033
234	2020	3806	5592	784CIP2_236	8052
235	2021	3807	5593	784CIP2 238	8096
236	2022	3808	5594	784CIP2_238	8096
237	2023	3809	5595	784CIP2 240	8113
238	2024	3810	5596	784CIP2_241	8126
239	2025	3811	5597	784CIP2 242	8132
240	2026	3812	5598	784CIP2_242	8137
241	2027	3813	5599	784CIP2 244	8137
242	2028	3814	5600	784CIP2 245	8159
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247	2033	3819	5605	784CIP2_250	8200
248	2034	3820	5606	784CIP2_251	8212
250	2035	3821	5607	784CIP2_252	8220
251	2036	3822	5608	784CIP2_253	8238
252	2037	3823 3824	5609 5610	784CIP2_254 784CIP2_255	8254
253	2039	3825	5611	784CIP2_255 784CIP2_256	8255
254	2040	3826	5612	784CIP2_256 784CIP2_257	8288 8296
255	2041	3827	5613	784CIP2_257	8329
256	2042	3828	5614	784CIP2_238	8362
257	2043	3829	5615	784CIP2_259	8429
258	2044	3830	5616	784CIP2 261	8436
259	2045	3831	5617	784CIP2_261	8448
260	2046	3832	5618	784CIP2_262	8472
261	2047	3833	5619	784CIP2 264	8502
262	2048	3834	5620	784CIP2_264 784CIP2_265	8504
263	2049	3835	5621	784CIP2 266	8507
264	2050	3836	5622	784CIP2 268	8509
265	2051	3837	5623	784CIP2 269	8515
266	2052	3838	5624	784CIP2 270	8519
267	2053	3839	5625	784CIP2 271	8530
268	2054	3840	5626	784CIP2 272	8532
269	2055	3841	5627	784CIP2 273	8532
270	2056	3842	5628	784CIP2 274	8539
271	2057	3843	5629	784CIP2_275	8541
272	2058	3844	5630	784CIP2_276	8543
273	2059	3845	5631	784CIP2_277	8593
274	2060	3846	5632	784CIP2_278	8595
275	2061	3847	5633	784CIP2_279	8615
276	2062	3848	5634	784CIP2_280	8620
277	2063	3849	5635	784CIP2_281	8621
278	2064	3850	5636	784CIP2_282	8623
279 280	2065	3851	5637	784CIP2_283	8625
281	2066	3852	5638	784CIP2_284	8628
282	2068	3853 3854	5639 5640	784CIP2_285	8628
283	2069	3855	5641	784CIP2_286 784CIP2_287	8629
284	2070	3856	5642	784CIP2_287	8630
285	2071	3857	5643	784CIP2_288	8631 8633
286	2072	3858	5644	784CIP2 290	8634
287	2073	3859	5645	784CIP2 291	8635
288	2074	3860	5646	784CIP2 292	8636
289	2075	3861	5647	784CIP2_293	8659
290	2076	3862	5648	784CIP2 294	8660
291	2077	3863	5649	784CIP2 295	8667
292	2078	3864	5650	784CIP2 296	8667
293	2079	3865	5651	784CIP2_297	8685
294	2080	3866	5652	784CIP2_298	8805
295	2081	3867	5653	784CIP2_299	8896
296	2082	3868	5654	784CIP2_300	8978
297	2083	3869	5655	784CIP2_301	9046
298	2084	3870	5656	784CIP2_302	9048
299	2085	3871	5657	784CIP2_303	9116
300	2086	3872	5658	784CIP2_304	9195
301	2087	3873	5659	784CIP2_305	9201
302	2088	3874	5660	784CIP2_306	9307
303	2089	3875	5661	784CIP2_307	9321
304	2090	3876	5662	784CIP2_308	9397
305	2091	3877	5663	784CIP2_309	9405
306	2092	3878	5664	784CIP2_310	9406
307	2093	3879	5665	784CIP2_311	9422

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
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309	2095	3881	5667	784CIP2 313	9512
310	2096	3882	5668	784CIP2 314	9632
311	2097	3883	5669	784CIP2_315	9661
312	2098	3884	5670	784CIP2_316	9664
313	2099	3885	5671	784CIP2_317	9691
314	2100	3886	5672	784CIP2_318	9700
315	2101	3887	5673	784CIP2_319	9716
316	2102	3888	5674	784CIP2_320	9721
317	2103	3889	5675	784CIP2_321	9870
318	2104	3890	5676	784CIP2_322	9887
319 320	2105	3891	5677 5678	784CIP2_323	9923
321	2106	3892 _. 3893	5679	784CIP2_324 784CIP2_325	9938
322	2108	3894	5680	784CIP2_325	9964
323	2109	3895	5681	784CIP2_326	10007
324	2110	3896	5682	784CIP2 328	10003
325	2111	3897	5683	784CIP2 329	10156
326	2112	3898	5684	784CIP2 330	10276
327	2113	3899	5685	784CIP2 331	10283
328	2114	3900	5686	784CIP2B_1	152
329	2115	3901	5687	784CIP2B_2	167
330	2116	3902	5688	784CIP2B_3	205
331	2117	3903	5689	784CIP2B_4	210
332	2118	3904	5690	784CIP2B_5	225
333	2119	3905	5691	784CIP2B_6	226
334	2120	3906	5692	784CIP2B_7	264
335	2121	3907	5693	784CIP2B_8	268
336 337	2122	3908 3909	5694 5695	784CIP2B_9	293
338	2123	3910	5696	784CIP2B_10 784CIP2B 11	293 293
339	2125	3911	5697	784CIP2B 12	302
340	2126	3912	5698	784CIP2B 13	311
341	2127	3913	5699	784CIP2B 14	352
342	2128	3914	5700	784CIP2B 15	358
343	2129	3915	5701	784CIP2B 16	368
344	2130	3916	5702	784CIP2B_17	393
345	2131	3917	. 5703	784CIP2B_18	477
346	2132	3918	5704	784CIP2B_19	508
347	2133	3919	5705	784CIP2B_20	508
348	2134	3920	5706	784CIP2B_21	515
349	2135	3921	5707 5708	784CIP2B_22	578
350	2136	3922	1	784CIP2B_23	588
351 352	2137	3923 3924	5709 5710	784CIP2B_24 784CIP2B_25	591 593
353	2138	3924	5711	784CIP2B_25	594
354	2140	3926	5712	784CIP2B_26 784CIP2B_27	619
355	2141	3927	5713	784CIP2B 28	620
356	2142	3928	5714	784CIP2B 29	654
357	2143	3929	5715	784CIP2B 30	692
358	2144	3930	5716	784CIP2B 31	753
359	2145	3931	5717	784CIP2B_32	758
360	2146	3932	5718	784CIP2B_33	787
361	2147	3933	5719	784CIP2B_34	833
362	2148	3934	5720	784CIP2B_35	838
363	2149	3935	5721	784CIP2B_36	870
364	2150	3936	5722	784CIP2B_37	891
365	2151	3937	5723	784CIP2B_38	891
366	2152	3938	5724	784CIP2B_39	921
367	2153	3939	5725	784CIP2B_40	924
368 369	2154	3940	5726	784CIP2B_41	932
	2155	3941	5727	784CIP2B 42	942

SEO ID NO:	SEQ ID	SEQ ID NO:	SRQ ID	Priority	SEQ ID
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length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		sequence	priority	}
	sequence			application	050
370	2156	3942	5728	784CIP2B_43	95B
371	2157	3943	5729	784CIP2B_44	968 992
372	2158	3944	5730	784CIP2B_45	
373	2159	3945	5731	784CIP2B_46	1025
374	2160	3946	5732	784CIP2B_47	1074
375	2161	3947	5733	784CIP2B_48 784CIP2B_49	1104
376	2162	3948	5734	784CIP2B_49	1114
377	2163	3949	5735 5736	784CIP2B 50	1262
378	2164	3950	5737	784CIP2B_51	1318
379	2165	3951 3952	5738	784CIP2B_52	1319
380	2166	3953	5739	784CIP2B 54	1328
381	2167	3954	5740	784CIP2B_55	1436
383	2169	3955	5741	784CIP2B_55	1464
383	2169	3956	5742	784CIP2B_50	1584
385	2170	3957	5743	784CIP2B 58	1617
386	2172	3958	5744	784CIP2B 59	1724
387	2172	3959	5745	784CIP2B 60	1728
388	2174	3960	5746	784CIP2B 61	1772
389	2174	3961	5747	784CIP2B 62	1809
390	2176	3962	5748	784CIP2B 63	1868
391	2177	3963	5749	784CIP2B 64	1898
392	2178	3964	5750	784CIP2B 65	1926
393	2179	3965	5751	784CIP2B 66	1965
394	2180	3966	5752	784CIP2B 67	1967
395	2181	3967	5753	784CIP2B 68	1995
396	2182	3968	5754	784CIP2B 69	2005.
397	2183	3969	5755	784CIP2B 70	2027
398	2184	3970	5756	784CIP2B 71	2055
399	2185	3971	. 5757	784CIP2B 72	2103
400	2186	3972	5758	784CIP2B 73	2106
401	2187	3973	5759	784CIP2B_74	2166
402	2188	3974	5760	784CIP2B_75	2175
403	2189	3975	5761	784CIP2B_76	2176
404	2190	3976	5762	784CIP2B_78	2236
405	2191	3977	5763	784CIP2B_79	2250
406	2192	3978	5764	784CIP2B_80	2300 .
407	2193	3979	. 5765	784CIP2B_81	2323
408	2194	3980	5766	784CIP2B_82	2340
409	2195	3981	5767	784CIP2B_83	2371
410	2196	3982	5768	784CIP2B_84	2399
411	2197	3983	5769	784CIP2B_85	2411
412	2198	3984	5770	784CIP2B_86	2428
413	2199	3985	5771	784CIP2B_87	2430
414	2200	3986	5772	784CIP2B_88	2439
415	2201	3987	5773	784CIP2B_89	2447
416	2202	3988	5774	784CIP2B_90	2461
417	2203	3989	5775	784CIP2B_91 784CIP2B 92	2487 2492
418	2204	3990	5776	784CIP2B_92	2512
419	2205	3991			2564
420	2206	3992	5778	784CIP2B_94	2678
421	2207	3993	5779	784CIP2B_95 784CIP2B_96	2816
422	2208	3994	5780	784CIP2B_96	2818
423	2209	3995	5781 5782	784CIP2B_97	2819
424	2210	3996		784CIP2B_98 784CIP2B_99	2943
425	2211	3997	5783 5784	784CIP2B_99 784CIP2B 100	3137
426	2212	3998	i	784CIP2B_100 784CIP2B_101	3137
427	2213	3999	5785		3160
428	2214	4000	5786	784CIP2B_102 784CIP2B_103	3323
429	2215	4001	5787 5788	784CIP2B_103	3360
431	2216	4002	5789	784CIP2B_104	3362
131	J	1 1003	1 3,03	10301128_103	J

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
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length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		sequence	priority	
	sequence			application	
432	2218	4004	5790	784CIP2B_106	3417
433	2219	4005	5791	784CIP2B_107	3418
434	2220	4006	5792	784CIP2B_108	3442
435	2221	4007	5793	784CIP2B_109	3442
436	2222	4008	5794	784CIP2B_110	3444
437	2223	4009	5795	784CIP2B_111	3855
438	2224	4010	5796	784CIP2B_112	3863
439	2225	4011	5797	784CIP2B_113	4090
440	2226	4012	5798	784CIP2B_114	4105
441	2227	4013	5799	784CIP2B_115	4142
442	2228	4014	5800	784CIP2B_116	4142
443	2229	4015	5801	784CIP2B_117	4149
444	2230	4016	5802	784CIP2B_118	4196
445	2231	4017	5803	784CIP2B_119	4202
446	2232	4018	5804	784CIP2B_120	4274
447	2233	4019	5805	784CIP2B_121	4304
448	2234	4020	5806	784CIP2B_122	4306
449	2235	4021	5807	784CIP2B_123	4311
450	2236	4022	5808	784CIP2B_124	4321
451	2237	4023	5809	784CIP2B_125	4323
452	2238	4024	5810	784CIP2B_126	4332
453	2239	4025	5811	784CIP2B_127	4488
454	2240	4026	5812	784CIP2B_128	4588
455	2241	4027	5813	784CIP2B_129	5569
456	2242	4028	5814	784C1P2B_130	5573
457	2243	4029	5815	784CIP2B_131	5577
458	2244	4030	5816	784CIP2B_132	5579
459	2245	4031	5817	784CIP2B_133	5582
460	2246	4032	5818	784CIP2B_134	5583 5584
461	2247	4033	5819	784CIP2B_135 784CIP2B 136	5585
462	2248	4034	5820 5821	784CIP2B_136	5591
463	2249	4035	5822	784CIP2B_137	5593
464	2250 2251	4036	5823	784CIP2B_138	5594
465	2251	4037	5824	784CIP2B_139	5594
467	2252	4038	5825	784CIP2B 141	5598
468	2254	4040	5826	784CIP2B 142	5602
469	2255	4040	5827	784CIP2B_143	5605
470	2256	4042	5828	784CIP2B_143	5608
471	2257	4043	5829	784CIP2B 145	5617
472	2258	4044	5830	784CIP2B_146	5620
473	2259	4045	5831	784CIP2B_147	5622
474	2260	4046	5832	784CIP2B 148	5623
475	2261	4047	5833	784CIP2B 149	5624
476	2262	4048	5834	784CIP2B 150	5625
477	2263	4049	5835	784CIP2B 151	5627
478	2264	4050	5836	784CIP2B 152	5628
479	2265	4051	5837	784CIP2B 153	5630
480	2266	4052	5838	784CIP2B 154	5632
481	2267	4053	5839	784CIP2B 155	5640
482	2268	4054	5840	784CIP2B 156	5641
483	2269	4055	5841	784CIP2B 157	5643
484	2270	4056	5842	784CIP2B 158	5647
485	2271	4057	5843	784CIP2B 159	5649
486	2272	4058	5844	784CIP2B 160	5658
487	2273	4059	5845	784CIP2B 161	5659
488	2274	4060	5846	784CIP2B 162	5667
489	2275	4061	5847	784CIP2B 163	5672
490	2276	4062	5848	784CIP2B 164	5674
491	2277	4063	5849	784CIP2B 165	5678
492	2278	4064	5850	784CIP2B 166	5680
493	2279	4065	5851	784CIP2B 167	5684
					

of tull- length sequence seque	SEO ID NO:	SEQ ID	SEQ ID NO:	T CPO TD	Thu!	
Length Sull mucleotide Sequence Se		_		SEQ ID	Priority	SEQ ID
nucleotide sequence length peptide sequence sequence Poptide sequence SEQ ID NO: in policity peptide sequence 09/488,725 494 2280 4066 5853 784CTP2E_168 5686 495 2281 4067 5853 784CTP2E_168 5686 497 2283 4068 5855 784CTP2E_170 5698 498 2284 4070 5855 784CTP2E_170 5698 499 2285 4071 5857 784CTP2E_173 5712 500 2286 4072 5858 784CTP2E_174 5720 501 2287 4073 5857 784CTP2E_174 5720 502 2288 4074 5860 784CTP2E_176 5730 503 2299 4075 5861 784CTP2E_178 5738 504 2290 4076 5862 784CTP2E_180 5740 507 2293 4079 5865 784CTP2E_180 5740 508 2294			_		docket number_	
Sequence						
Sequence			sequence			09/488,725
494 2280 4066 5652 784CIP2B_168 5686 496 2282 4068 5854 784CIP2B_170 5698 497 2283 4065 5853 784CIP2B_170 5698 498 2284 4070 5856 784CIP2B_171 5699 498 2285 4071 5857 784CIP2B_173 5719 500 2286 4072 5858 784CIP2B_173 5719 501 2287 4073 5859 784CIP2B_175 5727 502 2288 4074 5860 784CIP2B_175 5732 503 2289 4075 5861 784CIP2B_175 5732 504 2290 4076 5862 784CIP2B_175 5733 505 2291 4077 5863 784CIP2B_175 5733 506 2292 4078 5864 784CIP2B_175 5736 507 2293 4079 5863 784CIP2B_175 5736 508 2294 4076 5862 784CIP2B_175 5738 509 2295 4071 5863 784CIP2B_175 5738 509 2295 4078 5864 784CIP2B_185 5738 509 2295 4078 5864 784CIP2B_185 5744 509 2295 4078 5865 784CIP2B_185 5744 509 2295 4078 5865 784CIP2B_185 5746 509 2295 4078 5865 784CIP2B_185 5748 509 2295 4078 5865 784CIP2B_185 5748 509 2295 4078 5866 784CIP2B_185 5748 509 2295 4078 5867 784CIP2B_185 5748 509 2295 4078 5867 784CIP2B_185 5748 509 2295 4078 5867 784CIP2B_185 5748 511 2297 4083 5869 784CIP2B_186 5750 512 2288 4084 5870 784CIP2B_185 5750 513 2299 4085 5871 784CIP2B_186 5750 514 2300 4086 5872 784CIP2B_186 5750 515 2302 4088 5871 784CIP2B_186 5762 516 2302 4088 5874 784CIP2B_186 5762 517 2303 4089 5875 784CIP2B_186 5762 518 2304 4090 5876 784CIP2B_186 5762 518 2304 4090 5876 784CIP2B_187 5784 519 2305 4091 5877 784CIP2B_188 5762 510 2307 4088 5874 784CIP2B_199 5784 510 2307 4089 5871 784CIP2B_199 5784 511 2309 4086 5872 784CIP2B_199 5784 512 2288 4084 5870 784CIP2B_199 5784 514 2300 4086 5872 784CIP2B_199 5784 515 2301 4087 5873 784CIP2B_186 5762 515 2302 4088 5874 784CIP2B_199 5784 516 2302 4088 5874 784CIP2B_199 5784 517 2303 4089 5875 784CIP2B_199 5784 518 2304 4090 5876 784CIP2B_199 5784 519 2305 4091 5877 784CIP2B_199 5784 519 2305 4091 5877 784CIP2B_199 5784 519 2305 4091 5877 784CIP2B_199 5784 519 2305 4091 5877 784CIP2B_199 5784 519 2305 4091 5877 784CIP2B_199 5784 519 2305 4091 5877 784CIP2B_199 5784 519 2305 4091 5877 784CIP2B_199 5885 520 2306 4092 5878 784CIP2B_200 5873 521 2308 4094 5880 784CIP2B_201 5885 522 2313 4096 5885 784CIP2B_200 5873 531 2317 40				sequence		
495 2291 4067 5853 784C1P2B_179 5698 496 2282 4068 5854 784C1P2B_170 5698 497 2283 4069 5855 784C1P2B_170 5698 498 2284 4070 5855 784C1P2B_171 5712 590 2286 4071 5857 784C1P2B_171 5712 590 2286 4072 5858 784C1P2B_174 5720 590 2286 4073 5859 784C1P2B_174 5720 591 2287 4073 5859 784C1P2B_174 5720 591 2288 4074 5860 784C1P2B_176 5730 593 2289 4075 5861 784C1P2B_178 5737 594 2299 4075 5861 784C1P2B_178 5733 595 2291 4077 5862 784C1P2B_178 5733 595 2292 4078 5864 784C1P2B_178 5733 596 2292 4078 5864 784C1P2B_178 5733 597 2293 4079 5865 784C1P2B_18 5744 598 2294 4060 5866 784C1P2B_18 5744 598 2295 4060 5866 784C1P2B_18 5748 599 2295 4060 5866 784C1P2B_18 5748 599 2295 4061 5867 784C1P2B_18 5748 599 2295 4061 5867 784C1P2B_18 5748 591 2297 4083 5869 784C1P2B_18 5749 591 2297 4083 5869 784C1P2B_18 5750 591 2297 4084 5870 784C1P2B_18 5750 591 2299 4085 5871 784C1P2B_18 5750 591 2299 4085 5871 784C1P2B_18 5750 591 2299 4085 5871 784C1P2B_18 5750 591 2299 4085 5871 784C1P2B_18 5750 591 2299 4085 5871 784C1P2B_18 5761 591 2299 4085 5871 784C1P2B_18 5761 591 2299 4085 5871 784C1P2B_18 5761 591 2299 4085 5871 784C1P2B_18 5761 591 2299 4085 5871 784C1P2B_18 5761 591 2299 4085 5871 784C1P2B_18 5761 591 2299 4085 5871 784C1P2B_18 5761 591 2299 4085 5871 784C1P2B_18 5761 591 2299 4085 5871 784C1P2B_18 5761 591 2299 4085 5871 784C1P2B_19 5761 591 2290 4086 5872 784C1P2B_18 5761 591 2290 4086 5872 784C1P2B_19 5761 591 2290 4086 5872 784C1P2B_19 5761 591 2290 4086 5872 784C1P2B_19 5761 591 2290 4086 5872 784C1P2B_19 5761 591 2290 4086 5872 784C1P2B_19 5761 591 2290 4086 5872 784C1P2B_19 5761 591 2290 4086 5872 784C1P2B_19 5761 591 2290 4086 5872 784C1P2B_19 5761 591 2290 4086 5872 784C1P2B_19 5761 591 2200 4086 5872 784C1P2B_19 5761 591 2200 4086 5872 784C1P2B_19 5761 591 2200 4086 5872 784C1P2B_19 5761 591 2200 4086 5872 784C1P2B_19 5761 591 2200 4086 5872 784C1P2B_19 5761 591 2200 4086 5872 784C1P2B_19 5761 591 2200 4086 5876 784C1P2B_19 5761 591 2200 4086 5876 784C1P2B_19 5761 591 2200 4086 5876 784C1P2B_21 5784 591 2200 4086 58	494		4066	5053		
496 2287 4068 5854 784C1P2B_179 5698 497 2283 4069 5855 784C1P2B_171 5699 498 2284 4070 5856 784C1P2B_171 5699 499 2285 4071 5857 784C1P2B_173 5719 500 2286 4072 5858 784C1P2B_173 5719 500 2286 4071 5857 784C1P2B_173 5719 501 2287 4073 5859 784C1P2B_175 5727 502 2288 4074 5860 784C1P2B_175 5727 502 2288 4074 5860 784C1P2B_175 5727 503 2289 4075 5861 784C1P2B_177 5734 504 2290 4075 5862 784C1P2B_178 5739 505 2291 4077 5863 784C1P2B_178 5739 506 2292 4078 5862 784C1P2B_178 5739 507 2293 4079 5865 784C1P2B_180 5740 508 2294 4080 5866 784C1P2B_180 5740 509 2295 4081 5867 784C1P2B_180 5745 509 2295 4081 5867 784C1P2B_180 5745 510 2296 4082 5868 784C1P2B_182 5748 511 2297 4083 5869 784C1P2B_182 5745 512 2298 4084 5870 784C1P2B_184 5750 513 2299 4085 5871 784C1P2B_184 5750 514 2300 4086 5871 784C1P2B_186 5750 515 2298 4084 5870 784C1P2B_186 5750 515 2298 4084 5870 784C1P2B_186 5750 515 2298 4084 5870 784C1P2B_186 5750 515 2298 4086 5870 784C1P2B_186 5750 515 2298 4086 5871 784C1P2B_186 5750 515 2298 4086 5871 784C1P2B_186 5750 515 2298 4086 5871 784C1P2B_186 5750 515 2298 4086 5871 784C1P2B_187 5761 515 2300 4086 5871 784C1P2B_187 5761 515 2300 4086 5871 784C1P2B_187 5761 516 2300 4086 5872 784C1P2B_187 5761 517 2303 4089 5876 784C1P2B_187 5781 518 2300 4089 5876 784C1P2B_189 5762 520 2306 4092 5878 784C1P2B_193 5788 521 2307 4093 5879 784C1P2B_193 5788 522 2309 4094 5880 784C1P2B_193 5788 523 2309 4095 5876 784C1P2B_193 5788 524 2310 4096 5887 784C1P2B_193 5788 525 2311 4097 5883 784C1P2B_193 58818 524 2311 4097 5883 784C1P2B_193 58818 525 231 2307 4093 5879 784C1P2B_193 58818 526 2312 4098 5880 784C1P2B_193 58818 527 2305 4091 5877 784C1P2B_193 5788 529 2315 4001 5896 784C1P2B_200 5865 531 2317 4003 5897 784C1P2B_193 5788 532 2307 4093 5879 784C1P2B_193 58818 533 2314 400 5886 784C1P2B_200 5865 534 2314 400 5886 784C1P2B_200 5865 535 2313 4097 5883 784C1P2B_200 5865 536 2314 400 5886 784C1P2B_200 5865 537 2318 400 5889 784C1P2B_200 5865 538 2314 400 5889 784C1P2B_200 5865 531 2318 400 5899 784C1P2B_210 5895 534 2314				1		
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SOT 2293			4077	5863	784CIP2B 179	5739
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621	2407	4193	5979	784CIP2B_298	6167
622	2408	4194	5980	784CIP2B_299	6172
623	2409	4195	5981	784CIP2B_300	6173
624 625	2410	4196	5982	784CIP2B_301	6190
626	2411	4197	5983	784CIP2B_302	6194
627	2412	4198	5984	784CIP2B_303	6196
628	2413	4199	5985	784CIP2B_304	6197
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630	2415	4201	5987	784CIP2B_306	6198
631	2417	4202	5988 5989	784CIP2B_308	6214
632	2418	4204	5990	784CIP2B 309	6215
633	2419	4205	5991	784CIP2B_310 784CIP2B_311	6219
634	2420	4206	5992	784CIP2B 311	6226
635	2421	4207	5993	784CIP2B_312 784CIP2B_313	6229
636	2422	4208	5994	784CIP2B_313	6234
637	2423	4209	5995	784CIP2B_314 784CIP2B_315	6237
638	2424	4210	5996	784CIP2B_315	6238 6239
639	2425	4211	5997	784CIP2B 317	6239
640	2426	4212	5998	784CIP2B_317	6239
641	2427	4213	5999	784CIP2B_318	6240
642	2428	4214	6000	784CIP2B 320	6244
643	2429	4215	6001	784CIP2B 321	6245
644	2430	4216	6002	784CIP2B 322	6250
645	2431	4217	6003	784CIP2B 323	6252
646	2432	4218	6004	784CIP2B 324	6252
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648	2434	4220	6006	784CIP2B 326	6260
649	2435	4221	6007	784CIP2B 327	6261
650	2436	4222	6008	784CIP2B_328	6264
651	2437	4223	6009	784CIP2B_329	6265
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653	2439	4225	6011	784CIP2B_331	6270
654	2440	4226	6012	784CIP2B_332	6271
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658	2443	4229	6015	784CIP2B_336	6281
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661	2447	4233	6018	784CIP2B_339	6292
662	2448	4234	6019	784CIP2B_340	6294
663	2449	4235	6021	784CIP2B_343 784CIP2B_344	6312
664	2450	4236	6022	784CIP2B 344 784CIP2B 345	6312
665	2451	4237	6023	784CIP2B_345	6312
666	2452	4238	6024	784CIP2B 346	6322
667	2453	4239	6025	784CIP2B 347	6329
668	2454	4240	6026	784CIP2B 350	6331
669	2455	4241	6027	784CIP2B_350	6333
670	2456	4242	6028	784CIP2B_351	6334
671	2457	4243	6029	784CIP2B 353	6337
672	2458	4244	6030	784CIP2B 354	6339
673	2459	4245	6031	784CIP2B 355	6346
674	2460	4246	6032	784CIP2B 356	6348
675	2461	4247	6033	784CIP2B 357	6348
676	2462	4248	6034	784CIP2B 358	6350
677	2463	4249	6035	784CIP2B 359	6351
678	2464	4250	6036	784CIP2B 360	6355
679	2465	4251	6037	784CIP2B 361	6362

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684	2470	4256	6042	784CIP2B_366	6379
685	2471	4257	6043	784CIP2B_367	6380
686	2472	4258	6044	784CIP2B_368	6381
687	2473	4259	6045	784CIP2B_369	6392
688	2474	4260	6046	784CIP2B_370	6395
689	2475	4261	6047	784CIP2B_371	6397
690	2476	4262	6048	784CIP2B_372	6400
691	2477	4263	6049	784CIP2B_373	6401
692	2478	4264	6050	784CIP2B_374	6411
693	2479	4265	6051	784CIP2B_375	6411
694	2480	4266	6052	784CIP2B_376	6411
695	2481	4267	6053	784CIP2B_377	6416
696	2482	4268	6054	784CIP2B_378	6418
697	2483	4269	6055	784CIP2B_379	. 6422
698	2484	4270	6056·	784CIP2B_380	6423
699	2485	4271	6057	784CIP2B_381	6426
700	2486	4272	6058	784CIP2B_382	6427
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702	2488 2489	4274	6060	784CIP2B_384	6429
704	2499	4275	6061	784CIP2B_385	6430
705	2490	4276	6062	784CIP2B_386	6432
706	2491	4278	6063	784CIP2B_387	6432
707	2492	4278	6064 6065	784CIP2B_388	6438
708	2494	4279	6066	784CIP2B_389	6441
709	2495	4280	6067	784CIP2B_390	6446
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711	2497	4283	6069	784CIP2B_392	6459
712	2498	4284	6070	784CIP2B_394 784CIP2B 395	6461
713	2499	4285	6071	784CIP2B_395	6467
714	2500	4286	6072	784CIP2B_396	6468
715	2501	4287	6073	784CIP2B_397	6487
716	2502	4288	6074	784CIP2B_398	6491 6506
717	2503	4289	6075	784CIP2B_399	6514
718	2504	4290	6076	784CIP2B 401	6519
719	2505	4291	6077	784CIP2B 403	6521
720	2506	4292	6078	784CIP2B 404	6532
721	2507	4293	6079	784CIP2B 405	6536
722	2508	4294	6080	784CIP2B 406	6543
723	2509	4295	6081	784CIP2B 407	6544
724	2510	4296	6082	784CIP2B 408	6548
725	2511	4297	6083	784CIP2B 409	6551
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727	2513	4299	6085	784CIP2B 411	6552
728	2514	4300	6086	784CIP2B 412	6554
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735	2521	4307	6093	784CIP2B 419	6575
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738	2524	4310	6096	784CIP2B 422	6595
739	2525	4311	6097	784CIP2B 423	6599
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743	2529	4315	6101		6630
744	2530	4316	6102	784CIP2B_428	6631
745	2531	4317	6103	784CIP2B_429	6632
746	2532	4318	6104	784CIP2B_430	6633
747	2533	4319	6105	784CIP2B_431	6634
748	2534	4320	6106	784CIP2B_432	6639
749	2535	4321	6107	784CIP2B_433	6641
750	2536	4322	6108	784CIP2B_434	6644
751	2537	4323	6109	784CIP2B_435	6646
752	2538	4324	6110	784CIP2B_436	664B
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754	2540	4326	6112	784CIP2B_438	6654
755	2541	4327	6113	784CIP2B 439	6657 .
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759	2545	4331	6117	784CIP2B 443	6668
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773	2559	4345	6131	784CIP2B_457	6726
774	2560	4346	6132	784CIP2B_458	6727
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776	2562	4348	6134	784CIP2B 460	6730
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796	2582	4368	6154	784CIP2B_480	6844
797	2583	4369	6155	784CIP2B 482	6849
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799	2585	4371	6157	784CIP2B 484	6857
800	2586	4372	6158	784CIP2B 485	6861
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802	2588	4374	6160	784CIP2B 487	6875
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808	2594	4380	6166	784CIP2B 493	6894
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812	2598	4384	6170	784CIP2B_497	6914
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817	2603	4389	6175	784CIP2B_502	6935
818	2604	4390	6176	784CIP2B_503	6940
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828	2613 2614	4399	6185	784CIP2B_512	6967
829	2615	4400	6186	784CIP2B_513	6983
830	2616	4401 4402	6187	784CIP2B_514	6988
831	2617	4402	6188	784CIP2B_515	6996
832	2618	4404	6189	784CIP2B_516	7003
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834	2620	4406	6192	784CIP2B_518 784CIP2B_519	7017
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836	2622	4408	6194	784CIP2B_520 784CIP2B_521	7025
837	2623	4409	6195	784CIP2B 521	7025 7050
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840	2626	4412	6198	784CIP2B 525	7060
841	2627	4413	6199	784CIP2B 526	7064
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844	2630	4416	6202	784CIP2B 529	7072
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847	2633	4419	6205	784CIP2B 532	7088
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859	2645	4431	6217	784CIP2B_544	7126
860	2646	4432	6218	784CIP2B 545	7127
861	2647	4433	6219	784CIP2B_546	7130
862	2648	4434	6220	784CIP2B_547	7131
863	2649	4435	6221	784CIP2B_548	7144
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869	2655	4441	6227	784CIP2B_554	7190
870	2656	4442	6228	784CIP2B_555	7191
871	2657	4443	6229	784CIP2B_556	7203
872	2658	4444	6230	784CIP2B_557	7204
873	2659	4445	6231	784CIP2B_558	7208
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877	2663	4449	6235	784CIP2B_562	7221
878	2664	4450	6236	784CIP2B_563	7230
879	2665	4451	6237	784CIP2B_564	7237
880	2666	4452	6238	784CIP2B_565	7240
881 ·	2667	4453	6239	784CIP2B_566	7245
882	2668	4454	6240	784CIP2B_567	7250
883	2669	4455	6241	784CIP2B_568	7251
884	2670	4456	6242	784CIP2B_569	7255
885	2671	4457	6243	784CIP2B_570	7260
886	2672	4458	6244	784CIP2B_571	7265
887	2673	4459	6245	784CIP2B_572 784CIP2B 573	7268
888	2674	4460	6246		7279
889	2675	4461	6247	784CIP2B_574 784CIP2B 575	7279
890	2676	4462	6248	784CIP2B_575	7283
891	2677	4463	6249	784CIP2B_576	7287
892	2678	4464	6250 6251	784CIP2B 578	7301
893	2679	4465	6252	784CIP2B_578	7301
894	2680	4466 4467	6253	784CIP2B 580	7308
895	2681		6254	784CIP2B_580 784CIP2B_581	7309
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898	2685	4471	6257	784CIP2B 584	7326
900	2686	4472	6258	784CIP2B 585	7326
900	2687	4473	6259	784CIP2B 586	7334
902	2688	4474	6260	784CIP2B 587	7337
903	2689	4475	6261	784CIP2B 588	7339
904	2690	4476	6262	784CIP2B 589	7344
905	2691	4477	6263	784CIP2B 590	7355
906	2692	4478	6264	784CIP2B 591	7363
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908	2694	4480	6266	784CIP2B 593	7365
909	2695	4481	6267	784CIP2B_594	7368
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911	2697	4483	6269	784CIP2B_596	7372
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913	2699	4485	6271	784CIP2B_600	7381
914	2700	4486	6272	784CIP2B_601	7383
915	2701	4487	6273	784CIP2B_602	7387
916	2702	4488	6274	784CIP2B_603	7391
917	2703	4489	6275	784CIP2B 604	7393
918	2704	4490	6276	784CIP2B_605	7395
919	2705	4491	6277	784CIP2B_606	7397
920	2706	4492	6278	784CIP2B_607	7399
921	2707	4493	6279	784CIP2B_608	7405
922	2708	4494	6280	784CIP2B 609	7406
923	2709	4495	6281	784CIP2B_610	7406
	2710	4496	6282	784CIP2B_611	7409
924				<u> </u>	7410
925	2711	4497	6283	784CIP2B_612	1410
	2711 2712	4497 4498	6283	784CIP2B_612 784CIP2B_613	7411

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930	2716	4502	6288	784CIP2B_617	7422
931	2717	4503	6289	784CIP2B_618	7422
932	2718	4504	6290	784CIP2B_619 784CIP2B 620	7423
933	2719	4505	6291	784CIP2B_620 784CIP2B 621	7424 7426
934	2720	4506	L. —	784CIP2B_621 784CIP2B 622	7427
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938	2724	4510	6297	784CIP2B_625	7437
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963	2749	4535	6321	784CIP2B_650	7494
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967	2753	4539	6325	784CIP2B_654	7516
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969	2755	4541	6327	784CIP2B_656	7519
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977	2763	4549	6335	784CIP2B_664	7552
978	2764	4550	6336	784CIP2B_665	7554
979	2765	4551	6337	784CIP2B_666	7567
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981	2767	4553	6339	784CIP2B_668	7575
982	2768	4554	6340	784CIP2B_669	7576
983	2769	4555	6341	784CIP2B_670	7577
984	2770	4556	6342	784CIP2B_671	7579
985	2771	4557	6343	784CIP2B_672	7582
986	2772	4558	6344	784CIP2B_673	7587
987	2773	4559	6345	784CIP2B_674	7589
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993	2779	4565	6351	784CIP2B_680	7613
994	2780	4566	6352	784CIP2B_681	7623
995	2781	4567	6353	784CIP2B_682	7629
996	2782	4568	6354	784CIP2B_683	7630
997	2783	4569	6355	784CIP2B_684	7633
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1002	2788 2789	4574	6360	784CIP2B_689	7647
1003	2789	4575	6361	784CIP2B_690	7648
1005	2791	4576 4577	6362 6363	784CIP2B_691	7658
1006	2792	4578	6364	784CIP2B_692	7664
1007	2793	4579	6365	784CIP2B_693	7664
1008	2794	4580	6366	784CIP2B_695 784CIP2B_696	7674
1009	2795	4581	6367	784CIP2B_696	7675 7676
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1028	2814	4600	6386	784CIP2B_716	7759
1029	2815	· 4601	6387	784CIP2B_717	7760
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1038	2824	4610	6396	784CIP2B_726	7779
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	3019	4805	6591	784CIP2B_923	8393
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	3022	4808	6594	784CIP2B 926	8396
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nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
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1241	3027	4813	6599	784CIP2B_931	8406
	3028	4814	6600	784CIP2B_932	8409
1243	3029	4815	6601	784CIP2B_933	8410
1244	3030	4816	6602	784CIP2B_934	8414
1245	3031	4817	6603	784CIP2B_935	8415
1246	3032	4818	6604	784CIP2B_936	8419
1247	3033	4819	6605	784CIP2B_937	8426
1248	3034	4820	6606	784CIP2B_938	8430
1249	3035	4821	6607	784CIP2B_939	8431
1250	3036	4822	6608	784CIP2B_940	8432
1251	3037	4823	6609	784CIP2B_941	8433
1252	3038	4824	6610	784CIP2B_942	8434
1253	3039	4825	6611	784CIP2B_943	8438
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1255	3041	4827	6613	784CIP2B 945	8441
1256	3042	4828	6614	784CIP2B 946	8450
1257	3043	4829	6615	784CIP2B 947	8451
1258	3044	4830	6616	784CIP2B 948	8452
1259	3045	4831	6617	784CIP2B 949	8460
1260	3046	4832	6618	784CIP2B 950	8461
1261	3047	4833	6619	784CIP2B 951	8462
1262	3048	4834	6620	784CIP2B 952	8464
1263	3049	4835	6621	784CIP2B 953	8465
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1265	3051	4837	6623	784CIP2B 955	8470
1266	3052	4838	6624	784CIP2B 956	8471
1267	3053	4839	6625	784CIP2B 957	8473
1268	3054	4840	6626	784CIP2B 958	8474
1269	3055	4841	6627	784CIP2B 959	8475
1270	3056	4842	6628	784CIP2B 960	8476
1271	3057	4843	6629	784CIP2B 961	8480
1272	3058	4844	6630	784CIP2B 962	8482
1273	3059	4845	6631	784CIP2B 963	
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1275	3061	4847	6633	784CIP2B 965	
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1277	3063	4849	6635	784CIP2B_966	8492
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1281	3067		6638	784CIP2B_970	8499
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		4858	6644	784CIP2B_976	8542
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1288	3074	4860	6646	784CIP2B_978	8565
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1292	3078	4864	6650	784CIP2B_982	8578
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1295	3081	4867	6653	784CIP2B 985	8602
1296	3082	4868	6654	784CIP2B 986	8604
1297	3083	4869	6655	784CIP2B 987	8609
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1304	3090	4876	6662	784CIP2B 994	8651
1305	3091	4877	6663	784CIP2B 995	8654
1306	3092	4878	6664	784CIP2B 996	8655
1307	3093	4879	6665	784CIP2B 997	8657
1308	3094	4880	6666	784CIP2B 998	8665
1309	3095	4881	6667	784CIP2B_999	8668
1310	3096	4882	6668	784CIP2B_1000	8671
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1312	3098	4884	6670	784CIP2B_1002	8692
1313	3099	4885	6671	784CIP2B_1003	8706
1314	3100	4886	6672	784CIP2B_1004	8716
1315	3101	4887	6673	784CIP2B_1005	8719
1316	3102	4888	6674	784CIP2B_1006	8743
1317	3103	4889	6675	784CIP2B_1007	8764
1318	3104	4890	6676	784CIP2B_1008	8764
1319	3105	4891	6677	784CIP2B_1009	8764
1320	3106	4892	6678	784CIP2B_1010	8774
1321 1322	3107	4893	6679	784CIP2B_1011	8782
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1324	3110	4895 4896	6681	784CIP2B_1013	8827
1324	3110	4896	6683	784CIP2B_1014 784CIP2B 1015	8842
1326	3112	4898	6684	784CIP2B_1015	8842 8858
1327	3113	4899	6685	784CIP2B_1016	8871
1328	3114	4900	6686	784CIP2B_1017	8921
1329	3115	4901	6687	784CIP2B 1019	8927
1330	3116	4902	6688	784CIP2B 1020	8942
1331	3117	4903	6689	784CIP2B 1021	8994
1332	3118	4904	6690	784CIP2B 1022	9023
1333	3119	4905	6691	784CIP2B 1023	9028
1334	3120	4906	6692	784CIP2B 1024	9058
1335	3121	4907	6693	784CIP2B_1025	9058
1336	3122	4908	6694	784CIP2B_1026	9079
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1338	3124	4910	6696	784CIP2B_1028	9082
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1340	3126	4912	6698	784CIP2B_1030	9093
1341	3127	4913	6699	784CIP2B_1031	9101
1342	3128	4914	6700	784CIP2B_1032	9103
1343	3129	4915	6701	784CIP2B_1033	9105
1344	3130	4916	6702	784CIP2B_1034	9151
1345	3131	4917	6703	784CIP2B_1035	9161
1346	3132	4918	6704	784CIP2B_1036	9172
1347	3133	4919	6705	784CIP2B_1037	9174
1348	3134	4920	6706	784CIP2B_1038	9204
1350	3135 3136	4921 4922	6707 6708	784CIP2B 1039	9234
1351	3136	4922	6709	784CIP2B_1040 784CIP2B_1041	9235
1352	3137	4924	6709		9239
1353	3139	4925	6711	784CIP2B 1042	9256
1354	3140	4925	6712	784CIP2B_1043 784CIP2B_1044	9276
1355	3141	4927	6713		93 4 5 9379
1356	3142	4927	6714	784CIP2B_1045 784CIP2B 1046	9435
1357	3143	4928	6714	784CIP2B_1046 784CIP2B_1047	9435
	3144	4930	6716	784CIP2B 1047	9469
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1358					
	3145 3146	4931 4932	6717 6718	784CIP2B_1049 784CIP2B_1050	9500 9502

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1366	3152	4938	6724	784CIP2B_1056	9556
1367	3153	4939	6725	784CIP2B_1057	9575
1368	3154	4940	6726	784CIP2B_1058	9589
1369	3155	4941	6727	784CIP2B_1059	9599
1370	3156	4942	6728	784CIP2B_1060	9602
1371	3157	4943	6729	784CIP2B_1061	9606
1372	3158	4944	6730	784CIP2B_1062	9622 9623
1373	3159	4945	6731	784CIP2B_1063	9646
1374	3160	4946	6732	784CIP2B_1064	9747
1375	3161	4947	6733	784CIP2B_1065 784CIP2B_1066	9773
1376	3162	4948	6734 6735	784CIP2B_1066 784CIP2B 1067	9785
1377	3163	4949	6736	784CIP2B_1067	9801
1378	3164		6737	784CIP2B 1069	9811
1379	3165	4951	6738	784CIP2B 1070	9843
1380	3166	4952	6739	784CIP2B_1070	9854
1381	3167	4954	6740	784CIP2B_1071	9854
1382	3168	4955	6741	784CIP2B 1073	9864
1383	3170	4956	6742	784CIP2B 1074	9864
1385	3170	4957	6743	784CIP2B 1075	9871
1386	3172	4958	6744	784CIP2B 1076	9879
1387	3173	4959	6745	784CIP2B 1077	9881
1388	3174	4960	6746	784CIP2B 1078	9885
1389	3175	4961	6747	784CIP2B 1079	9901
1390	3176	4962	6748	784CIP2B 1080	9912
1391	3177	4963	6749	784CIP2B_1081	9916
1392	3178	4964	6750	784CIP2B_1082	9921
1393	3179	4965	6751	784CIP2B_1083	9925
1394	3180	4966	6752	784CIP2B_1084	9930
1395	3181	4967	6753	784CIP2B_1085	9949
1396	3182	4968	6754	784CIP2B_1086	9951
1397	3183	4969	6755	784CIP2B_1087	9959
1398	3184	4970	6756	784CIP2B_1088	9973
1399	3185	4971	6757	784CIP2B_1089	9982
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1401	3187	4973	6759	784CIP2B_1091	10021
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1407	3193	4979	6765	784CIP2B_1098	10132
1408	3194	4980	6766	784CIP2B_1099 784CIP2B_1100	10169
1409	3195	4981	6767	784CIP2B_1100 784CIP2B_1101	10217
1410	3196	4982	6768	784CIP2B 1101	10232
1411	3197	4983	6769 6770	784CIP2B_1102	10232
1412	3198	4984	6771	784CIP2B 1103	10279
1413	3199	4985	6772	784CIP2B_1104	33
1414	3200	4986 4987	6773	784CIP2C 2	271
1415	3201		6774	784CIP2C_2	848
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1417	3203	4989	6776	784CIP2C 5	864
1418	3204 3205	4990 4991	6777	784CIP2C 6	953
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1-16-	1				

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
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1428	3214	5000	6786	784CIP2C_15	2889
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1431	3217	5003	6789	784CIP2C_18	2905
1432	3218	5004	6790	784CIP2C_19	2948
1433	3219	5005	6791	784CIP2C_20	2956
1434	3220	5006	6792	784CIP2C_21	2959
1435	3221	5007	6793	784CIP2C_22	2965
1436	3222	5008	6794	784CIP2C_23	2966
1437	3223	5009	6795	784CIP2C_24	2970
1438	3224	5010	6796	784CIP2C_25	2985
	3225	5011	6797	784CIP2C_26	2987
1440	3226	5012 5013	6798 6799	784CIP2C_27	2993
1442	3227			784CIP2C_28	2993
1443	3228	5014 5015	6800	784CIP2C_29	3017
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1446	3232	5018	6804	784CIP2C_32 784CIP2C_33	3357
1447	3232	5019	6805	784CIP2C_33	3359
1448	3234	5020	6806	784CIP2C_34	3432 3438
1449	3235	5021	6807	784CIP2C_35	3439
1450	3236	5022	6808	784CIP2C_38	3463
1451	3237	5023	6809	784CIP2C_33	3466
1452	3238	5024	6810	784CIP2C 41	3466
1453	3239	5025	6811	784CIP2C 42	3467
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1463	3249	5035	6821	784CIP2C_52	3503
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1467	3253	5039	6825	784CIP2C_56	3531
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1470	3256	5042	6828	784CIP2C_59	3548
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1472	3258	5044	6830	784CIP2C_61	3553
1473	3259	5045	6831	784CIP2C_62	3564
1474	3260	5046	6832	784CIP2C_63	3567
1475	3261	5047	6833	784CIP2C_64	3572
1476	3262	5048	6834	784CIP2C_65	3573
1477	3263	5049	6835	784CIP2C_66	3574
1478	3264	5050	6836	784CIP2C_67	3583
1479	3265	5051	6837	784CIP2C_68	3615
1480	3266	5052	6838	784CIP2C_69	3623
1481	3267	5053	6839	784CIP2C_70	3629
1482	3268	5054	6840	784CIP2C_71	3666
1483	3269	5055	6841	784CIP2C_72	3667
1485	3270 3271	5056	6842	784CIP2C_73	3906
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nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
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1489	3275	5061	6847	784CIP2C_77 784CIP2C_78	3935
1490	3275	5062	6848	784CIP2C 79	3959
1491	3277	5063	6849	784CIP2C 80	3981
1492	3278	5064	6850	784CIP2C 81	4295
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1494	3280	5066	6852	784CIP2C 83	4360
1495	3281	5067	6853	784CIP2C 84	4362
1496	3282	5068	6854	784CIP2C 85	4371
1497	3283	5069	6855	784CIP2C 86	4373
1498	3284	5070	6856	784CIP2C 87	4376
1499	3285	5071	6857	784CIP2C_89	4378
1500	3286	5072	6858	784CIP2C_90	4382
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1505	3291	5077	6863	784CIP2C_95	4430
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1507	3293 3294	5079	6865	784CIP2C_97	4436
1509	3294	5080 5081	6866 6867	784CIP2C_98	4439
1510	3296	5082	6868	784CIP2C_99 784CIP2C 100	4440
1511	3297	5083	6869	784CIP2C_100	4441 4442
1512	3298	5084	6870	784CIP2C_101	4442
1513	3299	5085	6871	784CIP2C_102	4462
1514	3300	5086	6872	784CIP2C 104	4466
1515	3301	5087	6873	784CIP2C 105	4469
1516	3302	5088	6874	784CIP2C 106	4477
1517	3303	5089	6875	784CIP2C 107	4481
1518	3304	5090	6876	784CIP2C_108	4483
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1521	3307	5093	6879	784CIP2C_111	4490
1522	3308	5094	6880	784CIP2C_112	4499
1523 1524	3309	5095	6881	784CIP2C_113	4503
1525	3310 3311	5096 5097	6882 6883	784CIP2C_114	4506
1526	3312	5098	6884	784CIP2C_115 784CIP2C_116	4509
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1528	3314	5100	6886	784CIP2C_117	4516 4522
1529	3315	5101	6887	784CIP2C 118	4525
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1532	3318	5104	6890	784CIP2C_122	4529
1533	3319	5105	6891	784CIP2C_123	4532
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1536	3322	5108	6894	784CIP2C_126	4551
1537	3323	5109	6895	784CIP2C_127	4552
1538	3324	5110	6896	784CIP2C_128	4559
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1540	3326	5112	6898	784CIP2C_130	4568
1541	3327	5113	6899	784CIP2C_132	4585
1542 1543	3328 3329	5114	6900	784CIP2C 133	4592
1544	3339	5115	6901	784CIP2C_134	4609
1545	3331	5116 5117	6902 6903	784CIP2C_135	4616
1546	3332	5117	6903	784CIP2C_136	4617
1547	3333	5119	6905	784CIP2C_137 784CIP2C_138	4618 4620
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1549	3335	5121	6907	784CIP2C_140	4632
1550	3336	51.22	6908	784CIP2C_141	4634
1551	3337	5123	6909	784CIP2C_142	4638
1552	3338	5124	6910	784CIP2C_143	4639
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1554	3340	5126	6912	784CIP2C_145	4644
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1556	3342	5128	6914	784CIP2C_147	4668
1557	3343	5129	6915	784CIP2C_148	4677
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1559	3345	. 5131	6917	784CIP2C_150	4677
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1561	3347	5133	6919	784CIP2C_153	4690
1562	3348	5134	6920	784CIP2C_154	4691
1563	3349	5135	6921	784CIP2C_155	4727
1564	3350	5136	6922	784CIP2C_156	4730
1565	3351	5137	6923	784CIP2C_157	4734
1566	3352	5138	6924	784CIP2C_158	4757
1567	3353	5139	6925	784CIP2C_159	4764
1568	3354	5140	6926	784CIP2C_160	4786
1569	3355	5141	6927	784CIP2C_161	4793
1570	3356	5142	6928	784CIP2C_162	4825
1571	3357	5143	6929	784CIP2C_163	4826
1572	3358	5144	6930	784CIP2C_164	4850
1573	3359	5145	6931	784CIP2C_165	4853
1574	3360	5146	6932	784CIP2C_166	4855
1575	3361	5147	6933	784CIP2C_167	4856
1576	3362	5148	6934	784CIP2C_168	4867
1577	3363	5149	6935	784CIP2C_169 784CIP2C_170	4878
1578	3364	5150	6936	784CIP2C_170 784CIP2C_171	4880
1579	3365	5151	6937	784CIP2C_171 784CIP2C_172	4942
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1582	3368	5154	6940	784CIP2C_174	4952
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1584	3370	5156	6942	784CIP2C 178	4958
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1586	3372	5159	6945	784CIP2C 179	5590
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1593	3379	5165	6951	784CIP2C 185	5774
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1595	3381	5167	6953	784CIP2C 187	5806
1596	3382	5168	6954	784CIP2C 188	5852
1597	3383	5169	6955	784CIP2C 189	5892
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1599	3385	5171	6957	784CIP2C 191	6061
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1601	3387	5173	6959	784CIP2C 193	6160
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1604	3390	5176	6962	784CIP2C 196	6398
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			6965	784CIP2C 199	6469
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	sequence			application	
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1614	3400	5186	6972	784CIP2C_206	6691
1615	3401	5187	6973	784CIP2C_207	6695
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1619	3405	5191	6977	784CIP2C_211	6943
1620	3406	5192	6978	784CIP2C_212	7110
1621	3407	5193	6979	784CIP2C_213	7200
1622	3408	5194	6980	784CIP2C_214	7212
1623	3409	5195	6981	784CIP2C_215	7218
1624	3410	5196	6982	784CIP2C_216	7249
1625	3411	5197	6983	784CIP2C_217	7500
1626	3412	5198	6984	784CIP2C_218	7509
1627	3413	5199	6985	784CIP2C_219	7523
1628	3414	5200	6986	784CIP2C_220	7544
1629	3415	5201	6987	784CIP2C_221	7564
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1636	3422	5208	6994	784CIP2C_228	7943
1637	3423	5209	6995	784CIP2C_229	8175
1638	3424	5210	6996	784CIP2C_230	8216
1639	3425	5211	6997	784CIP2C_231	8225
1640	3426	5212	6998	784CIP2C_232	8271
1641	3427	5213	6999	784CIP2C_233	8397
1642	3428	5214	7000	784CIP2C_234	8466
1643	3429	5215	7001	784CIP2C_235	8503
1644	3430	5216	7002	784CIP2C_236	8953
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1655	3441		7013	784CIP2D_3 784CIP2D 4	3633
1656	3442	5228		784CIP2D_4 784CIP2D 5	3658
1657	3443	5229 5230	7015 7016	784C1P2D_5	3732
1658	3445	5231	7017	784CIP2D 7	4004
1659		5232	7017	784CIP2D 8	4700
1660	3446		7018	784CIP2D_8	4703
1661	3448	5233 5234	7020	784CIP2D 10	4774
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	3450	5236	7021	784CIP2D 12	4918
1664			7023	784CIP2D_12 784CIP2D 13	5159
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1668	3454 3455	5240	7026	784CIP2D_16 784CIP2D_17	8727
1670	3456	5241 5242	7027	784CIP2D 17 784CIP2D 18	8734
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1712	3498	5284	7070	784CIP2D 60	9501
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		5300 5301	7086	784CIP2D_76	9777
1770	3515		7087	784CIP2D 77	9787
1729	3515				
1730	3516	5302	7088	784CIP2D_78	9790
1730 1731	3516 3517	5302 5303	7088 7089	784CIP2D_78 784CIP2D_79	9790 98 4 2
1730	3516	5302	7088	784CIP2D_78	9790

of full- length No. of contig of contig ength nucleotide sequence ength nucleotide sequence ength sequence ength	SEO ID NO:	I SEO ID	SEO ID NO:	SEQ ID	Priority	1 450 75
Length Equil- Length sequence Sequence Sequence Length sequence Sequen		_			•	SEQ ID
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1735 3521 5307 7093 784CIP2D_83 10010 1736 3522 5308 7094 784CIP2D_84 10011 1737 3523 5309 7095 784CIP2D_85 10052 1738 3524 5310 7096 784CIP2D_86 10057 1739 3525 5311 7097 784CIP2D_87 10085 1740 3526 5312 7098 784CIP2D_87 10085 1740 3526 5312 7098 784CIP2D_87 10085 1741 3527 5313 7099 784CIP2D_90 10142 1742 3528 5314 7100 784CIP2D_92 10165 1743 3529 5315 7101 784CIP2D_92 10165 1744 3530 5316 7102 784CIP2D_93 10173 1744 3530 5316 7102 784CIP2D_94 10173 1746 3531 5317 7103 784CIP2D_94 10173 1746 3532 5318 7104 784CIP2D_94 10173 1747 3533 5319 7105 784CIP2D_95 10273 1748 3534 5320 7106 784CIP2D_9 4 10173 1749 3535 5321 7107 784CIP2D_9 5 10273 1749 3535 5321 7107 784CIP2D_9 10273 1749 3535 5321 7107 784CIP2D_9 10273 1749 3535 5321 7107 784CIP2D_9 10273 1749 3535 5321 7107 784CIP2D_9 10273 1749 3535 5321 7106 784CIP2D_9 10273 1749 3535 5321 7106 784CIP2D_9 10273 1750 3536 5322 7108 784CIP2D_9 10273 1750 3536 5322 7108 784CIP2D_9 10273 1751 3537 5323 7109 784CIP2D_9 10273 1752 3538 5324 7110 784CIP2D_9 4018 1751 3537 5323 7109 784CIP2D_9 4018 1751 3537 5323 7109 784CIP2D_9 4923 1754 3540 5326 7112 784CIP2D_9 4923 1755 3538 5324 7110 784CIP2D_9 4923 1756 3541 5327 7113 784CIP2D_10 4926 1755 3541 5327 7113 784CIP2D_10 4926 1755 3543 5329 7115 784CIP2D_10 4926 1756 3542 5328 7114 784CIP2D_10 4926 1757 3543 5349 5332 7116 784CIP2D_10 4926 1758 3549 5335 7117 784CIP2D_11 4962 1758 3549 5355 5331 7117 784CIP2D_11 4962 1759 3545 5331 7117 784CIP2D_11 4962 1756 3554 5330 7116 784CIP2D_12 4964 1759 3545 5331 7117 784CIP2D_12 4964 1759 3545 5331 7117 784CIP2D_11 4962 1756 3554 5330 7116 784CIP2D_12 4964 1759 3545 5331 7117 784CIP2D_11 4962 1760 3546 5332 7118 784CIP2D_11 4962 1760 3546 5332 7118 784CIP2D_11 4962 1760 3546 5337 7113 784CIP2D_11 4962 1760 3546 5337 7113 784CIP2D_11 4962 1760 3546 5337 7113 784CIP2D_11 5055 1760 3546 5337 7113 784CIP2D_11 5055 1760 3546 5337 7113 784CIP2D_11 5055 1760 3546 5337 7118 784CIP2D_11 794CIP2D_11 5055 1760 3556 5352 7138 784CIP2D_12 5056 1779 3556 5351 7131 784CIP2D_13 7772 1779 3556 53	1734	1 •	5306	7092		9867
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1771 3557 5343 7129 784CIP2F 3 4021 1772 3558 5344 7130 784CIP2F 4 4474 1773 3559 5345 7131 784CIP2F 5 4566 1774 3560 5346 7132 784CIP2F 6 4705 1775 3561 5347 7133 784CIP2F 7 4707 1776 3562 5348 7134 784CIP2F 8 4712 1777 3563 5349 7135 784CIP2F 9 5008 1778 3564 5350 7136 784CIP2F 10 5009 1779 3565 5351 7137 784CIP2F 11 5015 1780 3566 5352 7138 784CIP2F 12 5015 1781 3567 5353 7139 784CIP2F 12 5015 1782 3568 5354 7140 784CIP2F 14 7725 1783 3569 5355 7141 784CIP2F 16 8830 <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>						
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1784 3570 5356 7142 784CIP2F 16 8830 1785 3571 5357 7143 784CIP2F 17 9739						7725
1785 3571 5357 7143 784CIP2F 17 9739			5355			8828
4502				7142	784CIP2F_16	8830
1786 3572 5358 7144 784CIP2F 18 9896				7143	784CIP2F_17	9739
	1786	3572	5358	7144	784CIP2F_18	9896

TRADOCS:1416247.1(%C\$7011.DOC)

TABLE 7

IA	BLE 7		
SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location .	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine; M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	1	residue of	S=Serine, T=Threonine, V=Valine,
1	amino acid		
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
5359	337	1131	AHLSARLSALILDEVAILPAPQNLSVLSTNMKHLLMWSPVIAPG
ì		Ì	ETVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITA
}	1		TVPYNLRVRATLGSQTS/CLEHP/VSIPLIETQPSLPDL/RMEI
}	ł.	ļ	TKDGFHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSGGIP
			VHLETMEPGAAYCVKAOTFVKAIGRYSAFSOTECVEVOGEAIPL
1	1	l	1
1	1	1	VLALFAFVGFMLILVVVPLFVWKMGRLLQ/YLLLPRGGSSQTPW
1			KITQF
5360	2	1115	PRVRSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLK
1	}	}	CVASGHPRPDITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPED
l .		ì	SGKYTCRVSNRAGAINATYKVDVIQRTRSKPVLTGTHPVNTTVD
1 .	1		FGGTTSFOCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKF
	,	1	VVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYS
}	}	l	FRSAFLTVLPDPKPPGPPVASSSSATSLPWPVVIGIPAGAVFIL
1]	1	GTLLLWLCOAOKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPSL
1		1	
1		1	AALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTGHS
]	L	TPHTYTHPPPSCQLNSSHS
5361	3	925	HEGSISSANILLDDQFQPKLTDFAMAHFRSHLEHQSCTINMTSS
1		1	SSKHLWYMPEEYIRQGKLSIKTDVYSFGIVIMEVLTGCRVVLDD
1			PKHIQLRDLLRELMEKRGLDSCLSFLDKKVPPCPRNFSAKLFCL
	ļ		AGRCAATRAKLRPSMDEVLNTLESTQASLYFAEDPPTSLKSFRC
		1	PSPLFLENVPSIPVEDDESONNNLLPSDEGLRIDRMTQKTPFEC
1			SOSEVMFLSLDKKPESKRNEEACNMPSSSCEESWFPKYIVPSOD
	1	i	LRPYKVNIDPSSEAPGHSCRSRPVESSCSSKFSWDEYEQYKKE
	 	4879	SCOVEGCTRTYNSSOSIGKHMKTAHPDQYAAFKMQRKSKKGQKA
5362	2	4879	
			NNLNTPNNGKFVYFLPSPVNSSNPFFTSQTKANGNPACSAQLQH
}		1	VSPPIFPAHLASVSTPLLSSMESVINPNITSQDKNEQGGMLCSQ
1	1	i	MENLPSTALPAQMEDLTKTVLPLNIDRGSDPFLSLPAESSSIDL
			FPSPADSGTNSVFSQLENNTNHYSSQIEGNTNSSFLKGGNGENA
ļ			VFPSQVNVANNFSSTNAQQSAPEKVKKDRGRGQTGKERKPKHNK
} .	1		RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA
1		1	EIAOBLLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD
1	į .	1	PSFLOLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL
			ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH
		j	
1	{	1	TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN
	1	ľ	GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS
	1		ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH
1	1	1	SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT
1			VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISBDNVIQNFEKT
1	1		LEIIKTAMNSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ
i	1		NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL
	I .		QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE
1	1		MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKIHQYTPE
1	1		MILEIKKNOLKFAPFKCVVPTCTKTFTRNSNLRAHCOLVHHFTT
1			EEMVKLKIKRPYGRKSOSENVPASRSTOVKKOLAMTEENKKESO
i	1	1	PALELRAETQNTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS
1	1		EQCNTNALTNTQTKGRKIRRHKKEKEEKKRKKPVSQSLEFPTRY
			SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE
l.		1	ESEAGKESEETETKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL
1		1	HEMTPEEIESMTASVDVGKPPCDQLECKSSFTTYLNYVVHLEAD
1	1		HGIGLRASKTEEDGVYKCDCEGCDRIYATRSNLLRHIFNKHNDK
1			HKAHLIRPRRLTPGQENMSSKANQEKSKSKHRGTKHSRCGKBGI
1			KMPKTKRKKKNNLENKNAKIVOIEENKPYSLKRGKHVYSIKARN
1			
			DALSECTSRFVTQYPCMIKGCTSVVTSESNIIRHYKCHKLSKAF
1			TSQHRNLLIVFKRCCNSQVKETSEQEGAKNDVKDSDTCVSESND
1	1		NSRTTATVSQKEVEKNE*DEMDELTELFITKLINEDSTSVETQA
Į			NTSSNVSNDFQEDNLCQSERQKASNLKRVNKEKNVSQNKKRKVE
1		· ·	KAEPASAAELSSVRKEEETAVAIQTIEEHPASFDWSSFKPMGFE
i			VSFLKFLEESAVKOKKNTDKDHPNTGNKKGSHSNSRKNIDKTAV
1		1	TSGNHVCPCKESETFVQFANPSQLQCSDNVKIVLDKNLKDCTEL
L	_1		

Predicted Predicted Predicted Namino acid segment containing signal peptide			•	
Deginning corresponding corresponding corresponding corresponding corresponding corresponding to first amino acid amino acid residue of amino acid amino acid sequence sequenc	SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
No: nucleatide corresponding to first amino acid residue of saidue	_		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Corresponding to first maino acid main			location	Glutamic Acid, F-Phenylalanine, G-Glycine,
corresponding to first amino acid amino acid residue of amino acid residue of amino acid equence educated esquence educated esquence educated esquence educated esquence educated esquence educated esquence educated esquence educated esquence educated esquence educated esquence educated esquence educated esquence educated education, %=possible nucleotide deletion, %=possible nucleotide deletion, %=possible nucleotide education, possible nucleotide education, possible nucleotid	NO.			H=Histidine, I=Isoleucine, K=Lysine,
to first amino acid residue of amino acid residue of amino acid sequence sequence 5.563 8066 703 RECETORING SERVICE AND ENGINEERS				I-Leucine M-Methiopine N=Asparagine
amino acid residue of amino acid sequence dequen				nuncoline O-Glutamine P-Arginine
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DKOMDMAHMRCTCVGNGRGEMTCIAYSQLRDGCUDDTTYNVN DTFHKRHEESGMALCTCFGGGRGKHCDPUQCODSETSTFYOI GDSWEKYVHGVRYQCYCYGRGIGENHCQPLQTYPSSSGPVEVFI TETPSGQNSH9IQMAPQPSHISKYILRMRFKNSVGRWKEATIP GHLMSTIIKGLKPGVVYEQCLISIQQGGEVTKFDFTTTSTST PVTSNT\VTGETTFFSPLVATESEVTEITASSFVXSASDTV SGFRVFYELSEEGDBPQYLUPSTATSVIDLDLEGRKYIVN VYQISEDGBGLILISTSQTTAPDAPPPTVDQVDDTSITVRNSR PQAPITGYRIVYSPSVEGSSTEINLPSTANSVTLSDLQPGVQN ITIYAVEENQESTEVVIQETTGTRSDTVPSPRDLQFVEVTDV KVTIMMTPPESAVTGKYDVIPVILGEHGGKPLPSANTLSPLQPGVYN TILSPGGTTYTYFKVPANYHGRESKPITADGTYLLJNAFTNLQFVN ETDSTVLVRWTPPRAQITGYRLTVGLTRGQFRQYWTGPSVSKY PLRLQPASSTYVSLNALKMONGSPKATAGYFTLQGGSIV VSGLTGVEYYYTTQVLRDGGRAPRVTSDGGSIV VSGLTGVEYYYTTQVLRDGGRAPRVTSDGGSIV VSGLTGVEYYYTTQVLRDGGRAPRVTSDGGSIV VSGLTGVEYYYTTQVLRDGGRAPRVTSDGGSIV VSGLTGVEYYYTTQVLRDGGRAPRVTSDGGSIV VSGLTGVEYYYTTQVLRDGGRAPRVTSDGGSIV HADQSSCTF\DNLEWFGLETNVSYVTVKDDKSSVTSDTIIFAV PPPTDLFFTTN\ILGPTMATVN\APPPSLSTTPINGQCNSLEEVV HADQSSCTF\DNLEWFGLETNVSYVTVKDDKSSVTSDTIIFAV PPTDLFFTN\ILGPTMATVN\APPPSLSTTPINGTSDTIIFAV PPTDLFTN\ILGPTMATVN\APPPSLSTTIPNTQQCNSLEEVV HADGSSCTF\DNLEWFGLETNVSYVTVKDDKSSVTSDTIIFAV PPTDLFTN\ILGPTMATVN\APPPSLSTTPINGTSTLLT\SWFVKT GRMLQSLSIFFLSDN\AVULTNLLBGTEYVAVSVSCWCHESTP \LRGGKRTGLDSPJVTGJDFS\DTANSTVTVN\LTDFLUXFISPVKNE GRMLQSLSIFFLSDN\AVULTNLLBGTEYVAVSVSCWCHESTP \LRGGKRTGLDSPJVTGJDFS\DTANSTVTLNLLDFTGTEVV SIVALNGRESSPLLIGQGSTVSDVVRTLVN\LTANSTFVLLL\LSWFVKT SIVALNGRESSPLIGGSTVSDVALHDLHSGPPLFTLLL\LSWFVKT SIVALNGRESSPLIGGGSTVSDVALHDLHSGPPLFTLLL\LSWFV SIVALNGRESSPLIGGGSTVSVVALHDLHSGPPLFTLLL\LSWFV SIVALNGRESSPLIGGGSTVSVVALHDLHSGPPLFTLLL\LSWFV GVTPTSLSAQWTPPNVQLTGYRVTYFRENGFPREVVPR RGVTEATTIGLPGTTYNILYTLNNARSSPVUDASTALDAPS NLEFLATTINSLLVSWQPPRARITGYILKXERGSPREVVPR RGVTEATTIGLPGTTYNILYTLNNARSSPVUDASTALDAPS NLEFLATTNSLLVSWQPPRARITGYILKXERGSPREVVPR RGVTEATTIGLPGTTYNILYTLNNARSSPVUDASTALDAP SGQQPSVGQMTEBHGFFRTTPTTATPIRRRPRYPDVOGG ALSGTTISMAPPQDTSEYIISCHPVGTDGEDIGRANDCLEGG SGRWCHDMGVYKLGELNGWKTCLGGRGKGCTGGGGRGCDNC RGGGPSPGGTTGGSTYGQNYGGRYHATTNANCPIECFGGGFFCD HRATCYDDGKTYHVGEOWQREYLGALCCCTCFGGGGRGRCDNC RGGGPSPGGTTGGSTYGQNYGGRYHGTTSVFPVPPFTLWP		1		
DTHKKHEEGMMLACTCFGGGGRMCDPLOCOPSESTGTFYQI GDSMEXYUGWRYCYCTCYGGGGGMCDPLOTYPSSSGPEVEVI TETPSQPNSHPIONNAPQBSHISKYLLRMEPKNSVGRWEATIP GHANSTIKGLKPGVYYEGGLISIQQYGHQEVTRFDFTTTSTT PUTSIN'LVTGETTFFSPLVATESVTEITASSFVUSWSASDTV SGFRVYELSEEGGEPQYLVLBSTATSVANIP\DLLGRKYIVN VYGISEGGGSLILSTGTAPAPPPPDTVQVDTSIVYMSR PQAPITGYRIVYSSVEGSTSELMLPSTANSVTLSDLQPQVQYN ITIYAVENDGSTPVALQOGTTGFRSDTVPSPRDLQFVEVTDV KVTIMMTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\ABN TGLSPGVTYYFKVEAVSHGRESKPLTAQTTKLLDAPRILQPAVQYN ETDSTVLVXMTPPPRAQITGYRLTVGLTRAGQFRQYNVGPSVSKY PLRRLQPASEYTVSLVALKGNGESPKATGYFTLQGSIPPYN TEVTETTIVITTHTPAPRIGPKLGVRPSQGGAPPREVTSDSGSIV VSGLTPGVEYVYTTQVLROQGRDAP\LVNK\VVTPLSPFTLHH LEANPDTGVLTVSHRSTFTPDTTGYRTTPMGQGGALBEVV HADQSSCTP\DNLEVFGLEYNVSVYTVKDDKESVPISDTIIPAV PPPTDLRFTN/LLGPDTMXVTN\APPPSIDLTNFLVSSVKNCH GRMLGGLSIFFLSNN\AVVLTNLLBGTETYVVSVSVYCHGESTP VLRGRKTGLDSP\TGLDFS\DITA\NSFT\VHN\LPRSVKNTE GRMLGGLSIFFLSNN\AVVLTNLLBGTTVVSSVVSQHGESTP VLRGRKTGLDSP\TGLDFS\DITA\NSFT\VHN\LPRSVKNTE GRMLGGLSIFFLSNN\AVVLTNLLBGTTVVSSVVSQHGESTP VLRGRKTGLDSP\TGLDFS\DITA\NSFT\VHN\LPRSVKNTE GRMLGGLSIFFLSNN\AVVLTNLLBGGSTSATSIGLLFSSV SIVALNGRESSPLLIGQGSTVSDVRDLEVVAATFIELLI\SMD APAVTVRYYRITYGTGGDSFASKFISHVRTEIDRPSQAQVTDVQDNS ISVKNLDSSSPVTGSVGTVTVTYSSPEGGHLFFPDGEDTA ELQGLRTGGSTYSVSVALHDDMSGGPLGTGGTSTATPAPTLLKFT GUTPTSLAXMPSGCSGPLYGVTNIDRFKGLAFTLU DDDSIKIAMESPCGGVSRYRVTYSSPEGGHLEFPDGGEDTA ELQGLRTGSSTYSSVALHDDMSGGPLGTGGTSTATPAPTLLKFT GVTPTSLAXMPTGLGFSTYTSVLALKNDNASSPVUTDRYDSPERLAFTLU ELQGLRTGSSTYSSVALHDDMSGGPLGTGGTSTATPAPTLKFT GVTPTSLAXMPTGLGFTSYTIYLALKNNGKSPPLIGRTKTDE, QVTPTSLAXMPTGLGFTSYTIYLALKNNGKSPPLIGRTKTDE, QLVTLPHPNLLGGPTSYTIYLALKNNGKSPPLIGRTKTDE, QLVTLPHPNLLGGPTSYTIYLALKNNGKSPPLIGRTKTDE, GRGCFSTGTGGYNGVTRYTTSPLACTYGNGGGGGGGGFRCDLC SGGGFSTGCDNGRYNGTYSGVGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGFGCDNG RGGGFSFBGTTGGSTNGVGGGRGGAGCCGGGGGGGGGGGGGGGGGGGGGGGGGGGG		Į.		
GDSMEXYVIGURYQCYCYGRGIGEMHCQPLOTYPSSGFUVYT TETTSQPOSHPIONMAPOPHIS KYIMRRYMSVGKWEKATIP GHLMSYTIKGLKPGVYYEQQLISIQQYGHQEVTRFDFTTTSTST PVTSNT\VTGETTFFSPLVATSESVTEITASSYVSWASADTV SGFRVEYELSEEGDEGVLUFSTATSV\NITPLDFKKTIVN VYGISEGGGSLILSTSGTTAPDAPPDFTVQVDDTSIVVRWSR PQAPITGYRIVYSSSVEGSSTELLNBETANSVTLSDLQFOVQYN ITIYAVEENQESTPVIQOETTGTPSSDTVSPRRDLQFVEVTDV KVYIMMTPPESAVTGYRVDVIPVNLPGEGGQLPLSRNTF\ARN TGLSPGVTYYFKVFAVSHGRESKFLTAQQTTKL\DAPTHLQFVN ETDSTVLVRWTPPRAQITGYRLTVGLTRGQPRQYNVGSVSKY PLRNLQPASFYYTSLVATKKONGSSFAVTSTTLQQOSSIPPYN TEVTETTIVITMTPAPRIGFKLGVRFSQGGRAPREVTSDSGSIV VSGLTPGVEYVYTIQVLRQDQERDAP.IVTNLVVTTLPAPPTHLH LEANPDTGVLTVSWERSTTDITGYRITTTPTNGQQGNSLEVV HADQSSCTF\DNLEVPGLEYNNSVYTVDDKESVSTSPTNITLFTNTILTPFTNI'LGFTMRVTW\APPPSTBLTTRAFYTIL'LSAN PPPTDLFFTNI'LIGPTMRVTW\APPPSIDLTNFLVRSSPVKNE GRMLQSLSIFFISDN\AVVLINLBPGTEVYSVSVYEQHESTP \LRGQRKTGLDSP\GTGNFVUTWSTVYTVDDKESVSTSVEQHESTP \LRGQRKTGLDSP\GTGNFVUTWSTYVTWDDKESVSTSVEQHESTP \LRGQRKTGLDSP\GTGNFVUTWSTYVTWNDKESVSTVEQHESTP \TGYRIR\HHPEHF\SGRPEDR\VPHSNSITLTNLTPFGTEYVV SIVALNGRESSPLLIGQQSTVSDVPRDLEVVAAATPTSLLI\SWD APATVEYYRITTGETGONSPVQEFTVGSKSTATISGLKPGVD YTITYYAVTGRGDSPASSKPISINYRTEIDRFSQMQVTDVQDNS ISVXNLBSSSPVGTGNYTTT\FKNGG\FTKTXTAGPDTEMTI EGLQPTVEYVVSVYAQNPSGSSQPLVGTAVTNTICPRGGAFT UDSIKLAMBSSQCJUVGTAVTTSPROGVTTLTKNAGPEDTEMT ELQGLRGGSSYTVSVVALHDDMSGQPLIGTSTAIPAPDLKFT QVTPTSLSAQWTPDNQLTGYRVVTYPKSKTGPMKEINLAPDSS SVVVSGLWATKYEVSVYALMDTLTSARQGVYTLENWSPPRR RFGVTEATITGLEPGTEYTIVIALKNNQKSPPREVYERP RFGVTEATITGLEPGTEYTIVIALKNNQKSPPREVYERP RFGVTEATITGLEPGTEYTIVIALKNNQKSPPRIGLENTSPPRIVSP RRGVTEATITGLEPGTEYTIVIALKNNQKSPPRIGLENTSPPRIVSP ALSGTTISMAPFQDTSSYTISPTOTTTATPIRRFRPPPPNVGQ ALSGTTISMAPFQDTSSYTISPTOTTTATPIRRFRPPPPNVGQ ALSGTTISMAPFQDTSSYTISPTOTTTATPIRRFRPPPPNVGQ ALSGTTISMAPFQDTSSKRIGHTSPTTATPIRRFRPPPPNVGQ SSRHCHDRINGNYKKIGERNDGCCENGGGFKCLD SSRHCHDRINGNYKKIGERNDGCCENGGGFKCLD SSRHCHDRINGNYKKIGERNDGCCENGGGTCLDGGGFKCLD HRATCYDDGKTYHVEGQWGKSTIGAICSCTCGGGGGRKCDNC RFGGEPSPEGTTGQSYNQYSQRYQRTNTNVNCCPIECFMPLDVD ADRBSSRE PSDRENGPFGGSGERPFSTREFENNYATCLFVPRASSPFRLIMML			1	DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
TETPSQPNSHPJQMNAPQPSHISKYILKWRRYMSVGRWEATIP GHLMSYTIKGLKEGWVYSGQLISIQVGBVTRFDTTTSTST PVTSNT\VTGETTPFSPLVATSESVTEITASSPVUSWVSASDTV SGFRVEYELSEEGDEPQILVLPSTATSV\NIP\DLIPGKKYIVN VYQISEGDEGSLILSFSGTTAPADPPDPTVQVDDTSIVVRMSR PQAPITGYRIVYSPSVEGSTELNLPETANSVTLSDLQFGVQYN ITIYAVEENQESTPVVIQQETTGTPSTPSPRDLQFVEVIDV KVTIMMTPPESAVTGRVDVIPVNLPGEHGQRLPLSRNTF\AEN TGLSPGVTYYFKVFAVSHGRESKFLTAQQTIKLDAPTHLQFVN ETDSTVLVTMTPPPRAQITGYRLTVGLTREGQPRQTNVGSVSKY PLRNLQPASSYTVSLVATKKNGESPKATGVFTTLQFGSSIPPYN TEVTETTIVITWTPAPRIGFKLGVFAGYGEAPPEVYNSDGSIV VSGLTPGVEYVYTIQVLRDQCEDDAP\TVNK\VVTPLSPPTNLH LEANPDTGVLTVSWRSTSTPDITGYRITTPPTNOQCANSLEEVV HADQSSCTF\DNLEVPGEDYNVSVYVAVSVSSVYGHESTP VSGKTPGVEYVYTIQVLRDQCEDDAP\TVNK\VVTPLSPPTNLH LEANPDTGVLTVSWRSTSTPDITGYRITTPPTNOQCANSLEEVV HADQSSCTF\DNLEVPGEDYNVSVYTVSVSSVYGHESTP \LNGRQKTGLDSP\GTGIPF\DITAN\NSFT\VHN\LAPRA\TPI TGYRIR\HHBHF\GGRREEDR\VPHSRNSTITLINLTPGTEVVV SIVALNGRESSPLLIGQSTVSDVPRDLEVVAATPTELLI\SMD APAVTVRYYRITGGRGGNSPVGFTVGSKSTATIGGLKPGVD VSTIRKHEBESPLLIGQSTVSDVPRDLEVVAATPTELLI\SMD APAVTVRYYRITGGRGGNSPVGFTVGSKSTATIGGLKPGVD VTTSILSAGNTPSVYGVTTT\PKNGFG\FTVTGSKTATIGGLKPGVD DUSIKLAWSSPGGQVSKRYTYTSSPEDGIHELFPAPDGEEDTA ELQGLRPGSSTVSVVALHDDMSQPLGTTGSTAIPAPTDLKFT QVTPTSLSAQWTPPNVQLTGYRVYTTTPRKGFG\FTLENDFPGREEDTA ELQGLRPGSSTVSVVALHDDMSQPLGTGSTAIPAPTDLKFT QVTTSILSAQWTPPNVQLTGYRVYRVTTFRKGFGPEEDTA ELQGLRPGSSTVSVVALHDDMSQPLGTGSTAIPAPTDLKFT QVTTSILSAQWTPPNVQLTGYRVYRVTPKKTGPHARATIADPS SVVVSGLMVATKYEVSVYALKDTLTSRRAGGTFGRTLKP PURSTITIGLPGTDTVKYLYLINLANNQKSEPLLGRKKTDELP QUSTTITIGLPGTDTVKYLYLINLANNQKSEPLLGRKKTDELP REGVTEATITGLPGTTSVKYLYLINLANNQKSEPLLGRKKTDELP GLOVTTJHPNLHGPGILDVSTVQKTFTVTHGYDTGLGLAFGT SGQQPSVQQMIFERGFRRTTPFTTATFIRRRPPYPNVQG ALGQTTIGMAPPGDTESTYILGCHTGSGLAFGCHG SSRMCHNGWNYKIGERVDRGCENGMSCTLLGNGGFKCD HRATCYDGKTYHVEGONGKSTLGALCSCFGGGGRGUNCT SSRMCHNGWNYKIGERNDRGGREFKCD HRATCYDGKTYHVEGONGKSTLGALCSCFGGGGRGUNCT RPGGFSPEGTTGGSYNGYSQRYQRGRTTNTVNCPIECFPHDLDU ADREDSRE FECCTGGGGETPGASGKRGPAATTSLVLCIPSVPPVPFFTLWF PSPWRDGPFGGIRIDFFGRREFERREFENNAUTCLCUPVRASLFHRLIML	1			DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
TETPSQPNSHPJQMNAPQPSHISKYILKWRRYMSVGRWEATIP GHLMSYTIKGLKEGWVYSGQLISIQVGBVTRFDTTTSTST PVTSNT\VTGETTPFSPLVATSESVTEITASSPVUSWVSASDTV SGFRVEYELSEEGDEPQILVLPSTATSV\NIP\DLIPGKKYIVN VYQISEGDEGSLILSFSGTTAPADPPDPTVQVDDTSIVVRMSR PQAPITGYRIVYSPSVEGSTELNLPETANSVTLSDLQFGVQYN ITIYAVEENQESTPVVIQQETTGTPSTPSPRDLQFVEVIDV KVTIMMTPPESAVTGRVDVIPVNLPGEHGQRLPLSRNTF\AEN TGLSPGVTYYFKVFAVSHGRESKFLTAQQTIKLDAPTHLQFVN ETDSTVLVTMTPPPRAQITGYRLTVGLTREGQPRQTNVGSVSKY PLRNLQPASSYTVSLVATKKNGESPKATGVFTTLQFGSSIPPYN TEVTETTIVITWTPAPRIGFKLGVFAGYGEAPPEVYNSDGSIV VSGLTPGVEYVYTIQVLRDQCEDDAP\TVNK\VVTPLSPPTNLH LEANPDTGVLTVSWRSTSTPDITGYRITTPPTNOQCANSLEEVV HADQSSCTF\DNLEVPGEDYNVSVYVAVSVSSVYGHESTP VSGKTPGVEYVYTIQVLRDQCEDDAP\TVNK\VVTPLSPPTNLH LEANPDTGVLTVSWRSTSTPDITGYRITTPPTNOQCANSLEEVV HADQSSCTF\DNLEVPGEDYNVSVYTVSVSSVYGHESTP \LNGRQKTGLDSP\GTGIPF\DITAN\NSFT\VHN\LAPRA\TPI TGYRIR\HHBHF\GGRREEDR\VPHSRNSTITLINLTPGTEVVV SIVALNGRESSPLLIGQSTVSDVPRDLEVVAATPTELLI\SMD APAVTVRYYRITGGRGGNSPVGFTVGSKSTATIGGLKPGVD VSTIRKHEBESPLLIGQSTVSDVPRDLEVVAATPTELLI\SMD APAVTVRYYRITGGRGGNSPVGFTVGSKSTATIGGLKPGVD VTTSILSAGNTPSVYGVTTT\PKNGFG\FTVTGSKTATIGGLKPGVD DUSIKLAWSSPGGQVSKRYTYTSSPEDGIHELFPAPDGEEDTA ELQGLRPGSSTVSVVALHDDMSQPLGTTGSTAIPAPTDLKFT QVTPTSLSAQWTPPNVQLTGYRVYTTTPRKGFG\FTLENDFPGREEDTA ELQGLRPGSSTVSVVALHDDMSQPLGTGSTAIPAPTDLKFT QVTTSILSAQWTPPNVQLTGYRVYRVTTFRKGFGPEEDTA ELQGLRPGSSTVSVVALHDDMSQPLGTGSTAIPAPTDLKFT QVTTSILSAQWTPPNVQLTGYRVYRVTPKKTGPHARATIADPS SVVVSGLMVATKYEVSVYALKDTLTSRRAGGTFGRTLKP PURSTITIGLPGTDTVKYLYLINLANNQKSEPLLGRKKTDELP QUSTTITIGLPGTDTVKYLYLINLANNQKSEPLLGRKKTDELP REGVTEATITGLPGTTSVKYLYLINLANNQKSEPLLGRKKTDELP GLOVTTJHPNLHGPGILDVSTVQKTFTVTHGYDTGLGLAFGT SGQQPSVQQMIFERGFRRTTPFTTATFIRRRPPYPNVQG ALGQTTIGMAPPGDTESTYILGCHTGSGLAFGCHG SSRMCHNGWNYKIGERVDRGCENGMSCTLLGNGGFKCD HRATCYDGKTYHVEGONGKSTLGALCSCFGGGGRGUNCT SSRMCHNGWNYKIGERNDRGGREFKCD HRATCYDGKTYHVEGONGKSTLGALCSCFGGGGRGUNCT RPGGFSPEGTTGGSYNGYSQRYQRGRTTNTVNCPIECFPHDLDU ADREDSRE FECCTGGGGETPGASGKRGPAATTSLVLCIPSVPPVPFFTLWF PSPWRDGPFGGIRIDFFGRREFERREFENNAUTCLCUPVRASLFHRLIML	1		1	GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
GHLMSYTIKGLKPGVVTEGQLISIQQYGHQEVTEFFFTTTSTST PUTSTNT_VTOETTIPS PLVATESSTVYSETASSFVVSWASDIV SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN VYQISEDGEQSLILSTSQTTAPDAPPDFTVDQVDDTSIVVRWS PQAPITGYRIVYSPSVEGSSTEINLPETANSVTUSLQPGVQYN ITIYAVEENQESTFVVIQGETTGTRSDTVSPSRDLQFVGVYN KYTIMMYPESANTGYRDVIPVNIPGEGGRJEJLSRNTF\ARN TGLSPGVTYYFKVFAVSHGRSSKPLITAQQTTKL\DAPTHLQFVN ETDSTVLVWRTPPFRQITGYRLTVGLTRRGQPRQYNVGPSVSKY PLRNLQPASSYTVSLVAIKGNGESFKRATGVFTTLQPGSSIPPYN TEVTETTIVITWTPAPRIGFKLGVRSQCGARAFVTSDSGSI VSGLTPGASSYTVSLVAIKGNGESFKARTGVFTTLQPGSSIPPYN TEVTETTIVITWTPAPRIGFKLGVRSQCGARAFVTSDSGSI VSGLTPGASSYTVSLVAIKGNGESFKARTGVFTTLQPGSSIPPYN TEVTETTIVITWTPAPRIGFKLGVRSQCGARAFVTSDSGSI VSGLTPGASSYTVSLVAIKGNGESFKARTGVFTTLQPGSSIPPYN TEVTETTIVITWTPAPRIGFKLGVRSQCGARAFVTSDSGSIPYN TEVTETTIVITWTPAPRIGFKLGVRSQCGARAFVTSDSGSIPYN TEVTETTIVITYMTPAPRIGFKLGVRSQCGARAFVTSDSGSIPYN TEVTETTIVITYMYSWRSTTPDITGYRITTTPTNQQCANSLEEVV HADQSSCTF\DNLEVPGLEYNVSYTVTKDKTSSYVTGASSTVINE PPPTDLRFTN ILGDTMRVTM\APPSIDLTNFLUKYSSPVINE GRMLQSLSIFFLSDN\AVVLINLLPGTEVVVSSVYEQHESTP \LNGRQKTGLDSSP\CIDFS\DTANSTTLTNLTPGTEYVV SIVALNGREESPLLIQQQSTVSDVPRDLEVVAATPTSLLI\SWD APATVRYYRITYGTGGNSPVQEFTVQSKSTATIGGKPQUD YTITYAYTGRGGSPASKFISINYRTEIDKRSQMQTDVQCNNS ISVALNGRESSPVTTTYPKNGG\STRUTTARGGAPTUTOLTS SIVALNGRESSPVTGVTTTYPKNGG\STRUTTARGACPOTEMTI EGLQPTVEYVVSVYAQNSGESQPLVQTAVTNIDAPRGLAFTOV DVDSIKIAWESPQQVSYRVTTYSSPGOTIFELFPAPDTEMTI GGLQPTGSSTYTVSVVALHDDMSQPLIGTQSTAIPAPTDLKFT QVTPTSLSAQWTPPNVQLTGYRVRVTPKKKTGPMKEINLAPPSS SVVVSGIMVATKYEVSVYALMDTLTSAPQVOYTLTHAVSPFRR ARVTDATETTITISMRTKTETITGFQVDAVPANGGTFIQRTIKP DVRSYTITGLQPGTDYKIYLYYTLDNARSSPVYDDASTAIDAPS NLRFLATTPNSLUXWQPPRRATTGYIIKYEKPGSPPREVVPRP RRGVTEATITGLEPGTETTIVVIALKNNQKSEPLIGRKKTDELP QLVTLPHPNLHGPGELLDVPSTVQKTFYPTHPQYDTGMGIQLGCT SGQQSSVQQMIFEBHGFRRTTPFTTATPIHRRRPYPPNVCQB ALSQTTISMAPFQDTSSRTLEDFLORGRUFTGLAGRGFKCDP HRATCYDDGKTYHVEQPMQKSURGCLLCGNGGEFKCDP HRATCYDDGKTYHVEQPMGKSTIGALCSCCGGGGGRCCDNC RRGGEPSPEGTTGQSYNQYSQRYQRYNGRTNTNVNCPIECFMPLDVD ARRBSRE SIGGT				TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
PUTSINT\VITGETTPESPLUATESVITETASSFVUSWASASTV SGFRVEYELSEEGEBPOYLULPSTATSV\nlyDLLDCRKYYUN VQISEDGEGSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR PQAPITGYRIVYSPSVEGESTELNLPETANSVILSDLOPGVQYN ITIYAVEENGESTPVVIQQETTGTREDTVPSPRDLOPFVDYVD KVTIMWTPPESAVTGYRUDVIPVNLPGEHGGRIPLERNTF\AEN TGLSPGVYTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTHLOPFV ETDSTVLVRNTPPRAQITGYRLTVGLTRGOPRQYNVGPSVSKY PLRRIQPASSYTVSLVAIKGNGESPKATGYTTLQGESSIPYN TEVTETTIVITWTPAPRIOPKIGVPSGGEAPREVTNSGSIV VSGLTPGVEYYYTIQULRDOGERDAP\IVNK\VVTPLSPPTHLH LEAMPDTGVLTVSWERSTTPDITGYRITTTPTNGQGNSLEEVV HADQSSCTF\DNLEVFGENYNVTVKUDKESVPTSDGSIV GGMLOSSCTF\DNLEVFGENYNVTVKUDKESVPTSUFIFIA PPPTDLRFTM\ILGPDTMRVTM\APPESIDLTFLVRYSPVKNE GGMLOSSIFFLSDN\AVVLINLLPGTEYVVSVSSVYEQHESTP QRMLOSSIFFLSDN\AVVLINLLPGTEYVVSVSSVYEQHESTP TGYRIR\HHPEHP\SGFREDR\VPHSRSITLTNLTFGTEYVV SIVALNGRESSPLLIGQGSTVSDVPRDLEVVAATPTSLLI\SWD APAVTVRYYRITYGTGGSPQVGFTVTGSSTANTISGLKFGUD YTITVYAVTGRGOPASSKPISITRTFIDKPSGMQVTDVOONS ISVKNLPSSSPVTGYRVTTT\PKNGPG\PTKKTAGPDQTEMTI EGLQFTVEYVVSVYAQNPSGESQPLVOTAVNLDRREGLAFTDV DVDSIKINWESPGOVSKYRVTYSSPEGIHELFPAPDCEEDTA ELQGLRGGSEYTVSVVALHDDMSGPLTGTSTAIPAPTDLKFT GVTPTSLAQWTPPNVQLTGYRVTTPKRKTGPMKSINLAPDSS SVVNSGLMVATKVEVSVVALHDDMSGPLTGTSTAIPAPTDLKFT GVTPTSLAQWTPPNVQLTGYRVTTPKRKTGPMKSINLAPDSS NLRFLATTPNSLLVSMOPPRARITGYIIKYERPGSPFREVVPR RAVTDATETTITISMRTKTETTTGFQVDAVBNAGQTFIQRTIKP DVSSKTTTGLGPGTDKYILYTINNNASSFVVIDASTAIDARS NLRFLATTPNSLLVSMOPPRARITGYIIKYERPGSPFREVVPR RRGVTEATTTGLEPGTEYTIVIALKNNOKSSPVIDASTAIDARS NLRFLATTPNSLLVSMOPPRARITGYIIKYERPGSPFREVVPR RRGVTEATTITGLEPGTEYTIVIALKNNOKSSPVIDASTAIDARS NLRFLATTPNSLLVSMOPPRARITGYIIKYERPGSPFREVPRP SGQPSVGQOMIFERHGFRTTPPTTATPIHRPREVPYPNVGGE ALSGGTTGMSFOFDSEYIISGHPVGTGTSTAT LTGLTRGATYNIIVEALKDQQRHKVREEVUTVGNSVABGLNOT DDSCFDPTTVSHYAVGGENGOMMSCTCLGNCKGFFKCDD HRATCYDDGKTYHGENGOKEYLGAICSCTCFGGGRGRRCDNC RPGGEPSBGTTGGSTNQYSGRYHQRTNTNVNCPIECFMPLDVO ARREDSRE 5364 8066 703 RLCCGGGGGFGFGASGKRGPAATTSLVLCIPSVPPVPFFPLWP PSWRQPPGGIRRDFSRRLREARINJVATCLPVRASLSPRLIMM		1	1	CHINSYTIKGI KPGVVYEGOLISIOOYGHOEVTRFDFTTTSTST
SGFRVEYELSEGDEPGYLVLPSTATSV,NIP,DLLPGKKYIVN VYQISEDGQSLILSTSQTTAPDAPPDPTUQUDDTSIVTAMS PQAPITGYRIVYSPSVEGSSTELMLPSTANSVTLSDLQPGVQYN ITIYAVEENGESTPVVIQQETTGTPRSDTVPSRDLQFVEVTDV KVTIMWTPESAVTGKRQVDIPJVPSRDLQFVEVTDV KVTIMWTPESAVTGKRQVDIPJVPSRDLQFVEVTDV KVTIMWTPESAVTGKRQVDIPJVPSRDLQFVEVTDV KVTIMWTPESAVTGKRQVDIPJVSRDGCRQTAVLDSPNTI-\ABN TGLSPGVTYYFKVPAVSHGRESKPLTAQQTTKL\DAPTHLQFUN ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVQFSVSKY PLRNLQPASSYTVSLVALKGNGGSPKATGVFTLQGGSIPPXV TEVTETTIVITWTPARRIGPKLTVSLYDRKDVTLSPFTLHA LEAMPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV HADQSSCTF\DNLEVGGESRAVYTTVQNGKSVPISDTIIPAV PPPTDLAFTM/ILDFDTMRVTM\APPSIDLTFFLWYSSPVNE GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSVYEQHESTP \LGGGKTGLDSP\TGIDPS\DITA\NFT\VUM\LAPRA\TPI TGYRIR\HPEHF\SGFPREDR\VPHSRNSITLTNLTPGTEYVV SIVALNGRESSPLLIGQGSTVSDVPRDLEVVAATFTSLLI\SWD APAVTVRYYRITYGETGGSPPVDGFTDGSSTATTIGLKPGVD TTITYYAVTGRGSPASSKPISINYRTEIDKPSQMQVTDVDDNS ISVKLBSSSPVTGVRVTTI\PKNGPG\PTKTKTAGEPOTEMTI BELQGLRGGSFVTSVVALHDDMSQPLIGTGSTAIPAPTDLKFT QVTPTSLSQMTPDNVQLTGYRVRVTYSSPEGIHELFPAPDGEEDTA ELQGLRGGSFYTGVVALNDDMSQPLIGTGSTAIPAPTDLKFT QVTPTSLSQMTPPNVQLTGYRVRVTPFEKTGFMKEINLAPDSS SVVVSGLMVARKYFUSVYALKDTLTSRAGVYTTLENVSPPRR ARVTDATETTITISKRYKTETITGPQVDAVPANGQTIGTGKTDELP QVTPTSLSQMTPNVQLTGYRVRVTPFEKTGFMKEINLAPPSS SVVVSGLMVARKYFUSVYALKDTLTSRAGVYTTLENVSPPRR ARVTDATETTITISKRYKTETITGPQVDAVPANGQTIGTGKTDELP QLVTLPHPNLHGPEILDVPSTVQKTPFTHRFDYDTGNGIQLPGT SGQQPSVGQOMIFEBHGFFRTTPPTTATPIRRPRPYPNVOQB ALSQTTIGWAPFQOTESTYISTVALLKNNQKSEPLIGGKKTDELP QLVTLPHPNLHGPEILDVPSTVQKTPFTHRFDYDTGNGIQLPGT SGQPSVGQOMIFEBHGFFRTTPPTTATPIRRPRPYPNVOQB ALSQTTIGWAPFGOTESTYISTVALKKNNGKSEPLIGGKKTDELP GPGGFSPEGTTGSYNYYSTYALKOURGERGKTGLCGGGGFFKCD HRATCYDDGKTYHVGEQMGEVIGAICSCTCFGGGRGMCCNCR RPGGFSPEGTTGGSYNQYSQRYHQRTNTNVNCPIECFMPLDV ADREDSRE 5364 8066 703 RLCCGGGGETFGASSKRGPAATTSLVLLTJSVPPPVPPPVPFTLWP PSPWRQPPGGIRRDFSRLRREANLVATCLPVXASLSHRLMML	1	i		DAMENT ATTECTTOF COLVETS FS STEET ASSEVUS WVSASDTV
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PQAPITGYRIVYSPSVEGSTELNLPETANSVTLSDLQGGVQYN ITIYAVEENQESTPVVIQQETGTPSDTVPSPRPLQFVEVTDV KVTIMWTPPESAVTGYRVDVIPVNLPGEHGGRLPLSRNTF\AEN TGLSEGVTYYFKVPAVSHGRESKPLTAQOTTKL\DAPTNLOFVN ETDSTVLVRWTPPEAQTTGYLTUGLTRGGPGYNVGPSVSKY PLRNLQPASEYTVSLVAIKGNQESPKATGYTTLQGEGSIPPVN TEVTETTIVITWTPARRIGFKLGVRPSQGGAPREVTSDGGSIV VSGLTPGVEYVYTQVLDRQGGRDAF\TVNK\VVTPLSPPTNLH LEAMPDTGVLTVSHERSTTPDITGYRITTPTNGQQGNSLEEVV HADQSSCTF\DNLEVPGLEYNVSVTVKDDKESVPISDTIIPAV HADQSSCTF\DNLEVPGLEYNVSVTVKDDKESVPISDTIIPAV HADQSSCTF\DNLEVPGLEYNVSVTVKDDKESVPISDTIIPAV HADQSSCTF\DNLEVPGLEYNVSVTVKDDKESVPISDTIIPAV HADQSSCTF\DNLEVPGLEYNVSVTVKDDKESVPISDTIIPAV HADQSSCTF\DNLEVPGLEYNVSVTVKDDKESVPISDTIIPAV HADQSSCTF\DNLEVPGLEYNVSVTVKDDKESVPISDTIIPAV HADQSSCTF\DNLAVVLINLLPGTEYVVSVSVYSCHESTP \LRGRQKTGLDSP\TGLTGFSTTVANSTF\URN\TAPTSTLLTNLTPGTEYVV SIVALNGRESPLLIGQOSTVSDVRRDLEVVAATPTSLLI\SWD SIVALNGRESPLLIGQOSTVSDVRRDLEVVAATPTSLLI\SWD APAVTVRYRITYGGTGGNSPVQEFTVPGSKSTATISGLKPGVD YTITYYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVOONS ISVKNLPSSSPVTGYRVTTT\PKNGGQ\TRATTISDKPGALPTDV DVDSIKIAMESPQGQVSRYRVTYSSPEDGIHELFPAPDCEEDTA ELQGLRPGSEFYTVSVVALHDMSSQPLIGTGSTAIPAPTDLKEF DVDSIKIAMESPQGGVSRYRVTYSSPEDGIHELFPAPDCEEDTA ELQGLRPGSEFYTVSVVALHDMSSQPLIGTGSTAIPAPTDLKF QVTPTSLSAQNTPSNVQLITGFVRVTTYPKEKTGPMKEINLAPDSS SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR ARVTDATETTITISKRTKTETIFOFQDAVPANGQTPIQRTIKP DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSWGPPRARITGYLIXKEKPGSPFREVVPRP RFCVTEATITGLGPGTSTYLVIALKNNQKSPPLIGRKKTDBLP QLVTLPHNNLHOPBILLDVPSTVQKTPFVTHPGVDTONGQLCGT SGQOPSVGQMIFEBHGFRRTTPPTTATPIRHPRPPYPNVCQT SGQOPSVGQMIFEBHGFRRTTPPTTATPIRHPRPPYPNVCQT SSRWCHDNGVWYKIGEKNDRGGFRGDMMSCTCLGNGKGFKCDC HBATCYDDGKTTHVGEGNQKKYLGAICSCTCFGGGRGMCDNCR RPGGFSPBETGGSYNQVSGRYNGRTNTNVNCPLBCFMPLDVQ ADREDSRE FLCCTGGGGGTFGASGKRGPAATTSLVLCLIPSVPPVPFPFTLWP PPSWRQPPGGIRRDFSRLRERANLVATCLPVAASLPRLIMML	ì			SGFRVEYELSEEGDEPQILVEPSIAISV (NIF (DIMPGRAIIVA
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VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VTPLSPPTNLH LEANPDTGVLTVSWERSTTPDITGYRITTPTNGQQGNSLEEVV HADQSSCTF\DNLEVPQGLEYNVSVTVYDDKESVPISDTIIPAV PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE GRMLQSLSIFFLSDN\AVVLINLLPGTEYVVSVSSVYEQHESTP \LRGRQKTGLDSP\TGIDFS\DITA\NSPT\VHW\LAPRA/TPI TGYRIR\HHPEHP\SGRPREDR\VPHSRNSITLTNLTPGTEYVV SIVALMGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD YTITTYAVTGRGDSPASSKPISINVRTEIDKRSQMQVTDVQDNS ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI EGLQFTVEYYVSVYAQNPSGESQPLVQTAVTNIDRRKGLAFTDV DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT QVTPTSLSAQWTPPNVQLTGYRVTYPKEKTGPMKEINLAPDSS SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR ARVTDATETTITISMTRTTETITGFQVDAVPAMGQTFIQRTIKP DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTDNSLUSWQPPRRAITGYIKYERGSPPREVVPRP RPGVTEATITGLEFGTETTIYIJALKNNOKSEPLIGRKKTDELP QUVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGGIQLPGT SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRYPPPNVQGB ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPCTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVVTVONSVMBGLNQPT DDSCFDPYTVSHYAVGDEWGRMSESGFKLLCQCLGFGSGHFRCD SSRWCHDNGNYKTGEKNDROGENGOMMSCTLCHONKGEFKCDD HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGGGGWRCDNCR RPGGEPSPEGTTGGSYNQYSGRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE 703 RLCCTGGGGTFPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP	ł	I	1	
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DKGHDWGHMRCTCUGNGRGEWTCLAYSQLROGLOUDITYNU DTFHKRHBEGHMINCTCGGGGGRKRCDPUDQCOSSIGTFYC GDSHEKYVHGVRYOCYCYGRGIGEHCOPLOTYPSSSOPWEVE TETPSGPNSHIJGWARQPSHISKYILRWRPKNSVGRKEATI GHLNSTILKGLRGVVYSGQLISIQOYGHGETREPTTTSTS PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWASDI SGFRUYSLESEGDBPGVLUBETATSVINIPDLLDGRTYVY VQIJESDGEGGLILATSGTTAPDAPPDFTUDQVDDTSIVVRM PQAPIGGYRTYSPSVUSSESTEINLPETANSVILSDLQFBCVY VQIJESDGEGGLILATSGTTAPDAPPDFTUDQVDDTSIVVRM PQAPIGGYRTYSPSVUSSESTEINLPETANSVILSDLQFBCVY VQIJESDGEGGLILATSGTTAPDAPPDFTUDQVDDTSIVVRM PQAPIGGYRTYYSPSVUSSESTEINLPETANSVILSDLQFBCVY VQIJESDGEGGLILATSGTTAPDAPPDFTVDSVDTSLDQFBCVY VQIJESDGEGGLILATSGTTAPDAPPDFTVDSVDTSLDQFBCVY VQIJESDGEGGLILATSGTTAPDAPPDFTVDSVDLOPBCVY VQIJESDGEGGLILATSGTTAPDAPPDFTVDSPDLOPBCVY VQIJESDGEGGLILATSGTTAPDAPPDFTVDSVDLOPBCVY VQIJESDGEGGLILATSGTTAPDAPPDFTVDSPDLOPBCVY VQIJESDGEGGLILATSGTTAPDAPPDTTVDSPDLOPBCVY VQIJESDGEGGLILATSGTTAPDAPPDTTVDSPDLOPBCVY VQIJESDGEGGLILATSGTTAPDAPPDTLVSNOVING PAPANLOPS CONTINUENCE CHANGES PARAFORT TILDEGS TO PRILOPBC STOPPLOP TO THE TOTAL TO			1	
DITHKRHEGHMINTCRGQGGGRHKCDPUDQCOBSTGTFYC GDGWBKYVHGWTQCYCGGGIGEMCDQTPTSSGDPUCY GDGWBKYVHGWTQCYCGGGIGEMCDQTUTFSSGTPUCY TETPSQPNSHPIOWNAPQPSHISKYILRWRPKNSUGRKKEATI GHINSYTIKGLRGGVVFGQLISIQOYGHQSYTFDFTTTSTS PUTSNT\UTGETTPSSLVATSSSVTEITASSFVVSWSASDI SGFRUYYELSEGDBPQYLULGFATATSV\NIP\DLLDCHRYIV VYQISSDEGGLILETSGTTAPDAPPDTUDQVDDTSIVVNSW FQAPINGVRIVYSPSWEGSSTEINLPETANSVTLDDLQPGVQ ITIYAVERDOSTPVVIQQGTTGTPRSDTVDQVDDTSIVVNSW FQAPINGVRIVYSPSWEGSSTEINLPETANSVTLDDLQPGVQ ITIYAVERDOSTPVVIQQGTTGTPRSDTVDQVDTSIVVNSW FQAPINGVRIVYSPSWEGSSTEINLPETANSVTLDDLQFGVQ INTIYAVERDOSTPVIQFVIDQTTTRCDTVADPINLQFV KVTIMMTPPSAQITGVRLIVGLTRGGPQCNVGPSVSK PLRNLQPASETVSLVALKGNGSSKATGVFTTLQPGSSIPP TEVTETTLUTIVTMPAPARIGFKLAVPSSGGERFXVISDGSSIPP TEVTETTLUTIVTMPAPARIGFKLAVPSSGGERFXVISDGSSIPP LENDPTSULTVSWERSTFYDIGVRITTPTMGQOGNSLEEV HADQSSCTP\NNLEWFGLEXNVSVTVKDDKSSVISDTIIPP PPFDLRFTN\ILGPDTRVTV\APPPSIDLITHFLYXSPXNV GRMLGSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHEST \LBGRKGGLGSP\TGLDFS\DITAVSTVTVKDKSSVISDTIIPP PPFDLRFTN\ILGPDTRVTV\APPPSIDLITHFLYXSPXNV GRMLGSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHEST \LBGRKGGLGSP\TGLDFS\DITAVSTYTTPTMGQANSLEEV APAUTVRYTRITTGGTGGNGFVQEPTVSGSATTIGLAVFG SIVALINGRESPPLITOGGSTVSDVVRDLEVVANATFISLI\S APAUTVRYTRITTGGTGGNGFVQEPTVSGSATTIGLSLKFG YTTTVANTGRGDSPASSKPISINYTTEIDKSGMQVTDVQDD ISVXBLPSSSVTGXVTTTTPYFNGGQCTATATAPAFTLK SIVALINGRESPPLITOGGSTVSDVVRTPKEKTGFMKEINLAPDG EGLQPTVSVVSVYAQANAKVSVSVXALDDTLSFRAPATAPAFTLK DVDSIKIAMSEPGGQVSKYXVTYSSEBGIHBLFPAPDGEDD ELGQLAPTOSTVSVVALDDTLSFRAPSVVILDASTATDAB NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVP RPGVTESLSAQWTPSNVALDDTLSFRAPSVVILDASTATDAB NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVP RPGVTESLTTGLEFGTFTTTYTARRHRPRYPPNVQ ALSGTTISKAPPOTSETI ISCHPVOTTESPFAPVOTTENSSPP SVVVSGLMAARKYSVSVXALDDTLSFRAPSVVILDASTATDAB NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPRGNGGLGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		1	1	
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TETPSOPNSHIJOMNAPOSHISKYILRWEPKUSKIMKENTI GHINSYTIKGLKPOVYUSGOLISTOGYGHOETTROPETTSTS PUTSIN\UTGETTFSPLVATSESVTEITASSFVVSWVSASDI SGRVEYELSEEGBEPQYLVLDETATSVNIP\DLLEGRKYIV VYOISBOEGGELLISTGOTTAPDAPPOTVOVDDTSIVVRWS FQAPITGYRIVYSPSVEGSSTELKLPETANSVTLDLOPGVOY ITTYAVEENQESTPVIQOETTGTPSADTVSSPRLDLOPGVOY KVTIMMTPPESAVTGYRVDVIPVLDGEHGGREDPVSPRLDLOPGVOY KVTIMMTPPESAVTGYRVDVIPVLDGEHGGREDPVSVRT TGLSPGYVTYYKKVSAVHGRESKLTADOTTKL\DAPPNLOPF KVTIMMTPPESAVTGYRVDVIPVLDGEHGGREDPVSVRT KVTIMMTPPESAVTGYRVDVIPVLDGEHGGREDPVSVRT TGLSPGYVTYYKKVSAVHGRESKLTADOTTKL\DAPPNLOPF KVTIMMTPPESAVTGYRVDVIPVLDGETRGQPRQYNVGPSVSK PLRNLOPASETTVSUVAIKGNGESFKATGVFTILDPGSSIPPY TETVETTILVITWTPARFIGFKLGVRRSGOGRAPREVTEDSGSI VSGLTFOVEYYYTIQVLRRGGGERDAP\UTWK\VVTPLSPFTTM\ LEANPPOTGLTFTDITGYGITTPNGQGGASLEEV HADQSSCTF\DNLEVPGLEYNNSYTYKDDKSSYPISDTIIP PPPTDLEFTN\LLGPTGYLTVSUVASYTYKDDKSSYPISDTIIP PPPTDLEFTN\LLGPTGYNSYTYTKDDRSSYPISTIITP PPPTDLEFTN\LLGPTGYNSYTYTKDRSSYPISTIITP PPPTDLEFTN\LLGPTGYTAVGUNSYTYTKDDRSSYPISTIITP PPPTDLEFTN\LLGPTGYTAVGUNSYTYTKDDRSSYPISTIITP PPPTDLEFTN\LLGPGTSYTAVAVLTDLLDFTSYVGSSYVYEQHEST \LGGRKCGCSTF\NAVVLTNLLDFTSYVGSSYVYEQHEST \LGGRKCGCSTF\NAVVLTNLLDFTSYVGSSYVYEQHEST \LGGRKCGCSTF\NAVVLTNLLDFTSYVGSSYVYEQHEST \LGGRKCGCSTF\NAVVLTNLTDLPGTSYVASYSYVEQHEST SIVALNGRSSSPLIGGOGSTVGSPVGRTVFYVSSPEDGHAVLADRA\TT TTYVAYTGRGGSPASKPISTNYRTEIDITSLLTATILL\LAG APAVTVKYYRTYTTYTAYTGSPEDGHAVTTSLLL\LAG SIVALNGRSSSPLIGGSPUTGSVAUTHLORPGGOVTUTLENSPP ARVTDATETITISHRTKYETITGFQVDAVTNIDPRKILAFTI DVDSIKIANESPSOQVSRYRVTYSSSPEDGHAVEINLAPDE SUVVSGLWATKYESVYALDFUTLSRADGOVTTLENSPP ARVTDATETITISHRTKYETITGFQVDAVPANGGTPIORTI DVRSYTITIOLOPGTOKKYINTYTILANGRAGSSPVIDASTAIDAA NLRFLATTPDSLLVSWQPPRATITGYIIXYENGSPPEVVPP RPGGTSARAVFORDSTYNGKYANGSGNIGGERGCGGRAGCOM ALSGTTISAAPFOTDSTYIIACHTOTTATPIRRTRPYPPATOTT LTGLTRAGATYNIIVALGLEGGGFFGCGGRAGCOM ADRESRE DDSCCPDYTVSHYANGOGERMSCSSPVIOANTNYNCCTICGRGGFFKCI HEATCYDDGXTYTSHYANGGERMCSSMCGGGRAGCOMOOPSVAN RGGGGSPSPSRTGTGGSVANGYGSYNGTRYNTNYNCTICGGGGGRFCCS PPARETCYDGKYTGNTYNGGGRTYLGANGGONCOMOOPSVAN GSFGCTDBRKHYGINQWERTYLGANGCYCCIGGGRGCCOM CTANKCHGGGGSFTGA		1		GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
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TGLS PGUTYY FKVPANSHGRESKPLTAQQTTKL/DAPTHLQFV ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSK PLRNLQPASSTYUSLVAIKGNQESPKATGVFTTLQCSSIPPY TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSI VSGLTPGVEYVYTIQVLRDGQERDAP,1VNKVVTVTPLSPPTML LEARPDTGVLTVSWERSTTPDITGYRITTTPTNGQGNSLEEV HADQSSCTF DNLEVVGGLEYNVSVYTVKDVKSEVYISDTIIPP PPPTDLRFTH / LIGPTTNEYUM 'APPPSIDLTNFLVRYSPVKN GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSVYEQHEST \LRGQKTGLDSP\TGIDFS\DITA\NSFT\UNW\LAPPRA\TT TGYRIR\HPBEHF\SGRPREDF\VPHSRNSITITNLTPGTEYVV SIVALNGRESPLLIGQQSTVSDVPRDLEVVAAPPTSLLI\SK APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKFGV YTITYVAVTGRGBSPASSKPISINYRTEIDKPSQMQVTDVQDN ISVKWLPSSSPVTGYRVTTT\PKNSPG\PTTKTKAGFDCTEMT EGLQFTVEYVVSVYAANPSGSGDVLOTAVTNIDRYRGLAFTI DVDSIKAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDT ELQCLRFGSSTYTSVVALHDDMESQPLIGTQSTAIPAPTDLK; QVTPTSLSAQMTPNVOLIGTVRVTYFEKTGPMKSIINAPP SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPP ARVIDATETITISMTKTETITGFQVDAVPANGQTPIGRTIK DVRSYTTIGLGPGTDYKIVLYTLINDNARSSFVVIDASTAIDAE NLRFLATTPNSLLVSMQPFRARITGYIIKYEKGSPPREVVP RPGVTEATITGLEPGTEYTITVIALKNNQKSEPLIGRKKTDEI QLVTLPHPHLHGPEILDVBSTVQKKFPFVTHBFQTTGGTGLAGEFKCT SGQQPSVGQMIFEBIGFRRTTPPTTATPIHRPRPYPPNVG SGQQPSVGQMIFEBIGFRRTTPPTTATPIHRPRPYPPNVG ALSQTTISWAPFQDTSEYIISCHPVGTTGSSCHFRC SGRWCDNGWNTIGEKUNGQCGMMSCTCLGNGKGFFKCI DSCFDFYTVSHYAVGDEWERNSESGFKLLCQCLGFGSGFFRC SSRWCDNGWNTIGEKUNGQCGMMSCTCLGNGKGFFKCI GSGRPSPSFCTTGQSVNQYSQRYHQRTNTNNNCPIECFFMLDV ADREDSRE SSRCHCDNGWNYLGEKUNGQCGMMSCTCLGNGKGFFKCI GSGRPSPSFCTTGQSVNQYSQRYHQRTNTNNNCPIECFFMLDV ADREDSRE FSGREDSPSFCTTGQSVNQYSQRYHQRTNTNNNCPIECFFMLDV ADREDSRE SCHCDNGKHYNGEKUNGQCGMMSCTCLGNGKGFFKCI GSGRPSPSFCTTGQSVNQYSQRYHQRTNTNNNCPIECFFMLDV GDSGPSPSFCTTGQSVNQYSQRYHQRTNTNNNCPIECFFMLDV GDSGPSPSFCTTGQSVNQYSQRYHQRTNTNNNCPIECFFMLDV GDSGPSPSFCTTGQSVNQYSQRYHQRTNTNNNCPIECFFMLDV GDSGPSPSFCTTGQSVNQYSQRYHQRTNTNNNCPIECFFMLDV GDSGPSPSFCTTGQSVNQYSQRYHQRTNTNNNCPIECFFMLDV GDSGPSPSCTTGQSVNQYSQRYHQRTNTNNNCPIECFFMLDV GDSGPSPLCLLLAVLCLCTAPVSTGASKSKRQAQOMVOPOSPVAW GSKPGCTDNGKHYQIDTYPRUGDTYPREFKSMMUCTCIGAGGRGRI CTIANRCHEGGGSYKLGDTWRPHETGGYMLECVCLGNAKGEF		1	1	
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EWKCERHTSVOTTSSGSGPTDVRAMVGOPOPHOPPPYCHCUT DEGVUTSVOMQLA TYCONKUM, CUCLOKISVSCOSTANTOTYO GRSNOSPCULPTYTGGTYSCTTEGRQDGHLMCGTTSNYEDQO KYSCTCHITHLVUGTGGNSNALGHEPILVNNHYTGLTSGER DMMKNGOTTONYDADQKFGFCPMAHERICTTNEGVWTRIGDGM DROHDMSHMRGCTGKGRGSEWTCHSGOLDGETGTFYGI GDSMEKVYHGRVGCKGRGSEWTCHSGOLDGETGTFYGI GDSMEKVYHGRVGCVGGRGGRWKCDPVDQCDGSETGFYGI GDSMEKVYHGRVGCVGGRGGWCDQTGTYSSGSPWUF TETPSQFNSHFJGMRAPQSSHISKYLLRMFPRMSVGRKKEATIP GHLMSVTIKGLKRGVTGGGGTGTYGGTGTFYGI GGLSWSTYTIKGLKRGVTGGGGTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT		1		ITCTSRNRCNDODTRTSYRIGDTWSKKDNRGNLLOCICTGNGRG
DSGWYSVGMCLA* KTOSKKML\CTCLGKGVSCGETAVTOTYG GRSNGSPCVLEFTYKGTPSCTTERGODGHLMCSTTINTEDOD KYSFCTDHTVLVQTRGGNSNALCHFPELYNHMYTDCTSEGER DMKKKGCTTONIDADKFGFCPMAAHGELGTTHSGVATKIGDOM DKQHDMGHMMTCTCVGRGRGBWTCLAYSQLEDOCLVDDLTYNNN DTFHKHEEGHMLACTFCGGGRGBWTCLAYSQLEDOCLVDDLTYNNN DTFHKHEEGHMLACTFCGGGRGBWTCLAYSQLEDOCLVDDLTYNNN DTFHKHEEGHMLACTFCGGGRGBWTCLAYSQLEDOCLVDDLTYNNN DTFHKHEEGHMLACTFCGGGRGBWTCLAYSQLEDOCLVDDLTYNNN DTFHKHEEGHMLACTFCGGGGRGWACDPLOGTYDSSCOPUSVUT GDSMEKYVHGWYCOCYCYGRGIGSWLODPLOGTYDSSCOPUSVUT TTDSGDNSHIPLOMADSSUTTLAMSPROWERASDTV GGFRYEYELGSBODEDOYLVLREATASV\NIP\DLLAGRATIVN VOLISBCROGGLLLAGTGTTADAPPDTVDQVDDTSIVVRWS SCFRYEYELGSBODEDOYLVLREATASV\NIP\DLLAGRATIVN VOLISBCROGGLLLAGTGTADAPPTVDQVDDTSIVVRWS TITLYAWERNQSTFVUIQUETGTRASVTUSHQFVGVGVT KVTIMMTTPSSAVTGTVDIPTDAPPTVDQVDDTSIVVRWS TOLSGCRYTTYRVTAVSHGRSSKPLTAQCTTKL\DAPTNLQFVWN KVTIMMTTPSSAVTGTVDVIPTVDLTARGOPRGNVBSPUKTY\AEN TGLSGVTYTTVAVFAYSHGRSSKPLTAQCTTKL\DAPTNLQFVWN ETDSTVLURWFDPSAVTGTVDVIPTVDLTARGOPRGNVBSVGVK FLRHIQPASSTTVSLVALKGRGSKAATGVFTTLQGSSIPPTVA TRVTETTILTIVTTRYAGTGTSVAVDTTURGOPRGNVBSVSKST LRHIQPASSTTVSLVALKGRGSKAATGVFTTLQGSSIPPTVA TRVTETTILTIVTTRYAGTGTSVAVDTTURGOPRGNVBSVSKY FLRHIQPASSTTVSLVALKGRGSKAATGVFTTLQGSSIPPTVA TRVTETTILTIVTTRYAGTGTGSVAVTVALDGGSSIPPTVA HADGSSCTP\DHLEVRGLEYNXYVTVKDDKESVFISDTSITIS VSGLTFGVEVYTTIQVLRGGGEADPLVANTYTSLAGSSIPPTVA HADGSSCTP\DHLEVRGLEYNXYVTVKDDKESVFISDTSITIS CREMCGSLSIPPTGVRKTVATLYCHTGFTGVAVSSVYEQUESTFF ALRGCRGCLDSPLYAGTTGTSLLAVANTYTSLATILATGGTEVVAV SIGNAMGRESSILLGGGSTVSVSVTTYCDGKSSVFISDTSITIS GRAMGSLSIPPTGVRKTVATLYFGSSTATISGLKGGVU TOTATAL\GREESSILLGGGSTVSVSVTTYGDKSSVFIDATGTTLATGGTEVVAV SIGNAMGRESSILLGGGSTVSVSVTTYGDKSSVFIDATGTTLATGGTEVVAV SIGNAMGRESSILLGGGSTVSVSVTTYGDRSSTATISGLKGGVU TOTATALAGRGSSTATISGTGFTGTGTGTGTGTGTATK BGLGQDTVAVTATAGTGTGSSKFITTYTALAGDQTTENTT GRAMGATATTURGGGSTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT			}	EWKCERHTSVOTTSSGSGPFTDVPAAVVODODUDODDDVCUGUD
GISNOSPCULPTYNGCRYPSCTTERGQOSHALGETSTANNOGO, KYSPCTUHTHLVOTEGOSHANGLOFPELVINNHYTOTSGGRE DMMKKGOTTONYDADOKPGFCPMAHERICTTUNGVWYRIGDOM DROMDMANGCTOKGRGGEWTLASGOLROCIUDTYNNN DFFHKHREGGMMLNCTCFGGGGRWKCDPUDQCDGETGTPGJ GGSMEKYVHGWYGCVGGGGGWKCDPUDQCDGETGTPGJ GGSMEKYVHGWYGCVGGGGGWKCDPUDQCDGETGTPGJ GGSMEKYVHGWYGCVGGGGGWKCDPUDQCDGETGTPGJ GGSMEKYVHGWYGCVGGGGGWKCDPUDQCDGETGTPGJ GGSMEKYVHGWYGCGGGGWKCDPUDQCDGETGTPGJ GGSMEKYVHGWYGCGGGGWKCDPUDQCDGETGTPGJ GGSMEKYVHGWYGCGGGGGWCDPUDQCDGTGTFGGG GGMEKYVHGWYGCGGGGGWCDPUDQCDGTGTTGGGGGWKGATJ GGLSSTTIKGGGGGGAGGWCGPUTGGGGGGAGGWKGATJ GGLSSTTIKGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA		l		DSGVVYSVGMOLA * KTOCNKOMI. \ CTCL CNCVCOCETA I TOCTUCA
KYSPCTIHYULVTROGNSMALCHFFFIYMTNITOCTSEGRER DMMKGGTTGNYDADQRGGTGTAMGELTTMEGGWYRIGODW DKQHDMSHMRCTCYGNGGGEWTCLAYSQLEDGCUVDLITYMYN DFMKRHEGEMHLACTCYGNGGGEWKGDPVOCQDSGTGTFYQT GDSMEXYWIGVRYCYCYGRGIGEWHCQDLGTYPSSSGDPWYFT TETPSQNSHIPLGWANDOPSHISYTLIMSERVSWASDTV TETPSQNSHIPLGWANDOPSHISYTLIMSERVSWASDTV GGNEKYWIGVRYCYCYGRGIGEWHCQDLGTYPSSSGDPWYFT TETPSQNSHIPLGWANDOPSHISYTLIMSERVSWASDTV GGNEKYWIGVRYCYCYGRGIGEWHCQDLGTYPSSSGDPWYFT TETPSQNSHIPLGWANDOPSHISYTLIMSERVSASDTV GGNEKYWIGVRYCYCYGRGIGEWHCQDLGTYPSSSGDPWYFT TETPSTTVINGLTFYSPSUADSTATSVANIPADLLGRAYTY GHLMSYTIKGLKRGWYFROGLISTOTTHOPSTOPWASDTV SGFRYEFELSEGDEPQYLVLESTATSVANIPADLLGRAYTY VXGISGREGOLISTSTATABYTLSDLQPCVONN TITYAVERNOSSTSTELLLESTGATABYTLSDLQPCVONN TITYAVERNOSSTSTELLLESTGATABYTLSDLQPCVONN TITYAVERNOSSTSTELLLESTGATABYTLSDLQPCVONN TITYAVERNOSSTSTELLASTGATABYTLSDLQPCVONN TITYAVERNOSSTSTELLASTGATABYTLSDLQPCVONN TITYAVERNOSSTSTELLASTGATABYTLSDLQPCVONN TITYAVERNOSSTSTELLASTGATABYTLSDLGPCVONN TETPSTTIVITWTPAFALGFLGWYRSGGGEAPRYTYSDLGSSIV VSGLTFGWEYVTTIQUARDOGRAPALVNKVYTYLDGSSIV TETPSTTIVITWTPAFALGFLGWYRSGGGGARPEVTSDLGSSIV TETPSTTIVITWTPAFALGFLGWYRSGGGARPEVTSDLGSSIV TETPSTTIVITWTPAFALGFLGWYRSGGGARPEVTSDLGSSIV TETPSTTIVITWTPAFALGFLGWYRSGGGARPEVTSDLGSSIV TETPSTLATABYTLSTATAGATA TETPSTTIVITWTPAFALGFLGWYRSGGARPETTSDLGSSIV TETPSTLATAGATA T	1		}	GNSNGEPCVI.DETVNCPTEVCCTTECPOPCIU NOCTTONICO
DMMKMGGTTQNYDADQKFGFCPMAHEBICTTMEGMYRIGOD DRQHDMSHMMRCTCVGNGRGEBTCLAYSQLBQCUYDDITYNWN DTFHKRHEGIMILOTCRGGGRGNKCDPVDQCDSETGTFYQT GDSMEKYUNGVCYCYGGGGIGCHQCDLGTYPSSGPWUFUI TETSSQDNSHFIQMAPQSHISYYLLRWFDXSGVGNKEATIP GRLMSYTIKGLKGWVCGCGUGGIGCQYGQWFUFSSGPWUFUI TETSSQDNSHFIQMAPQSGHISYYLLRWFDXSGVGNKEATIP GRLMSYTIKGLKGWVCGCGUGGIGCQYGQWFUFSTGSTF PYTSNYLVGETTFEFDLWATSSSYTEITASSFVUSWASADTV SGFRYEVELSEGDDERQYLLUFSTASVAIRQMSGAVGUGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	1	ļ	1	KYCECTDUTY VOTECCHONON CHEET INTERPREDE
DKQHDMSHMRCTCYGNGRGENTCLAYSQLEDGCLYDDITYMY DIFHKRHEEGHINLCTCGGGGGRMCDPUDCOGBRGTFYQI GDSMEKYVIGVRYQCYCYGGGGGEMHODPLOTYPSSGDPWEYI TETPSQCMSHI JORNADQSHISYLLAWPROSUGRKEANII GHANSTYI KGLKPGVYYEGGLIS JQQGGGVTREDPTTTGTTT PTTSTYLTGILKPGVYYEGGLIS JQQGGGVTREDPTTTGTTT PTTSTYLTGILKPGVYYEGGLIS JQQGGGVTREDPTTTGTTT PTTSTYLTGILKPGVYYEGGLIS JQQGGGVTREDPTTTGTTT PTTSTYLTGILKPGVYYEGGLIS JQQGGGVTREDPTTTGTTT PTTSTYLTGILKPGVYYEGGLIS JQQGGGVTREDPTTTGTTT PTTSTYLTGILKPGVYYEGGLIS JQQGGGVTREDPTTTGTTT PTTSTYLTGILKPGVYYTEGEDGEDPYLVJBSTYLTABDLOFGVYYYI VYQIS BDGGGSLILGTSQTTTAPDAPPDFYTVDVDDTISIVYWRS PQAPIGTRIVYSSVGSTELHLEPTANSVILBSLQFGVYYYY KUMTUPESSAVTYSVGATIGAUTGANDENGAVYYSVBOLGFVEYTY KVTIMTTPESSAVTYSVGATIGAUTGANDENGAVYSVSTYSDGGAVYYYY RUMTUPESSAVTYSVGATIGAUTGANGAVYTYKKDAPTHAGPGSSIV VAGITFGVYYYTYKVFAVSHGRESKPLTAQQTTKLANDATSTYLDGSSIV VSGITFGVYYTIQUKAROGSRDAYLTWALVFLGPGSSIPY TGVYTETTIVINTPAPRIGFKLAVFRSQGGSAPRYTGDGSSIV VSGITFGVYYTIQUKAROGSRDAYLTWALVFLGPGSSIPY VSGITFGVYYTIQUKAROGSRDAYLTWALVFLGPGSSIPTIDISISIT LEANINGSETPLEDDYANVLTYLLAPTSEVVSVSSVYEQHESTP VSGITFGVYYTIQUKAROGSRDAYLTWALVFLAFTSVATA PPPTDLARTYN LIBPTMSVTAYAPPDFLITTRTTSPTTTVYN HADDSSCTYP\NBLEVGLEYNVSVYTVKNDESVPISDTIIDITIPAP PPPTDLARTYN LIBPTMSVTAYAPPDFLITTRTTLFTGTFVV SIVALINGBESPLITGQGSTVSDVYRDLEVVAATTTSLILIYARVA PPPTDLARTYN LIBPTMSVTAYAPPDFLITTRTTLFTGTFVV SIVALINGBESPLITGQGSTVSDVYRDLEVVAATTTSLILIYAR AFAVTYNTYSITYGTGGSSVGGVTVYOSKATATIGGLAFTDV TGYRIN,HSPEPTVTGTGGSSVGGVTVYOSKATATIGGLAFTDV TGYRIN,HSPEPTVTGTGGTGSVGGVTVYOSKATATIGGLAFTDV DVBS IKIAMSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ì			DIMENSOCITION OF POWER PROPERTY OF THE POWER POWER PROPERTY OF THE POWER POWER PROPERTY OF THE POWER PROPERTY OF THE POWER PROPERTY OF THE POWER PROPERTY OF THE POWER POWER PROPERTY OF THE POWER POWE
DTFHKRHESGHMLATCTGGGRGNRKCDPVOQCOSETGTTYQU GDSMEXYUNGVYCYCYGGGGGEMGQDLTTYSSGPVEVUI TETPSQRNSHIQWANQOSHISKYLLRWFXNSVGRKKEATIT GHLMSYTIKGLKGAVVEGGLIS LQQVGGGVTGPTTSTSTT GHLMSYTIKGLKGAVVEGGLIS LQQVGGGVTGPTTSTSTT PYTSNT VYGETTPESPLWATGESVELTASSFVVSWASSDFY SGFRVEHLSEGDEPQYLWLDSTATSVNIP JOLLDGRKYIW VGISEDGGGLILSTSGTTADDAPPDPYTDVDUDTSIVTRWS POARITGYRIVYSPSWGSSTELMLPPTANSYTLAGUTVAL NOTHANDERGENGETPVALOGETTGTREADTVSPROLGGVGVTDV KVTIMPTPESSAVTGYRDVIPVIPVSPROLGGVGVTDV KVTIMPTPESSAVTGYRDVIPVIPVSPROLGFVSVTDV KVTIMPTPESSAVTGYRDVIPVIPVSPROLGFVSVTDV KVTIMPTPESSAVTGYRDVIPVIPVSPROLGFVSVTDV KVTIMPTPESSAVTGYRDVIPVIPVSPROLGFVSVTDV KVTIMPTPESSAVTGYRDVIPVSPROLGFVSVTDV KVTIMPTPESSAVTGYRDVIPVSPROLGFVSVTDV KVTIMPTPESSAVTGYRDGYNGVSSVSV FLRRIGAPASETVITVIAVERSFROMITYGLTRGGPRQVNVGSSSVSV FLRRIGAPASETVITVIAVERSFROMITYGLTRGGPRQVNVGSSSVSV FLRRIGAPSSAVTITVIAVERSFROMITYTHTGGGRSFRATVSTTLGGGSSIPPYN TEVTETTIVITVITVAPRIGGKLGVNSSOGGGARREVTSDGSSIPPYN TEVTETTIVITVITVAPRIGGKLGFVLGVNSSOSGARREVTSDGSSIPPYN TEVTETTIVITVITVAPRIGGKLGFVLGVNSSAVTGNOMSST VSGLTGGVEVYTITVIAVERSFRATIVITVITVISPPTNILL LEAMPDTSVITVIAVERSFTIPDITGYRITTPTTGGGGSARREVTSDGGSSIPPYN TEVTETTIVITVIAVERSFTIPDITGYRITTPTTGTUSYSSSTVENGHESTP LEAMPTSVITVIAVERSFTATIVITVITAVERSFTSTIPTITGYRITTPTMGGGNSLEVERS GRMQSLSIFFLISDNAVVITNILLDFTSVVSSSVYEGHESTP LARGGKTGLSSPASSRYSISINYTASISCHAPATOVANA APAVTTRYKITTGGGSSPASSRYSININYTSILDFSQWQVTDUDGDS SIVALMGRESSPLIGQGSTVSDVPRDLEVVAATPTSLLILSCHGVD YTITYVAVTGRGDSSPASSRYSININYTSILDFSQWQVTDUDGTSMT SELQPTVSVVSVAQAPSGGSGDLVQTAVTNIDEPKGLAFTDV DVDS ILAMESGGOQGVSTVTVTSSSEDGOGHELFPAPDGGEDTMT SELQPTVSVVSVAQAPSGGSGDLVQTAVTNIDEPKGLAFTDV DVS SILAMSGGOQGVSTVTVTSSSEDGOGHELFPAPDGGEDTMT SELQPTVSVVSVAQAPGGSGDLVQTAVTNIDEPKGLAFTDV DVS SILAMSGGOQGVSTVTVTSSSEDGOGHELFPAPDGGEDTMT SELQPTPSVVSVAQAPGGGSGDLVQTAVTNIDEPKGLAFTDV DVS SILAMSGGOQGVSTVTVTSSSEDGOGHELFPAPDGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1	ì	ł	DMMANCGITQNYDADQRFGFCPMAAHEEICTTNEGVMYRIGDQW
GDSMEXYVIGURYCCYCRGGIGEMICOPLOTYPSSSCPUVUT TETPSQOMSHI PIQONAPQPSI SKYLLEMRYSKIRKEATIP GHLMSYTIKGLKPGVVYEGOLISIQOYGHQEVTRIPTTTSTST PYTSNTVYOGGTTFFFFPLVATSSSVTETTASSTVSWASASDTV SGFRVEYELSEGGEPQLIVLPSTATSV\NIP\DILLPGRYIYN VXGISGGGGGLILSTSGTTAPAPPPTTYDDTSIVVAWSR PQAPITOYRIVYSFSVEGSSTELNLPTANSVTLEDLQFGVQYN ITIYAVEENQESTPVVIQGTTGTRSDTVPSPROLQFVEYTDV KVTIMTTPPESAVTGYRDVIUPUNGGGGGGYNGVBSVSKYN KVTIMTTPPESAVTGYRDVIUPUNGGGGGYNGVBSVSKYN FORDTVILWRYPPRAQITGYRLTVOLTRRGGYNGVBSVSKYN FIRRIQPASETTVSLVAX KONGESPRATGYPTILQPSSIPPN TEVETTYLVIHYPRARIGKLAVPSGGGSRYTDSGGSIV VSGLTFGVEYYYTIQULEDGGERDAP\IVAK\VVTELSPTNLE FLARLQPASETTVSLVAX KONGESPRATGYPTILQPSSIPPN TEVETTYLVIHYPRARIGKLAVPSGGGGAFVSDSGGSIV VSGLTFGVEYYYTIQULEDGGERDAP\IVAK\VVTELSPTNLE FLARLQPASETTYSLVAX KONGESPRATGYPTILQPSSIPPN TEVETTYLVIHYPARSTSTYDHIGVRITTPTHGGGGNSLEEV VSGLTFGVEYYYTIQULEDGGERDAP\IVAK\VVTELSPTNLE FLARLQPASETTYSLVAX KONGESPRATGYPTILQPSSIPPN TEVETTYLVIHYPARSTSTYDHIGVRITTPTHGGGGNSLEEV VSGLTFGVEYYYTIQULEDGGERDAP\IVAK\VVTELSPTSDGGIV VSGLTFGVEYYYTIQULEDGGERDAP\IVAK\VVTELSPTSDGGIV VSGLTFGVEYYYTIQULEDGGERDAP\IVAK\VVTELSPTSDGGISLEV HADDSSCTF\NNLEVVGLEYNSVYTVKDDKSSVYEOHESTD VLGRCKGTGLSP\TOLTAYNSTPTVLGYSYSSVYEOHESTD VLGRCKGTGLSP\TOLTAYNSTPTVLGYSYSSVYEOHESTD VLGRCKGTGSP\TOLTAYNSTPTVLGYSYSSVYEOHESTD VLGRCKGTGSPTLICQCTTYSVYTYKDDKSSVYEOHESTD VLGRCKGTGSPTLICQCTTYSVYTYKDRDKATATILISM APAVTVRYYRITYGTGGGSTSPVCBTTPTGSKSTATILISMA APAVTVRYYRITYGTGGGSTSSKSFRISHTNTFILDKRGMQTTVLOONS ILSWENGSSKSFRISHTSVTTSSPEDGULELPPAPDGEDTM BGLQPTVEYVVSVYAQNDSGGSQPLVGTAVTNIDRRGGLAFTDV DVDSIKJAMESPGGOVSTKYVTYSSPEDGULELPPAPDGEDTM BGLQPTVEYVVSVYAQNDSGGSQPLUTGGTAIJAPTDUKFT QVTTSLSAGMTYTSSPEGGURELPPAPDGEDTM BLGGLBPGSEYTVSVVALHDDMESQPLIGTGSTAIJARDP RACTGATGTTISMATGTTISMTKTETTITSGODAVPANGMENINAPOTS SUVUSIGNATATYSPETGATTITSMTKTETTITSGODAVPANGMENINAPDTS SUVUSIGNATATYSPETGATTITSMTKTTTTTGFOODAVPANGMENINAPDTS ARCTGATGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
TETESQÜNSHIQANDAÇISIISKYILEMERNINGURIKATIP GHLNSYTIKUKRPOVYSEQLISIQYGHQEYTETTASTST PYTSINT VTGETTFESPLATSESYPETTASSPVUSWISASDTV SCERVEYELISEGGEPQILLESTASTVINDLERKEYIV VYQISEGGEOGLILISTGOTTAPDAPPPTVQVDUTSIVWAKS PQAPITGYRIVYSPSVEGSTELINIPETANSVILSDLQPGVYN ITITAVEENGSTPVVIQGETTGTRSDTVPSRPDLGFVEVTDV KVTIMMTEPESAVTGYRUVIPVINDGEHQGRIPLISNITT\ABN TOLSPGVTYYTKYRAVSIGGESKPLTAQOTTIADPSPOKTYLOPGSSIPPYN RVTIMMTEPESAVTGYRUVIPVINDGEHQGRIPLISNITT\ABN TOLSPGVTYYTYKYRAVSIGGESKPLTAQOTTIADPSVKY FLRRILQPASETVISLVAIKKNOSSENTAQOTTIADPSVKY FLRRILQPASETVISLVAIKKNOSSENTATQOTTIADPSVKY FLRRILQPASETVISLVAIKKNOSSENTATQOTTIADPSVKY FLRRILQPASETVISLVAIKKNOSSENTATQOTTIADPSVKY FLRRILQPASETVISLVAIKKNOSSENTATQOTTIADPSVKY FLRRILQPASETVISLVAIKKNOSSENTATQOTTIADPSVKY FLRRILQPASETVISLVAIKKNOSSENTATQOTTIADPSVKY FLRRILQPASETVISLVAIKKNOSSENTATOTIADPSOGGEAPREVTSDOSGIV VSGITPGVEYVYITOVLBOGGERAPAPIVATGSSIPPYN FEVTETTIVITAVTSRGERAPAPIVATAVATTIADPSOGGEAPREVTSDOSGIV VSGITPGVEYVYITOVLBOGGERAPAPIVATGSPSIPTITIADP FRANCISETVINIA TOLSPATATAVATAVATAVATAVATAVATAVATAVANAVATAVANAVATAVANAVATAVANAVATAVAT	1			DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
GRLMSTTIRGLKPGVVYEGGLISIQQYGHGEVTRDFTTTSTST PYTSNT\VTGSTTFFFFFLANTSSNYETITASTYLWSSASDTUT SGF#VEYELSEGDEPQTLVLPSTATSV\NIP\DILLGRRYIYM VXGISGGGGGLILSTSGTTAPDAPPDFTVQVDVDTSIVVRWSR PQAPITGYRIVYSPSVEGSTELNIPETANSVTLSDLQPGVQYN ITITAVERNGSSTPVVIQGETGTF#SDTVPSPRDLQFVGVTDV KVTIMNTPPSSAVTGYRVDIVPNLDGEHGGPNGVBVSKYK PQAPITGYRIVYSPSVEGSSTELNIPETANSVTLSDLQPGVQYN KVTIMNTPPSSAVTGYRVDIVPNLDGEHGGYMVGPSVSKY PLRALQPASETTVSLVAY KKNQSSFRAGVPTTLQPGSSIPPN TGLSPGVTYYKVFAVSGRRSSFPLTAQQTTKL\DAPTNLQPVN PLRALQPASETTVSLVAY KKNQSSFRAGVPTTLQPGSSIPPN TEVTETTVI UNTPAPRAGIGFKLAVPSQGGAFVTSDGSGIV- VSGLTPGVBYVYTIQULENGGERDAP\IVK\VTPLSPPTNLH LEAMPDTGULTVSHESSTPDITGYRITTPTNGCQGTSLEEVV HADQSSCTP\DMLEVPGLETNVSVTVKDDKSSVPISDGTIFAV PPPTDLRFTN\ILDPTRTVTM\APPBSIDLTNFLVSYSPKNE GRMLQSLSTPLEDN\AVVLTLLDGTSTVVSVYEQHESTF \LRGRKGGLDSP\TG1DF\$\DITA\NSFT\VHN\IAPPAT\TPL TGYRIP\HTGSTRAFTYSGTGGGNSPVSTRYDTSLLIVANS PPPTDLRFTN\ILDPGTSVVV SIVALNGRESSPLLIGQSTVSDVRRDLEVVAATPTSLLI\SWD APAVTWYRYTITYGTGGGNSPVSTRNSTBGLKPOV TITYTAVTGGGGSPASKISTNYTTEIDKPSQMVTDVQDMS ISVANDRSSSPVTGYNVTTT\PKNOFQ\PTKTTTGGLKPOV TTITYTAVTGGGGSPASKISTNYTTSLTBCKAPOV TTITYTAVTGGGGSPASKISTNYTTSLTBCKAPOV DUSSILAMESGGGVSKTRVTYSSPEDGHELPPAPDGEDTA ELGGLPGGSSVTVSVVALHDDHSSQPLIGGAVTLENDSPRR GRAVTDATTTITISTRGTTTTVINGRKGGAVTLENDSSPRR ARVTDATTTTITISTRGTTTTVINGRSQPAVTLENDSSPRR ARVTDATTTTITISTRGTTTTVINGRSQPAVTLENDSSPRR ARVTDATTTTITISTRGTTTTVINGRNGSPPLIGRKTTDLP UNSTITUTISTRGTTTTTTTTTTTTTTTTRAFTLATTTRAFTLATTTLEPTDLKFT QLYTTSHANDRYSTYSVALHDDHSSQPLIGGAVTTLEPTLKFT QLYTTSHANDRYSTYSVALHDDHSSQPLIGGAVTTLEPTLKFT QLYTTSHANDRYSTYSVALHDDHSSQPLIGGAVTTLEPTLKFT QLYTTSHANDRYSTYSVALHDDHSSQPLIGGAVTTLEPTLAGGTSPRC SGQDSVGQMIFEBHGFRTTTPTTATTIRRRFRFYPPNVGG ALSGTTISMAPGTOFTTYTYTINGNARSSPVTANSSPRRINGFT PROTTERTTTTTSRTTTTTTRAFTCTTTTRAFTRAFTPTTATTRAFTLANDRSS SUVUSIANATTYTANAFTYSTYTATTRAFTTTRAFTRAFTPTTATTRAFTRAFTPTTATTRAFT CGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1	ł	ł	GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
GRLMSTTIRGLKPGVVYEGGLISIQQYGHGEVTRDFTTTSTST PYTSNT\VTGSTTFFFFFLANTSSNYETITASTYLWSSASDTUT SGF#VEYELSEGDEPQTLVLPSTATSV\NIP\DILLGRRYIYM VXGISGGGGGLILSTSGTTAPDAPPDFTVQVDVDTSIVVRWSR PQAPITGYRIVYSPSVEGSTELNIPETANSVTLSDLQPGVQYN ITITAVERNGSSTPVVIQGETGTF#SDTVPSPRDLQFVGVTDV KVTIMNTPPSSAVTGYRVDIVPNLDGEHGGPNGVBVSKYK PQAPITGYRIVYSPSVEGSSTELNIPETANSVTLSDLQPGVQYN KVTIMNTPPSSAVTGYRVDIVPNLDGEHGGYMVGPSVSKY PLRALQPASETTVSLVAY KKNQSSFRAGVPTTLQPGSSIPPN TGLSPGVTYYKVFAVSGRRSSFPLTAQQTTKL\DAPTNLQPVN PLRALQPASETTVSLVAY KKNQSSFRAGVPTTLQPGSSIPPN TEVTETTVI UNTPAPRAGIGFKLAVPSQGGAFVTSDGSGIV- VSGLTPGVBYVYTIQULENGGERDAP\IVK\VTPLSPPTNLH LEAMPDTGULTVSHESSTPDITGYRITTPTNGCQGTSLEEVV HADQSSCTP\DMLEVPGLETNVSVTVKDDKSSVPISDGTIFAV PPPTDLRFTN\ILDPTRTVTM\APPBSIDLTNFLVSYSPKNE GRMLQSLSTPLEDN\AVVLTLLDGTSTVVSVYEQHESTF \LRGRKGGLDSP\TG1DF\$\DITA\NSFT\VHN\IAPPAT\TPL TGYRIP\HTGSTRAFTYSGTGGGNSPVSTRYDTSLLIVANS PPPTDLRFTN\ILDPGTSVVV SIVALNGRESSPLLIGQSTVSDVRRDLEVVAATPTSLLI\SWD APAVTWYRYTITYGTGGGNSPVSTRNSTBGLKPOV TITYTAVTGGGGSPASKISTNYTTEIDKPSQMVTDVQDMS ISVANDRSSSPVTGYNVTTT\PKNOFQ\PTKTTTGGLKPOV TTITYTAVTGGGGSPASKISTNYTTSLTBCKAPOV TTITYTAVTGGGGSPASKISTNYTTSLTBCKAPOV DUSSILAMESGGGVSKTRVTYSSPEDGHELPPAPDGEDTA ELGGLPGGSSVTVSVVALHDDHSSQPLIGGAVTLENDSPRR GRAVTDATTTITISTRGTTTTVINGRKGGAVTLENDSSPRR ARVTDATTTTITISTRGTTTTVINGRSQPAVTLENDSSPRR ARVTDATTTTITISTRGTTTTVINGRSQPAVTLENDSSPRR ARVTDATTTTITISTRGTTTTVINGRNGSPPLIGRKTTDLP UNSTITUTISTRGTTTTTTTTTTTTTTTTRAFTLATTTRAFTLATTTLEPTDLKFT QLYTTSHANDRYSTYSVALHDDHSSQPLIGGAVTTLEPTLKFT QLYTTSHANDRYSTYSVALHDDHSSQPLIGGAVTTLEPTLKFT QLYTTSHANDRYSTYSVALHDDHSSQPLIGGAVTTLEPTLKFT QLYTTSHANDRYSTYSVALHDDHSSQPLIGGAVTTLEPTLAGGTSPRC SGQDSVGQMIFEBHGFRTTTPTTATTIRRRFRFYPPNVGG ALSGTTISMAPGTOFTTYTYTINGNARSSPVTANSSPRRINGFT PROTTERTTTTTSRTTTTTTRAFTCTTTTRAFTRAFTPTTATTRAFTLANDRSS SUVUSIANATTYTANAFTYSTYTATTRAFTTTRAFTRAFTPTTATTRAFTRAFTPTTATTRAFT CGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
PUTSNY VYGISEGGEPCILLETSTATS VIP LIDERRY IV W SCFREVERLESEGGEPCT VILLETATS VIP LIDERRY IV W VGISEGGESTELLETSTATA PRAPP POPT VID VDDTS I VYRSE BOAPITO'S I VYSESGEGSE EILLETETATS LIDLEPCRY IV W VGISEGGESTELLETSTATS LIDLEPCRY IV W VGISEGGESTELLETSTATS LIDLEPCRY IV W VGISEGGESTELLETSTATS LIDLEPCRY IV W VGISEGGESTELLETSTATS LIDLEPCRY IV W IT I VALUER OF THE VALUE OF THE VALUE OF THE VERY INTERPRET VILLE OF THE VERY INTERPRET VILLE OF THE VERY INTERPRET VILLE OF THE VERY INTERPRET VILLE OF THE VILLE				GHLNSYTIKGLKPGVVYEGQLISIQQYGHOEVTRFDFTTTSTST
SSFRVEYELSEEGGEPGYLVLPSTATSV\NIP\DLEGRYIVN VYGISEGGESGLILISTGAPAPAPPDYDYDVDDTSIVYRWSR PQAPITGYRIVYSSPVEGSSTELRIPETANSVTLGDLQFQVDYN ITITAVEENGCSTPVVIQOETTGYRBZDYSPRDLGFVEVTDV KVTIMMTPDESAVTGYRVDVIPVNLPGERGGRLPLSRNTP\AEN TGLSPGVTYYFKVEAVSHGRESKPLTAQTTKL\DAPHILOPUN ETDSTVLVRWTPPRAGITGYRLTVGLTRGQFRGYNVGPSVSKY PLRNLQPASETYUSLVAIKGNGESPKATGYTTLQGSIPYN TEVTETTIVITWTPRAFICFKLGVRPSGGSIPYN TEVTETTIVITWTPRAFICFKLGVRPSGGSIPYNGFSVSKY PLRNLQPASETYUSLVAIKGNGESPKATGYTTLQSSIPYN TEVTETTIVITWTPRAFICFKLGVRPSGGSIPYNGFSVSKY PLRNLQPASETYUSLVAIKGNGESPKATGYTTLGSSIPYN TEVTETTIVITWTPRAFICFKLGVRPSGGSIPYNGFSSIPYN TEVTETTIVITWTPRAFICFKLGVRPSGGSIPYNGFSSIPYN HADGSCTF\DNLEWPGLEYNVSVTYKDDKSSVPISDTIIDAV PPPTLLEFTN\LLGGGTYNDVTTVKADKSSVPISDTIIDAV PPPTLLEFTN\LLGGGTYNDVTTVKDKSSVPISDTIIDAV PPPTLLEFTN\LLGGGTYSDVPRDLEVVASTYTSPVGNTE GRALGSLSIPFLSN\LAVVLINLLPGTEVVSVSSVYEQHESTF \LRGRKTGLDSP\TGIDFS\DITA\NSFT\VIN\LAFRA\TPTI TGYRIN\HPPEHT\SGGREDRO\LYPASTYTIVATYTSUTSCTSTLINLTDTGTTYV SIVALMGREESPLLIGQGTYSDVPRDLEVVASTYTITLINLTGTTYV SIVALMGREESPLLIGQGTYSDVPRDLEVVASTYTITLINLTGTTYV SIVALMGREESPLIGQSTYSDVPRDLEVVASTATISGLKFGVD YTITVVAVTGRGDSPASSKPISINYRTEIDKPSGMQUTTVQMNS ISVKLIPSSSPVTGYRVTTITYRGRGCD\FSKSTATISGLKFGVD YTITVVAVTGRGDSPASSKPISINYRTEIDKPSGMQUTTVQMNS ISVKLIPSSSPVTGYRVTTITYRGRGCD\FSKSTATISGLKFGVD YTITVVAVTGRGDSPASSKPISINYRTEIDKPSGMQUTTVQMNS ISVKLIPSSSPVTGYRVTTITYRGRGCD\FTKTATGAPDOTEMTI BGLQPTYEVVSVYAQNPSGESQPLVQTAVTNIDRRKGLATTDUKT QVTPTSLSAQGVSRYNTYSSSEDOIHELFPAPDGEDTA ELGGLAPGSSVTVSVALMDMRSQPLIGTXTAATDUKT QVTPTSLSAQGVSRYNTYTSSSEDOIHELFPAPDGEDTA ARVIDATETTITISMTKTEITIFGVDAVPANGNGRINLADSS SVVVSGLMVANKKYSVYALAUTLTSFRAGSPUTDATIAPTUKKT QVTPTSLSAQGVSRYNTYTYPKRGCD\FTKTATAATDUKT QVTPTSLSAQGVSRYNTYTYPKRGCD\FTKTATAATDUKT QVTPTSLSAQGVSRYNTYTYPKRGCD\FTKTYPROGGRATAATDUKT QVTPTSLSAQGVSRYNTYTYPKRGCD\FTKTATAATDUKT QVTPTSLSAQGVSRYNTYTYPKRGCD\FTKTATAATDUKT QVTPTSLSAQGVSRYNTYTYTYPKRGCD\FTKTATAATDUKT QVTPTSLSAQGVSRYNTYTYTYPKRGCD SVVVSGLMWAYLYLGGGRGCTGCHATGTYTHAATAATAATAATAATAATAATAATAATAATAATAATAA		1	ĺ	PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
VYGISEGEGISILISTSGTTAPDAPPPTVDGVDTSITVRMSR POAPITOTRIVYSPSVEGSTELLNPETVLIGDIGPGVGYN ITITAVEENGESTPVIIQGETGTPREDTVPSPRDLGFVEVTDV KVTIMTPPEAAVTGYRVDVIPVNLPGENGGRLEISRNTY,AEN TGLSPGVTYYFKVFAVSHGRESKELTAQCTTKL\DAPTHLGFVN ETDSTTVLVMTPPRAGITGYRLTVGLTRRGOPRGYNVGEVSKY PLRNLQPASETVSULVAI KNONGESPKATTUGPGSISIPYN TEVTETTIVITWTPARGITGYRLTVGLTRRGOPRGYNVGEVSKY PLRNLQPASETVYSLVAI KNONGESPKATVTGPGSISIPYN TEVTETTIVITWTPARGITGYRLTVGLTRRGOPRGYNVGEVSKY PLRNLQPASETVYSLVAI KNONGESPKATVTGPGSISIPYN TEVTETTIVITWTPARGITGYRITTTPTNGQGNSLEEVV HADGSSCTF\DNLEVPGLEYNVSVTTVKDDKESVPISDGISLPV HADGSSCTF\DNLEVPGLEYNVSVTTVKDDKESVPISDGISLPV HADGSSCTF\DNLEVPGLEYNVSVTTVKDDKESVPISDGISLPV HADGSSCTF\DNLEVPGLEYNVSVTTVKDDKESVPISDTIIPAV GRMLGSISIFFLSDN\AVVLINLLPGTEVVSVSSVYEGHESTF \LKGRGKTGLDSP\TGTSDF\DITAVAVTANLPTSELTITATTPTTEYVV SIVALNGRGESPLLIGOGSTVSDVPBLEAVAPTSLLI\SWD APAVTVRYYRITYGETGGRSPVGEFTVPGSKSTATISGLKPGVV YTITYAVTGRGDSPASSKPISINYRTEIDRSGMQVTTVQMDN ISVALBSSSEVTGNRVTTT\PNNGGG\PTKTKTAGPDQTTEMTI BGILOPTVEYVVSVYANDPSGSGDLVQTAVTNIDRSGLAFTDV DVDSIKIAMESPQGVGSKYNTYSSPEGIHELPPAPDGEEDTA ELGGLAPGSEYTVSVVALHDDMESGPLIGTGSTAIPAPDLKFT QVTPTSLSAGNTPNNGLOTGYRVRYTPKEGNREINLADDS SVVUSGLMVARKYESVYALKDDITGSTAIPAPDLKFT QVTPTSLSAGNTPNNGLOTGYRVRYTPKEGNREINLADDS SVVUSGLMVARKYESVYALKDTLTSRPAQGVVTTLENVSPPRR ARVIDATETITISMGPFRRITTIVTALKNNGKSEPLIGRKTNDELP GNASTTITISLPGFGTVIVYTLNINAMSSEVVIDASTAIDAPS NLAFLATTPNSLLVSNGPPRRITTYTATATVIXKSPEGISPREVVPRR REGUTEATITISLPGFGTVIVYTLNINAMSSEVVIDASTAIDAPS NLAFLATTPNSLLVSNGPPRRITTYPTATRINGSEPLOCHGFRGGHFRCD SGROGPSVGGOMIFERHIGRATTPTTATTFURNGLOCHGRGGRIGGNGCHGCHCR RGGGSISPSEGTTGSNNQYSGRYHQRTNTNVNCPIECFMPLDVQ ADLESSEE SSRNCLDNGWNYKIGEKMDRGENGGMSGTCLGNGKGEFKCDP HEATCYDDGKTYHVAGGNOKEYLGALGCCTGNGKGEFKCDP HEATCYDDGKTYHVAGGNOKEYLGALGCCTGGNGKGCNNC RGGGGGSFSEGTTGGSNNQYSGRYHQRTNTNVNCPIECFMPLDVQ ADLESSER CTIANGCHEGGGGSYKGFAGTSTSVVGETWREVYCGGSNGRFCCSK PEAESTCPBVTTNYNCOTYESTGASKKRGNGLLLCCTCINGRG ENCCERHTSVOTTSSGSGPFTDVRAAVYQOPHPCPPYGHCUT DSGVYJSVGMGLA*KTGGNGALA\TCLTGGTSGSGRT	1	1		SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLDGPRVTIM
POAPITGYRITYSSVEGSTELMLPETANSVTLSDLQPCUQYM ITIYAVEWAGESTPVVLQQCRTGPRBSTOPSPDLQFVEVTDV KVTIMWTPPESAVTGYRVDVIPVNLPGEHQGRLPLSRNTP\AEN TGLSPGVTYYFKVFAVSHGREKGTAQTTKL\DAPTHLQFVM ETDSTVLVRWTPPRAGITGYRLTVGLTRGGPRGYNVGPSVSKY PLRHLQPASETYUSLAIRGNGESPKATGYPTTLQPSIPYMY TEVTETTIVITWTPRAGITGYRLTVGLTRGGPRGYNVGPSVSKY PLRHLQPASETYUSUAIRGNGESPKATGYPTTLQPSIPYMY TEVTETTIVITWTPPRAGITGYRLTVGLTRGGRERDPUTSDSGIV VSGLTPGVEYYYTIQVLRGGGERDAPLVTNGGGSLEEVV VSGLTPGVEYYYTIQVLRGGERDAPLVTNCGGSLEEVV VSGLTPGVEYYYTIQVLRGGERDAPLVTNCGGSLEEVV PPDTDLRFTM/ILDPTMRVTW\APPPSIDLTNFLVRSPYRNA GRMLQSLSTFISINA\CVULTNLLPGTEVVSSVYEGHESTP \LRGRKTGLDSP\TGIDFS\DITA\NSFT\VHA\LAFRA\TPTI TGYRIR\HPBIF\SGRFBD\VPHSRTTLUTLTPGTEYVV SIVALMGREESPLLIGQSTVSDVPRDLEVVAATPTSLLI\SWD APAVTVRYYRITGEGGSPSVGEFTVPGSKSTATISGLKPGVV YTITYVAVTGRGSDSPASSFISINYRTEIDLAIPDTEYVV YTITYVAVTGRGSDSPASSFISINYRTEIDLAIPDTEYVV YTITYVAVTGRGSDSPASSFISINYRTEIDLAIPDTEYVV YTITYVAVTGRGSDSPASSFISINYRTEIDLAIPDTEYVV YTITYVAVTGRGSDSPASSFISINYRTEIDLAIPDTEYVV YTITYVAVTGRGSDSPASSFISINYRTITNDRKGALFTDV DUSSIKIAMESPGGGVSRYNTYTSSEDGIUELPPAPDGEDTA ELQGLRPGSEYTVSVVALHDDMESQPLGTGYSTAIPATDLKFT GUTPTSLSAGATPPNVQLTGYRWYTPKKTGPMKSIMLARDSS SVVVSGLMVARKYEVSVVALHDDMESQPLGTGYSTAIPATDLKFT QVTPTSLSAGATPPNVQLTGYRWYTPKKTGMKSIMLARDSS SVVVSGLMVARKYEVSVVALHDTMSSPERAGOVVTTLENVSPPRR ARVTDATEITTISHBYRTEITIGFGVANGGOFTLORTSTLDAP DVSSYTITGLOPGTDYKTYLYTLINDARSSSVVUDASTADAPS NLAPLATTPHSLLVSNOPPARIOTSTITISHBYRNGOFTLORTINGP REGUTEATITGLEPGTEYTYVALANGKSEPLIGRKKTDELP QLVTLJHHNLHGPEILDVPSTVCKTFFTHREYDTPNGQG ALSQTTISMAPFQDTSEYIISCHPVATDEBPLCFRVFDETSTSAT LTGLTRGATVAIVTALAROORNINGERTYPTATTIRHPRPYPPNVGG ALSQTTISMAPFQDTSEYIISCHPVATDSVMSGLNQT DDSCFOPPTTVSHTAVGDGWCRYLGETGTGNSTGGGRGRCNCC RPGGESSPEGTTGGSYNQYSQRYHQRTNTNVNCPIECFMPLDV DSCFOPPTTVSHTAVGDGWCRYLGETGTGNSTGGGRGRCNCC RPGGESSPEGTTGGSYNQYSQRYHQRTNTNVNCPIECFMPLDV QSKPGCYDNGKHYQINQWBRTYLLGNALVCTCYGGSRGFNCESK PEARETCFDRYTNTYRYGDTYSRRBHSTGGYMLECVCLGRGSGRI CTIANGCHEGGGSYNQTSVVGGETWRCPTYGFTGHGGGGGG INCTSRNCCHDGTATSYRIGDTWSKKONRGNLLOCICTGNGG EWCCRHTSVOTTSSGSGPFTDVRAAVYQOPHPCPPYGHCUT DSGCVYSVGWGALA**TGGGMASLAV	1			VYQISEDGEOSLILSTSOTTAPDAPPDPTVDOVDDTGTUDBUGB
ITITAVEENGESTPVJQQETIGTPREDTVPSPENDLQFUEVTDV KVTIMMTPESAVTGRAVDIPALIDERDLPLSANTPI\AEN TGLSGUTYYFKVEAVSHGRESKULTAQOTTKL\DAPTHLQFUN ETDSTVLVAWTPPRAQITGYRLTVGLTRRGGPRGYKNGSVSKY PLRALGPASETTVSLVAAIRGNGSSPKATTVPTTLQFGSSIPYN TEVTETTIVITMTBARIGFKLGWREGGGRAP; MVTFLSPPTNLH LEAMPDTGVLTVSNERSTTPDITGYRITTTPTNGQGASLERVV HADGSSCTF VDNLEVPGLEVMVSVTYTVALVRDKSSVEJSPTIIDAV HADGSSCTF VDNLEVPGLEVMVSVTYTVALVRDKSSVEJSPTIIDAV PPPTDLRFTN/ILDFDTMSVTVA\APPSIDLTNFLVRYSPVKNE GRMLQSLSIPFLSDN\AVVLINLEPCTEVVVSVSVYVEYDHESTF \LGGRKGTGLDSP\TGIDFS\DITA\MSFT\UMINLAPGATYDIT TGYRIR\HHPEHF\SGRREDR\PMSRTTLINLITDTETYVV SIVALNGRESSP\LTIGGGTSVDVPRDLXAAPTSLLI\SWD APAVTRYYRITYGETGGRSPVGSFTVPGSKSTATISGLKFGVV YTITVYAVTGRGDSPASSFYISINYRTEIDSGAWPTOVDNS ISVKULPSSSPYTGRVTTT\PKNGPG\PTKTKTAGPOCTEMTI EGLOPTVEYVVSYVYANPSGESGGLVQTAVTNIDRSGAMTDVODNS ISVKULPSSSPYTGRVTTT\PKNGPG\PTKTKTAGPOCTEMTI EGLOPTVEYVVSYVYANPSGESGGLVQTAVTNIDRSGLATTDV DVDSIKIAMESPGQQVSKYRVTYSSPEGGIHELFPAPDGEEDTA ELGGLLPGSSEYTVSVVALHDDMESGPLIGTGSTAIPATDLKFT QVTFTSLSAGATPPNVOLITGYRVRVTPKEKTGPMKEINLAPDS SVVVSGLMVARKYEVSVALLDDLTSRPAQGVVTTLENVSPPRR ARVTDATETITISHSVTETETITGFQVDAVPRNGGTPLGRTIPDDLKFT QVTFSTITGLOPGTDYKIYLYTLINDRARSSSVVIDASTALDAPS MLEFLATTPNSLLVSNQPPRARITGYILKYEKGSPREVVPRR PROGTEATITISHSVTETITIVTALKNNGKSPELIGRKKTDELF CLVTLEHNNLHGPELIDVPSTVQKTFFTTHRGVDTORIQLD-FGT SGQOFSVGGOM(FIEBEIGRRTTPPTTATPITRPRPYPPNVGG SGADFSVGGOM/FIEBEIGRRTTPPTTATPIRRPRPYPPNVGG SGROFSVGGOM/FIEBEIGRRTTPPTTATPIRRPRPYPPNVGG SARNCIDNGWNYKIGEKWDRGGENGOMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGGQWGYLYGLGCCLGFGGGHRCD SRRCIDNGWNYKIGEKWDRGGENGOMSCTCLGNGKGFKCDP HEATCYDDGKTYHVGGGWGYLYGLGCLGFGGGGRGCNCCR RGGGFSFEGTTGGSNQYSGRYHQRTNTWNCPIECFMPLDVQ ADEEDSRE SGRCGVFNGKHYGINQWSRTYLCNALVCTCYGGSRGRCDSC PPGGFSFECTTGGSNQYSGRYHQRTNTWNCPIECFMPLDVQ ADEEDSRE SGRCGVFNGKHYGINQWSRTYLCNALVCTCYGGSRGRTCESK PPEAETCPDFYTTNTYNCPTFERENGENTCTLGRGGGRTS CTIANRCHEGGGGSYKIGDTWRRPHETGYMLCCVCLGNGGGHT CKPIAEKTSVOTTSSGGGFTDVRAAVYQOPHPCPPYGHCUT DSGVYJSWGMALA*TTGGRGMALVACTCURGGGGRTAUTOTYG				POAPITGYRIVYSPSVEGSSTELNI, DETANGUTT EDI ODGUGUST
KVTIMWTPPESAVTGYRVDUPVNLPGEHGGRLPLESMTP\AEM TGLSFGUTYFKVFASHGRESKPLTGYTKLOPTKLOPVN ETDGTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY PLRNLQPASEYTVSLVAIKGNGESKRATGVETTLGGSSIPYM TEVTETTIVITTTPAFIGGKLGVFRSGGGRAFEVTISGSGIV VSGLTPGVEYVYTIQVLRDGGGRDAP\IVNK\VYTLSPPTNLH LEANPDTGVLTVSMESTTPDITGYGTTPTHOGGGGSLEEVV HADGSSCTP\DNLEVPGLEYNUSVTVKDDKESVPISDTIIPAV PPTDLRFTN/ILGPDTMRVTW\APPSIDLTHFINGYSPVKNE GRMLQSLSIFFLSDN\AVVLTNLLDGTTYVVSVSSVYRGHESTE \LRGCRGKTGLDSP\TGIDFS\DITA\NSFY\UPWIAPRA\TPTI TGYRIR\HPBEHF\SGRFRBR\VPRSNSITLTNLTFOTFYVV SIVALNGRESSPLLIGGGSTVSDVPRDLEVVAATPTSLLI\SWD APAVTVRYRITYGETGGNSPVGEFTVPGSKSTATISGLKPGV YTITYYAVTGRGDSPASSKPISINYRTEIDKPSGMYDTUQDNS ISVKMLPSSSSPVTGYRVTTT\KNMPG\PYKTKTAGPDQTEMTI BGLQPTVEVVVSVYAQNPSGSSQPLVATNINDRYRGLAFTDV DVDSIKIAMESSGQQVSRYRVTYSSPEDGIHELFPAPDGEEDTA ELIGGLRPGSETYTSVVALIDDMESGJTUTGGTATIAPATDLKFT OVTPTSLSAQWTPPNVQLTGYRVTVPKEKTGPMEINLAPDSS SVVVSGLMVAIKYEVSVYALKDTLTSRPAGGVVTLENVSPPRR ARRYDDATETTITISMFKTETITGFOUNDAPPANGGTPIGRIIR DVRSYTITGLQPGTDKKITLYTIANDARSSPVVILDATAIDAPS NLAFLATTTRISLLSWBOPRRAITSJVLKEKEGSPPPEUVPRP RPGGTEATITGLEPGTTSYTIYALAKNQKSEPLIGRKKTDELP QLVTLPHPNLHGPEILDVPSTVQKTFPVTHGYDTGMGIGLPGT SGQOFSVGQOMIFEBHGFRRTTPPTTHGYRPRYPPWOGG ALSGTTISMAFFQDTSETIISCHPVGTDEEPLQFRVGTSTSAT LTGLTRGATYMI IVEALKOORKWKRETHRRPRPYPPWOGG ALSGTTISMAFFQDTSETIISCHPVGTDEEPLQFRVGTSTSAT LTGLTGRATYMI IVEALKOORKWKRETHRRPRPYPPWOGG ALSGTTISMAFFQDTSETIISCHPVGTDEEPLQFRVGTSTSAT LTGLTRGATYMI IVEALKOORKWKRETHRRPRPYPPWOGG ALSGTTISMAFFQDTSETIISCHPVGTDEEPLQFRVGTSTSAT LTGLTGRATYMI IVEALKOORKWRTTERRPRPYPPBVOGG ALSGTTISMAFFQDTSETIISCHPVGTDEEPLQFRVGTSTSAT LTGLTGRATYMI IVEALKOORKWRTSKSGFKLLCCLGFGSGHRCDKC RPGGESSFEGTTGGSNQYGGRYAGTTNTNVNCPIECFMPLDVQ ADREDSTE GRGGFFDFTGTTGGSNQYGGRYAGTTNTNVNCPIECFMPLDVQ OSKPGCYDNGRHYGUTGDTFGASKKRORGMLDCTCLGAGGGIS CTIANCCHEGGGSYKIGDTMRFRETOGYMLECVCLONGGGIS CTIANCCHEGGGSYKIGDTMRFRETOGYMLECVCLONGGGIS CTIANCCHEGGGSYKIGDTMRFRETOGYMLECVCLONGGGIS CTIANCCHEGGGSYKIGDTMRFRETOGYMLECVCLONGGGIS CTIANCCHEGGGSYKIGDTMRFRETOGYMLECVCLONGGGIS CTAANCCHEGGGSKIGDTMRFRETOGYMLECVCLONGGGIS CTAANCCHEGGGSKIGDTMRFRETOGYMLE	1	1		ITIYAVEENOESTPVVIOOETTCTPDengunenppi Approximent
TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVM ETDSTVLVUKWTPPRAQIT GVRLTUGHTGQPRQYMYGSVSKY PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYM TEVTETTIVITHTPAPRIGFKLGVRPSQGGARAFEVTSDSGSIV VSGLTPGVEYVTTIQLVLDQGGRDAP JVMK\VVTPLSPPTNLH LEAMPDTGVLTVSMERSTTPDITGVRITTPTMGQGGNSLEEVV HADQSSGTP\DALEVGLEVTNSVTVLDKOSEVPJSDTIIPAV PPPTDLRFTM/ILGPDTMRVTW\APPSIDLTNFLVRYSPVKNE GRMLQSLSIFFLSDN\AVVLTNLLDGTTYVUSVSSYFQCHESTTP \LLGRQKTGLDSP\TGTFS\DTF\JNFT\VJM\ATAPRA/TPI TGVRIR\HHPEHP\SGRPESBR\VPHSRNSITLTNLTPGTEYVV SIVALNGRESSPLLIGQGSTVSDVPGHVVAATPTSLLI\SWD APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKRGVD YTITVYAVTGRGDSPASSKPISINNTETINLTPGTEYVV SIVALNGRESSPLUGGQSTVSDVPGFQFYTKTHAGPDOTEMTI EGLQPTVEVVSVYAQNPSGESQDLVQTAVTNIDRFKGLASTDV DVDSIKLAMESSPQGVSYRVTYSSPEDGHTLFPAPDGEEDTA ELQGLRPGSEYTVSVVALIDDMESGPLIGTQGTAIPAFDGEEDTA ELQGLRPGSEYTVSVVALIDDMESGPLIGTQGTAIPAFDLKFT QVTPTSLSAQHTPPNVQLTGYRVRYTERETGPMERINLAPDGS SVVVSGAMVATKYEVSYALKDTLIRSQVVVTLENSPPR ARVTDATETITISWRTKTETITGFOVDAVPANGGTPIGRTIKP DVRSYTITIGLOPGTDKKYLYTYLANDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSWQPPRARITSTIIKYERGSPPREVVPRP REGGTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP QLVTLPHNILGPEILDVSTVQKTPTHEYGDTGMGIGLPGT SGQQPSVGQOMIFEBHGFRETTPPTTATPIRRPPRPYPPNVQD ALGOTTISMPFQDTSSYIISCHPWGTDEEPLQFRVPGTSTSTAI LTGLTRGATYNIIVELKDOQRHKYREVVTVGNSVEGGLNQFDT DDSCPPPTTVSHYAVGDBMENNSSGFKLLCCLGFGSGHFRCD SSRNCHBNOWNYKIGEKMPRQGENCOMFCLGKKGDFT DDSCFPPTTVSHYAVGDBMENNSSGFKLLCCLGFGSGHFRCD SSRNCHBNOWNYKIGEKMPRQGENCOMFCLGKGRGNFS PSHKCHDNOWNYKIGEKMPRQGENCOMFCLGRKGGFEKCDP HEATCYDDGKTYHWGDFWGRYSFLAGALCSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGGSYNQSGYRYRTTNTNVCTIECFMBLDVQ QSKPGCYDNGHVANGTVGDTYFERNADCTCLGRKGGFSIS PSHKCHDNOWNYKIGEKMPRQDENCYMANDCTCLGRKGGRIS CTIANNCHEGGGGFTGASGKRGPAATTSLULCIPSVPPPPFFTLMP PSHWRGDPFGGIRRDFSRLREEANLANATCLGVGRSGFNCESK PRAEETCFDKYTGNTTRVGDTYFERNADCTCLGRGGGIS CTIANNCHEGGGGSYKIGDTWRPHETGGYMLECVCLGNGKGBIF CKPIANGTSYVGTTSSSSGPFTDWRANVYQCQPHPOPPTGHCVT DSGVYYSVGMLA**TROGDYKGML*CTCLGRGGGSGFTGGGG ENKCERHTSVGTTSSSSGPFTDWRANVYCOCCHORGGGIS TCTSRNCCHDQDTRTSVRIGDTWRANVYCOCCHOPPPTGHCVT DSGVYYSVGMLA***TOCCHKGMCMCMCTCLGGGGGGFRCCO	1			KVTIMWTPPESAVTGYPUDUT DUNIT DOBUGODY DE COMPE'
ETDSTYLVRWTPPRAQITGYRLIVGLTRRGQPRQYNVGPSVSKY PLRNIQPASEYYSULAI KONDSSIRAVPITLQPGSSIPYN TEVTETTIVITWTPAPRIGPKLGVRPSQGGAPREVTSDSGSIV VSGLTFGVEYYTIQVLRDGQGRDAP, LYNK, VVTLSSPPTNLH LEANPDTGVLTVSMERSTTDDITGYRLTTTPTRGQCGRSLEEVV HADQSSCTF\DNLEVPGLEYNVSVTVKDDKSEVJSDTIIPAV PPPTULRFIN/ILGPTMRYTW\ADPSILDTHFLWYSPYDYND GRMLQSLSIPFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP \LRGQRKTGLDSP\TGIDFS\DITA\NSFY\UNH\ARPA\TPI TGYRIR\HHPEHF\SGRPREDN\VPHSNSITITNLTFGTYVV SIVALNGRESSFLIGQQSTVSDVPRDLEVVAATPTSLLIN\SWD APAVTVRYTRIYGGTGNSPVQETFVSSSTATISGLKFGVD YTITVYAVTGRGGDSPASSRPISINVRTEIDKPSQMQVTDVQDNS ISVKMLPSSSPVTGRYNTT\PKNOPG\PTIKTKTAGPDQTEMTI EGIQPTVEVVVSVYAQNPSGESQPLVQTAVTNIDRFKGLAFTDV DVDSIKIAMESPQQVSRYRVTYSSPEDGIHELFPAPDGEEDTA ELIGGLRAPSEYTVSVVALDDDMESQFLTGGSTATAPDLKFT QVTPTSLSAQMTPPNVQLTGYRRVTYSPEDGIHELFPAPDGEEDTA ARVIDATETITISMSFYGTYNTYSPEDGIHELFPAPDGEEDTA ARVIDATETITISMSFYGTYNTYSPEDGIHELFPAPDGEEDTA ARVIDATETITISMSFYGTYNTYSPEDGIHELFPAPDGEEDTA ARVIDATETITISMSFYGTYNTYNLDNARASSPVUTIENVSPFRA ARVIDATETITISLBGTEYTIYVIALKANGKSEPLIGRKKTDELF QLATLPHNLIGPSELDVSTVKYTPYTHPRYDTGRGIQLFGT SGQQPSVQQMIFEEHGFRRTTPPTTATPIRKFRPPYPRVGGE ALSQTTISMAFFQDTSEYIISCHVGTDEEPLQFRVOTSTSAT LTGLTRGATYNIIVELLDVSTVKYTHGSVTGGIQLFGT SGQQPSVQQMIFEEHGFRRTTPPTTATPIRKTRPRPYPRNGGE ALSQTTISMAFFQDTSEYIISCHVGTDEEPLQFRVFGTSTSAT LTGLTRGATYNIIVELLKOQORKWREYTGGALGSCTCLGNGGGFRCD SSRKCHBNGVWAYKIGKWBROGGENGQMMSCTCLIGNGKGEFKCDP HEATCYDDGKTYHVGEQWGKSYLGALGSCTCFGGGRGRCDNGR RPGGESPEGTTGGSYNQYSGRYARTNTNVNCPLECFMBLDVQ ADREDSER PSEMROPPGGIRRDFGRASKKGPAATTSLVLCIFSVPPPVPFFTLMF PSEMROPPGGIRRDFGRASKKROPAGHVDCTCLGAGGRIS CTIANGCHEGGGSYKIGDTMRPHETGGYMLECVCLONGKGBKT CKPLAKECFPHAAGTSYVVGETWEKPYQGWNDCTCLGAGGRIS CTIANGCHEGGGSYKIGDTMRPHETGGYMLECVCLONGKGBKT CKPLAKECFPHAAGTSYVVGETWEKPYQGWNDCCLCIGNGGGIS CTIANGCHEGGGSYKIGDTMRPHETGGYMLECVCLONGKGBKT CKPLAKECFPHAAGTSYVVGETWEKPYQGMVDCCLGIGNGGGGGF EMCCERHTSVGOTTSSASGPFTDWAAVYQPQPPHOPPPFGHCVT DSGVVYSVGOTTSSASGPFTDWAAVYQPQPPHOPPPFGHCVT DSGVVYSVGOTTSSASGPFTDWAAVYQPQPPHOPPPFGHCVT DSGVVYSVGOTTSSASGPFTDWAAVYQPQPHOPPPFGHCVT DSGVVYSVGOTTSSASGPFTDWAAVYQPQPPHOPPPFGHCVT	1	1		TGLSPGVTVVFKVFAVGUGDECKDI MAGORMUT AND DOCUMENT
PLRNIQPASSTYTSUVALKGKGSPKATGYPTLQPGSSIPYM TRVTETTIVITMTPAPRIGPKGKAPREVTSDSGSIV VSGLTPGVEYVYTIQVLRDGQGRDAP\IVNK\VYTELSPPTNLH LEAMPDTGVLTVSWERSTTPDITGYRTTTPTMGQGGMSLEEVV HADOSSCTP\DNLEWPGLEYMVVYLDDKESVJESTIIPAV PPPTDLAFTN\ILGPDTMVTW\DNLFGTFVVVSVSVYEQHESTP GRMLQSISIPFISDN\AVVLTNLLPGTFVVVSVSVYEQHESTP \LRGRQKTGLDSP\TGIDFS\DLTA\NSFT\VHM\IAPRA\TPI TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTKLTFGTFYVV SIVALNGRESSPLIGQGSTVSDVFBLEVVAATFISLLI\SWG APAVTVRYRITGETGGNSPVQBFTVVGSKSTATISGLKRGVD YTITVAVTGRGSPASSRPISINNTRTIDKSQMQVTDVQDNS ISVKWLPSSSPVTGTVTTT\PNNGPG\FTEKTKTAGPDQTEMTH EGLQPTVEYVVSVYAQNSSGSQPLVQTAVTNIDRPKGLAFTDV DVDSIKLAMESSQGVGSRYRVTYSEDGIHELPPADGEDTA ELQGLRPGSEYVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT QVTPTSLSAQWTPPNVQLIGYRVRVTPKEKRPWEINLAPDDS SVVVSGLMVATKYEVSVYALNDDMESQPLIGTQSTAIPAPTDLKFT QVTPTSLSAQWTPPNVQLIGYRVRVTPKEKRPWEINLAPDDS SVVVSGLMVATKYEVSVYALNDTLAFRPAQGVVTILENVSPPRR ARVTDATETITISSRTKTEFITGFQVDAVPANGGTFIQRTIKP DVSSYTITGLQFGTDYKIYLYTLANANSESPVULDATALDASS NLAFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP REGUTEATITGLEPGTFYTIYVIALKNNKSEPLIGKKTDELP QLVTLPHPNLHGPEILDVDSTVQKTFVTHPGYYDTGGIQLPGT SGQQPSVGQOMIFEEHGFRRTTPPTTATFIRRRPPYPPNVGDE ALGGTTJSMAPFQDTSEYIIGHDFSFLOCKGFGCGLGFGSGHFRCD SSRWCHDNGVNYKIGEKNDQGENGQMSCTCLONGGFFKCD HEATCYDDGKTYHVGEQWGKEYLGAICSCTCFGGGGRWGCDNGR RGGEBSPFGTTGOSYNQYSQRYHQRTNTWNVCPIECFMPLDVQ ADREDSRE \$103 RLCCTGGGEGTPGASGKRGFAATTSLVLCIPSVPPPFFTLMP PPSWRROPPGGIRIDFSRLRREANLVATCLPVRASLPHRLMNL RGFGFGLLLLAWLCLGTAVPSTGASKSRQAQMVQPQSPVAVS QKPGCYDNGKHYQINQQMERTYLGNALVCTCLYGGSGFFNCESK PPSERETCPKYTGNTYRCDTTTERFKDSMIMDCTCLGGGRGFIS CTIANRCREGGGSKLGDTWRPHETGGYMLECVCLGNGKGBWT CKPLARCKFPOHAAGTSTVVGETWERPYGMMMUDCTCLGGGRGRI CTIANRCREGGGSKLGDTWRPHETGGYMLECVCLGNGKGBWT CKPLARCKFPOHAAGTSTVVGETWERPYGMMMUDCTCLGGGRGRI CTIANRCREGGGSKLGDTWRRPHETGGYMLECVCLGNGKGBWT CKPLARCKFPOHAAGTSTVVGETWERPYGMMMUDCTCLGGGRGRI CTIANRCREGGGSKLGDTWRRPHETGGYMLECVCLGNGKGBWT CKPLARCKFPOHAAGTSTVVGGTWERPYGMMMUDCTCLGGGRGRI CTIANRCREGGGSKLGDTWRRPHETGGYMLECVCLGNGKGBWT CKPLARCKFPOHAAGTSTVVGGTWERPYGMMMUDCTCLGGGRGRI CTIANRCREGGSFTVCTSSGGFFTUVRAAVYOPPOPPPPPPTGHCVT DSGVV		1		ETDOTTI I I WETDODA OLITICADE MICHINDO CONTROLO
TEVTETTIVITMTPAPRIGERGNAP\UNK\VVTPLSPPTNLH VSGLTPGVEVYTIOVLREGGERDAP\UNK\VVTPLSPPTNLH LEANPDTGVLTVSWERSTTPDITGYRITTIPTNGGGRSLEVV HADGSSCTP\DMLEVPGLEYNVSYYTVKDKESVPISTIIPAV PPPTDLEFTNT/LIGPTRYTW\MPPSIDLINFRYSPVKNE GRMLQSLSIFFISDN\AVVLTNLLPGTEVVSVSSVYEQHESTP \LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHM\IAPRA\TPI TGYBIR\HHPEHF\SGRPREDR\PYPGSKTATISGLKPGVD SIVALNGREESPLLIGQGSTVSDVPRDLEVVAATFISLI\SWD APAVTVXYRITYGETGGNSPVDETYPGSKTATISGLKPGVD YTITYYAVTGRGDSPASSKPISINYRTEIDKPSGWQVTDVQDNS ISVKWLPSSSPVTGYRVTTT\PKNGGG\STWKTAGGDQTEMTI BGLQPTVEVVVSVYAQNDSGESGPLVQTAVTNIDRPKGLAFTDV DVDSIKIAMESPQGQVSRYRVTYSSPEDGIHELPPAPDGEEDTA ELQGLRPGSSYTVSVVALHDDMESQPLIGTGSTAIPAPTDLKFT QVTPTSLSAQWTPPRVQLITGYRVYTPKKRGPMPETULAPDS SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTLENVSPPRR ARVTDATETTIISHSWTKTETITGFODAVPANGGTPIQRTIKP DVRSYTITGLQPGTDYKIYLYTINDNARSSPVVIDASTATDAPS NLAFLATTPNSLLVSWQPPRARITGYITKYERGSPPREVVPRP REGVTEATITGLEPGTEYTIYVLANNKSEPLIGRKKTDELP QLVTLPHPALHGPEILDVPSTVQKTPFVTHPGVDTGGGLQLPGT SGQQPSVQQQMIFEEHGFRRTTPPTTATPIRHRPRYPPRVGGE ALSGTTISMAPFQDTSEYIISCHPVGTOEBELQFRVPGGTSTSAT LTGLTRGATYNIIVEALKDQGRKKYBEVVYVGRSVREGLNOPT DDSCFPDYTVSHYAVGDBWRMSESPKLLCOCLGFSGHPRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHYGEGWGEYLGAICSCTGGGGRGRGCDNG RPGGESPEGTTGGSYNQYSGRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE 5366 703 RLCCTGGGGGTPGASKRGFAATTSLVLCIPSGGGRRCDNG RPGGGESPFGTTGGSTNAYSGGTYHGNANVCTCTYGGSRFFNCESK PSHEBSPFGTTGGSYNQYSGRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE CTIANRCREGGGSKLODTWRPHETGGYMLECVCLGNGKGEFKC PPEBETCFDKYTGNTYKVCDTYTERKFSMHIDCTCIGAGGRGIS CTIANRCREGGGSKLODTWRPHETGGYMMUDCTCLGGGGR ICTIANRCREGGGSKLODTWRPHETGGYMMUDCTCLGGGGR CTIANRCREGGGSKLODTWRPHETGGYMMUDCTCLGGGGR ITCTSNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGRGGR ITCTSNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGRGGR ITCTSNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGRGGR ITCTSNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGRGGR ITCTSNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGRGGR EKKCRHTSVQTTSSGGFFTOVRAAVYQDPRQPPPPYGHCVT DSGVVYSVGMAU'AFCGGSKGALTOTTGTGGTWGMTDDTCTCLGGGGGR				DI DNI ODA CEVENOVI IN THE TOTAL THE
VSGLTFOVEVYTIOURENGGERDAP, IVNK, VVTPLSPPTNLH LEAMPDGGVLTVSWERSTTPDITGYRITTPTTMGQCGMSLEVV HADQSSCTF\DNLEVPGLEYNVSVTVKDKSSVPISTIIPAV PPPTDLRFTN\ILGPTMRVTW\APPSIDLTMFLVRYSPVKNE GRMLQSLSIFFLSM\AVVLTNLTGTVVVSSVYVEQHESTP \LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA\TPI TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTLLTGTTYVV SIVALNGRESSPLIGQGSTVSDVPRDLEVVAATFTSLII\SUKP APAVTVRYRITTGETGGNSPVQEFTVPGSKSTATISGLKPGVD YTITVYAVTGRGSPASSKPISINYRTEIDKSGMQVTDVQDNS LSVKULPSSSPVTGVRVTTT\PKNGC\PTKRTKIGPOTEMTH EGLOPTVEYVVSVYAQNSGESQDLVQTAVTHIDRPKGLAFTDV DVDSIKIAMESPQGVSRYRVTYSSPEDGIHELPPAPDGEEDTA ELQGLRPGSEYTVSVVALHDDMESQPLIGTGSTAIPAPTDLKFT QVTPTSLSAQMTPPNVQLTGYRVRVTPKEKTGPMEINLAPDGS SVVSGIMMATKYEVSVYALKDTLIKYEKGSPPEVVPPP RARVTDATETITISMRTKTETITGFQVDAVPANGGTPIGRTIKP DVRSYTITGLGPGTDYKIYLYTLNDNARSSPVUIDASTAIDAPS NLRFLATTYPNSLUSWGPPRAR ITG;KYEKGSPSPEVVPPP REGGTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP QLVTLPHPNLHGPBILDVFSTVGKTFFVTHRGYDTGMGIQLPGT SGQQPSVGQOMIFEHGFRRTTPTTRIRRRPRPYPNVGGE ALSGTTISMAPFQDTSEYIISCHPVGTDEFELGRKKTDELP COUTLINGREFIKENDINGTURT DDSCFPPYTVSHYANGDEMBRMSESGFKLLQCLGFGSGHFRCD SSRNCHDNGVNYKIGEKNDRGGENGMMSCTCLONGKGFFKCDP HEATCYDDGKTTHVAGENDRAGGENGGMNSCTCLONGKGFFKCDP HEATCYDDGKTTHVAGENDRAGGENGGMNSCTCLONGKGFFKCDP HEATCYDDGKTTHVAGENDRAGGENGGMNSCTCLONGKGFFKCDP HEATCYDDGKTTHVAGENGRAGGENGGMNSCTCLONGKGFFKCDP RPGGPSPEGTTGGSYNQVSQRYHQRITNTNNCPIECFMPLDVQ ADREDSRE 5366 703 RLCCTGGGGTFGASGKRGPAATTSLVLCIPSVPPPVPFFTLMP PPSWRQPPGGIRNDFSRLRREANLVATCLPVRASLPHRIMML RGGGPSPLLLLLAVLCLGTAVPSTGASKSKRQAQOMVQPQSPVAVS QSPGCYDNGHHYQINQOMENTYLAUNCTCYGGSGFNTCSK PEAEETCPDKYTGNTYRVGDTYERPKDSMIWDCTCTGAGGRGRIS CTIANNCCHGGGGSKLGDTWRPHETGGYHLECVCLGNGKGEWT CKFJARKCNDQDTRTSYRIGDTWSKKDNRGNILQCICTGNGRG EWKCERHTSVQTTSSGGGFTUVRAAVYQPOMPQPPPYGHCVT DSGVVYSSVGMOLA*KTGGSKGFTUVRAAVYQPOMPQPPPYGHCVT DSGVVYSGVGMCLA*KTGGSKGFTUTSKATUTGTYGGGGFTUTSK	1			PERNEQPASETTVSEVATKGNQESPKATGVFTTLQPGSSIPPYN
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HADGSCIF\DNIEVEGLEYNGVTVKDDKESVPISDTIIPAN PPPTDLRFTH/ILGPDTMRTW\APPPSIDITNIPSYPVKNE GRMLQSLSIFILSDN\AVVLTNLLDCTSYVVSUSSVYEQHESTE \LRCQRKTGLDSF\TGIDFS\DITA\NSFT\VHH\IAPRAYFPI TGYRIR\HHEHEH\SGRPREDB\VPHSRNSITLINLTPGTEYVV SIVALNGREESPLLIGQGSTVSDVPRDLEVVAATPTSLLI\SWD AFAVTVRYYRITGETGGKSPVQEFTVPESKSTATISGLKFGVD YTIITVAVTGGESPASSKPISINVRTBIDRYSGMQVTDVQDNS ISVKMLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI EGGLQPTVEYVVSVYAQNDSGESQPLVQTAVTNIDRYKGLAFTDV DVDSIKLAMESSGQQGSRYRVTYSPEDGIHELPPAPDGEEDTA ELQCLRPGSSYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT QVTPTSLSAQWTPPNVQUTGYKVRVTPEKTGEMKEINLAPDSS SVVVSGLMVATKYEVSVYALKDVLITSRRAGGVVTLENVSPPRR ARVTDATETITISMRTKXETITGGVDAVPANGGTPIQRTIKP DVRSYITIGLQPGTDYKIYLYTLNUANRSSPVIDASTAIDAPS NLARLATTNSLLVSWQPPRRRITGYIIKVEKGSPPREVVPRP RPGYTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP OLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVGQOMIFEBHGFRRTTPPTTATPIRHPRFYPPNVOQE ALSGTTISMAPFQDTSEYIISCHPVGTDESPLOFRVPGTSTSAT LTGLIRGATYNIIVSALKOQORKVYREVVTVGNSVNEGLNQTP DDSCFDPYTVSHYAVGDEWERMSSEGFKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKWDRGGENGQMMSCTCLGNGKGFKCDP HEATCYDDGKTTHVGEQWGKSYLGIGSCTCTGNGKGFKCDP HEATCYDDGKTTHVGEQWGKSYLGIGSCTCTGNGKGFKCDP HEATCYDDGKTTHVGEQWGKSYLGIGSCTCTGNGKGFKCDP PPSWRROPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGGGPGLLLAVLCCGTAVPSTGASKSKQAQQMVOPOSPVAVS QSKPGCYDNGKHYQINQWGRTYLDAVCTCLGGRGGRIS CTIANRCHEGGGSYKIGDTWRRPHETGGYMLECVCLGRGKGEWT CKPIARCHEGGGSYKIGDTWRRPHETGGYMLCCCLGRGRGRIS CTIANRCHEGGGSYKIGDTWRRPHETGGYMLCCCLGRGRGRG ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSPFIDVRANYQOPPHPCPPPPGGCTT DSGVVYSVGMOLA*KTQGNGKDL\CTCTCGCGCETAVTGTYG	1			VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
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GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVUSVSSYYEQHESTE \LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\lapra\TPI \TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITITNLTPGTEYVV SIVALNGRESEPLLIGQSTYSDVPRDLEVVAATPTSLLI\SND APAVTVRYYTYTGETGGNSPVGSKTATISGLKPGUD YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI BGLQPTVEYVVSYVAQNPSGPLVQTAVTNIDRPKGLAFTDV DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA ELQGLRPGSSYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT QVTPTSLSAQMTPPNVQLITVRVTYFKEKTGPMKBINLAPDS SVVVSGLMVATKYEVSVYALKDTLTSRPAGGVVTTLENVSPPRR ARVYDATETTITISWRTKTETITGFQDAVPANGGTPIQRTIKP DVRSYTTGLGPGTDYKIYLIDDARSSPVIDASTALDAPS NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP RPGVTEATIGLEPGTEYTIYVIALKNNQKSEPLIGTKKTDELP GLYTLPHPNLMFGEILDVSTVAFFVYHDEYDTONGLOLPGT SGQQPSVGQWIFEHGFRRTTPPTTATPIRRPRPYPPNVQGE ALSQTTISWAPFQDTSEYIISCHPVGTDEFLQFRVFGTSTSAT LTGLTRGATTNITVEALKDQRKKVREEVVTVGNSVREGLNQFT DDSCFPPYTVSHYAVGDEWERWSESGFKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKWDRQGENCGMMSCTCLGNKGEFKCDP HEATCYDDGKTYHVGERWGKEVIGATCSCTCFGGGGRGRCDNCR RPGGEFSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE FLCCTGGGETPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGIRNDFSRALRREANLVATCLPVRASLPHRLNML RGPGFGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPSPVAVS QSKPGCYDMSKHYONQWSGYSTYCNSNWEDCVCLGRGGGRGIS CTIANRCHEGGGSYKIODTWRPHETGSYMLECVCLGRIGGERIS CTIANRCHEGGGSYKIODTWRPPETGSYMLECVCLGRIGGERIS CTIANRCHEGGGSYKIODTWRPPETGSYMLECVCLGRIGGERIS CTIANRCHEGGGSYKIODTWRPPETGSYMLECVCLGRIGGERIS CTIANRCHEGGGSYKIODTWRPPETGSYMLECVCLGRIGGERIS CTIANRCHEGGGSYKIODTWRRPHETGSYMLECVCLGRIGGERIS CTIANRCHEGGGSYKIODTWRRPHETGSYMLECVCLGRIGGERIS CTIANRCHODDTRTSYRIGDTWSKKDNRGNLLQCICTGVRGG EWKCERHTSVOTTSSGGGFTTUVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGWQLA*KTQGGNACVLCCCTTGVTGYG EWKCERHTSVOTTSSGGGFTTUVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGWQLA*KTQGGLA*KTQCANGALCCCCTTAVTTYG	1			HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
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CLEGRGKTGLDSP\TGIDFS\DITA\MSFT\VIW\LAPRA/TPT TGYRR\HPPEHF\SGRPREDR\VPHSRNSITLTNITGTETYVV SIVALNGREESPLLIGQGSTYSDVPRDLEVVAATPTSLIL\SND APAVTVRYYRITYGETGGNSPVDEFTVPGSKSTATISGLKPGVD YTITYYAVTGRGDSPASSKPISINYRTEIDKPSGMQVTDVQDNS ISVKMLPSSSPVTGYRVTTT\PKNGGC\PTKKTKTAGPDGTEMTI EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA ELQGLRPGSSYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT QVTFTSLSAGMTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS SVVVSGLMVATKYEVSVYALKDTLTSFAPAGGVTTLENVSPPRR ARVTDATETITISMRTKTETITGFQVDAVPANGGTPIQRTIKP DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSMQPPRARITGYIIXYEKPGSPPREVVPRP RPGVTEATITGLSPGTEYTYLALKNNOKSEPLIGRKKTDBLP QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGMGIQLPGT SGQQPSVGQGMIFEBHGFRRTTPPTTAFTIRRPRPYPPNVAGE ALSGTTISMAPFQDTSEYTISCHPVGTDESPLCFWPGTSTSAT LTGLTRGATYNIIVEALKDQORHKVREEVVTVGNSVNEGLNQPT DDSCFPPYTVSHTAVGDEWERMSESGFFLLCQCLGFGGGHRCD SSRKCHDNGGNYKIGEKUNGGENGGMMSCTCLGNKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGGGRRCDNCR RPGGFBSPEGTTGGSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE 5366 8066 703 RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGFGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDMGKHYQINQWERTYLCNALVCTCYGGSRGFNCESK PEAEFTCFDKYTGNTTRVQDTYERPKDSMIMPCTCLGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGMKGEWT CKPIAEKGPÜHAAGTSYVVGETWERPYQGMMVDCTCLGAGGGRI CTIANRCHEGGGSYKIGDTWRRPHETGGYMLECVCLGMKGEWT CKPIAEKGPÜHAAGTSYVVGETWERPYQGMMVDCTCLGGGSGR ITCTSRNRCNDDDTRTSYRIGDTWRRPHETGGYMLCCVCLGRAGGEWT CKPIAEKGPÜHAAGTSYVVGETWERPYQGMMVDCTCLGGGSGR ITCTSRNRCNDDDTRTSYRIGDTWRRPHETGGYMLCCVCLGRAGGEWT CKPIAEKGPÜHAAGTSYVVGETWERPYQGMMVDCTCLGGGSGR ITCTSRNRCNDDDTRTSYRIGDTWRRMVDCTCLGGGGGRIS EWKCERHTSVQTTSSGSGPFTDVRAAVYDQPHPROPPYGHCVT DSGVVYSVGMQLA**KTQGNKGML\CTCLGROVSCQCTAVTTTYG				GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEOHESTP
TGYRIR\HHPEHF\SGRPREDR\UPHSRNSITLTNLTPGTEYVV SIVALNGREESPLLIGQGSTVSDVPRDLEVVAATPTSLLI\SMD APAVTVRYYRITYGETGGNS PVQEFTVPGSKSTATISGLKPGVD YTITYYAVTGRODSPASSKPISINYRTEIDKPSQMQVTDVQDNS ISVKMLPSSSPVTGYRVTTT\PKNOFG\PTKTKTAGPDQTEMTI EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV DVDSIKIAWESPQGVSRYRVTYSSPEDGIHELFPAPDGEEDTA ELQGLRPGSEYTVSVVALHDDMESQPLGTQSTAIPAPTDLKRT QVTPTSLSAGAMTPPNVQLTWRVTPYREKTGPMKEINLAPDSS SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR ARVIDATETTITISWRTKTETITGFQVDAVPANGGTPIQRTIKP DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP RPGGTEATITGLEPGTEYTIVVIALKNOKSEPLIGRKKTDELP QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVGQMIFEEHGFRRTTPPTTATPHRRPRPYPPNVGQE ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT LTGLTRGATNNIIVEALKDQORHKVREEVVTVGSVREGLNQPT DDSCFPPYTVSHYAVGDEWRMSSSGFKLLOCLGFGSGHPRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGGRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE 5366 6066 703 RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGIRGDFSRCLRREENLVATCLPVRASLPHRLINML RGFGGGLLLLAVLCLGTAVPSTGASKSKROAQOMVQPSPVAVS QSKPGCYDNGKHYQINQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYTERPKDSMIMDCTCIGAGRGFIS CTIANRCHEGGSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGMMVDCTCLGBGSGR ITCTSRNCNDQDTRTSYRIGDTWSKKDNRGNLLOCICTGNRGG EWKCEHTSVQTTSSGSGFTTDVRAAVYQDQPPHPQPPPFGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGRGVSCOPTAVYQTYG	1	ľ		\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPT
SIVALNGREESPLLIGQGSTVSDVPRDLEVVAATPTSLLI\SMD APAVTVRYYRITYGETGGNS PVQEFTVPGSKSTATISGLKPGVD YTITYYAVTGRGDSPASSKPISINYRTEIDKBSQMQVTDVQDNS ISVKWLPSSSPVTGRVTTT\PKNGPG\PTKYKTAGPDQTEMTI EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDR KGLAFTDV DVDSIKLAWESPQGQVSRYRVTYSSPEDGIHELFPAPPGEEDTA ELQCLRPGSEVTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT QVTPTSLSAQWTPPNVQLIGTVRVATPKEKTGPPMEINLAPDSS SVVVSGLMVATKYEVSVYALKDTLTSRPAGGVTTLENVSPPRR ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP DVRSYTITGLQPGTDYKIYLYTLHDNARSSPVVIDASTAIDAPS NLAFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP QLVTLPHPNLHGPBILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRRPRPPPPPNVQQE ALSQTTISWAPFQDTSEYIISCHPVGTDEBFLQFRVPGTSTSAT LTGLTRGATNNIIVEALKDQQRHKVREEVVTVGNSVREGLNQPT DDSCFDPYTVSHYAVGDEWBERMSESGPKLLCQCLGFGSGHFRCD SSRWCHDNGWNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRWCDNCR RPGGEPSPEGTTGQSYNQVSQRYHQRTNTNVNCPIECFMPLDVQ ADREDGRE 5366 8066 703 RLCCTGGGGGTPGASGKRGPAATTSLVLCIPSVPPPVFFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLINML RGFGGGLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFPKYTGNTYRVGDTYBERPKDSMIMDCTCIGAGRGFIS CTIANRCHEGGGSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYGGRMMVDCTCLGBGSGR ITCTSRNCCNDQDTRTSYRIGDTWSKKDNRGNLLCCICTGNGRG EWKCENHTSVQTTSSGGGFTTDVRAAVYQPQPPPPPPFPCHVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGRGSCFRAVTGTYG	ļ .	J J		TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLINI,TPGTEYIN
APAVTVRYYRITYGEGGRS PVOEFTVEGSKSTATISGLKPGVD YTITYYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTUQDNS ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI EGLQFTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV DVDS IKIAWESPGGVSRYRVTTSSPEDGHHELPPAPDGEBDTA ELQGLRPGSETYVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS SVVVSGLWVATKYEVSVYALKDTLTSRPAGGVVTTLENVSPPRR ARVTDATETITISWRTKTETITGFQVDAVPANGQTPIQRTIKP DVRSYTITGLOPGTDYKYLYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTPNSLUSWQPPRARITGYIIKYEKPGSPPREVVPRP REGVTEATITGLEPGTETTIYVJALKNNQKSEPLIGRKKTDELP QLVTLPHPNLHGPEILDVPSTVQKTPPVTHEGYDTGGIQLPGT SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPPYPNVGQE ALSGTTISWAPFODTSEYIISCHPVGTDEEPLOFRVFGTSTSAT LTGLTRGATYNIIVEALKDQGRKKVREEVVTVGNSVNEGLNQPT DDSCFPPYTVSHYAVGDQRKKVREEVVTVGNSVNEGLNQPT DDSCFPPYTVSHYAVGDGWKEVLGAICSCTCFGGGRGWRCDNCR RPGGEPSPECTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE \$366 703 RLCCTGGGGGTPGASGKRGPAATTSLVLCIPSVPPPYFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLINML RGFGPGLLLLAVLCLGTAVPSTGASKSKRQAQMVQPOSPVAVS QSKPGCYDNGKHYQINQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYTERPKDSMINDCTCIGAGRGRIS CTIANRCHGGGSYKLGDTWRRPHETGGWMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSVVVGETWERPYGGWMMVDCTCLGAGRGGRI CTIANRCHGGGGSYKLGDTWRRPHETGGWMLCCTCTGAGRGGRI CTIANRCHGGGGSYKLGDTWRRPHETGGWMLCCCLGGRGGEWT CKPIAEKCFDHAAGTSVVVGETWERPYGGWMMVDCTCLGAGRGGRI CTIANRCHGGGGSYKLGDTWRRPHETGGWMLCCCLTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPPPPGPPYGHCVT DSGVVYSVGMQLA*KTGGNKGML\CTCLGIGGSCETAVTOTYG	1		'	SIVALNGREESPLLIGOOSTVSDVPRDI.EVVAATPTSLITI SWD
YTITYYAVTGGGDSPASSRISINYRTEIDKPSQMQVTDVQDNS ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTXTKTAGPDQTENTI BGLQPTVEYVVSVYAQNPSGESQBLVQTAVTNINPRGLAFTDV DVDSIKIAWESPQGQVSRYRVTYSSPEDGHELFPAPDGEEDTA ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS SVVVSGLMVARKYEVSVYALKDTLITSRPAQGVVTTLENVSPPRR ARVIDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP DVRSYTITGLOPGTDYKIYLYTHDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSWQPYRALNTQYIIKYEKPGSPPREVVPRP RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVQQQMIFEEHGFRRTTPPTTATPITAHPRPYPPNVQQE ALSQTTISWAPFQDTSEYIISCHPVGTDEBPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVVTVCNSVMEGLNQPT DDSCFDPYTVSHYAVGDBWERNSESGFKLLQCLGFGSGHPRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGFFKCDP HEATCYDDGKTYHVGEOWQKEYLGALCSCTCFGGQRGWCCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDGRE 5366 8066 703 RLCCTGGGGGTPGASGKRGPAATTSLVLCIPSVPPPVFFFTLWP PPSWRRQPPGGIRRDFSRLRREANLVATCLPVRASLPHKLNML RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLCNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYPERPKDSMIWDCTCLGAGRGRIS CTIANRCHEGGQSYKLGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRLGDTWSKKNNRGNLLQCICTONGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNRKQML\CTCLGNGVSCETAVTQTYG	1			APAVTVRYYRITYGETGGNS PVOFFTVPGSKSTATIGGLVPCVP
ISVKMLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDOTEMTI EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV DVDSIKLAWESPGGQVSRYRVTYSSPEDGIHELPPAPDGEEDTA ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT QVTTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMERINLAPDSS SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR ARVTDATETTITISWRIKTETITGFQVDAVPANGGTPIQRTIKP DVRSYTITGLQPGTDVKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSWQPPRARITGYIIYKPKPGSSPREVVPRP RPGGTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGMGIQLPGT SGQQPSVGQQMIFEBHGFRRTTPPTTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQORHKVREEVVTVGNSVNEGINQPT DDSCFDPYTVSHYAVGDEWERMSESGPKLLCQCLGFGSGHPRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGGSYNQVSQRYHQRTNTNNNCPIECFMPLDVQ ADREDSRE 5366 8066 703 RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVFFFTLWP PPSWRROPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERYLGAILVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIMDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGSYMLECVLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ICTTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQQNKQML\CTCLGROCSCGETAVTOTYG				YTITYYAVTGRGDSDASSKDISTNYDTEIDKRSOMOUTDKADAG
EGLQPTVEYVVSYYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV DVDSIKIAWESPQGVSTRVTYSSPEDGIHELIPPAPDGEEDTA ELQGLRPGGSYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR ARVTDATETTITISWRTKTETITGFQVDAVPANGGTPIQRTIKP DVRSYTITGLQPGTDYKIYLYTLINDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP RPGGTEATITGLEPGTEYTIYVIALKNNQKSEPLIGKKTDELP QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVGQQMIFEBIGFRRTTPPTTATPIRHRPPYPPNVGQE ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQORHKVREEVVTVGNSVNEGLNQPT DDSCFDPYTVSHYAVGDEWBRMESGFKLLCQCLGFGSGHRCD SSRWCHDNGWNYKIGEKWDRQGENQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE \$1666 703 RLCCTGGGGGTPGASGKRGPAATTSLVLCIPSVPPPVFFFTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGFGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERYILGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIMDCTCIGAGRGFIS CTIANRCHEGGQSYKIGDTWRRPHETGSYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQQPQPPPPPFGCVT DSGVVYSVGMQLA*KTQQNKQML\CTCLGGNOSCGETAVTOTYG				TSVKWI.DSSSDVTGVDVTTTV DVMGDC\ DTWTTTM GDCCT
DVDSIKIAMESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA ELQGLRPGSSYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR ARVTDATETITISWRTKTETTTGFQVDAVPANGGTPIQRTIKP DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP QLVTLPHENLHGPEILDVPSTVQKTPFVTHEGYDTONGIQLPGT SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSSYIISCHPVGTDESPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT DDSCFPPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHPRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGGRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE \$166 703 RLCCTGGGGGTPGASGKRGPAATTSLVLCIPSVPPPVFFFTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRRSLPHRLNML RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQMVQPQSPVAVS QSKPGCYDNGKHYQINQWERTYLCNALVCTCYGGSRGFNCESK PPEAETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLCCVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPPPPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG				FGLOPTVEVVVCVVAONDECECOPT VOMALERYT DE STATE
ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR ARVTDATETITISWRTKYETITGFQVDAVPANGGTPIQRTIKP DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSWQPRARIGYIIXYEKPGSPPREVVPRP RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSEYIISCHPVGTDEBPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT DDSCFDPTYVSHAVGDBWERMSSSGFKLLQQCLGFGSGHPRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE 5366 8066 703 RLCCTGGGGGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGFGPGLLLLAVLCLGTAVPSTGASKSKRQAQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PPAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGSYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGMLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQBTAVTQTYG	1	į į		DUDGINIAMEGROCOMORNAMICORRESCONDINGUES DE COMO
QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR ARVTDATETTITISWRTKTETTTGFQVDAVPANGQTPIQRTIKP DVRSYTITGLQPGTDYKIVLYTLINDNARSSPVVIDASTATDAPS NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP QLVTLPHPNLHGPEILDVESTVQKTPFVTHPGYDTGNGTQLPGT SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSEYIISCHPVGTDEBPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVVTVCNSVNEGLNQPT DDSCFDPYTVSHYAVGDEWGRMSESGFKLLCQCLGFGSGHPRCD SSRWCHDNGVNYKIGEKNDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE 5366 8066 703 RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFFTLWP PPSWRROPPGGIRTDFSRRLRREANLVATCLPVRASLPHRLNML RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGRGCTAVTOTYG				ELOCI PROCESTATO AND AND AND AND AND AND AND AND AND AND
SVVVSGLMVATKYEVSVYALRDTLTSRPAQGVVTTLENVSPPRR ARVTDATETTITISWRTKTETITGFQVDAVPANGGTPIQRTIKP DVRSYTITGLQFGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSWQPPRARITGYIIKYEKFGSPPREVVPRP RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRRRPRYPPNVGQE ALSGTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVMEGLNQPT DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKWDRGGENGOMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE 5366 703 RLCCTGGGGGTPGASGKRGPAATTSLVLCIPSVPPPVFFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTCNTYRVCDTYFERFKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPPPPPPPGHCVT DSGVVYSVGMQLA*KTQQNKQML\CTCLGRGVSCQETAVTGTYG	1 1			ELOGERPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
ARVIDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP QLVTLPHPNLHGPEILDVPSTVQKTPFVTHREYDTGRGIQLPGT SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVMEGINQPT DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE 5366 703 RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVFFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGFGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNCNDQDTRTSYRIGDTWSKCDNRGNLLQCICTGNGGG EWKCRPHTSVQTTSSGSGPFTDVSKAVYQQPPPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNCML\CTCLGNGVSCQETAVTQTYG	}			QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
DVRSTITGLOPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSWOPPRARITGYIIKYEKPGSPPREVVPRP RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP OLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVMEGLNQPT DDSCFDPYTVSHYAVGDEWBRMSESGPKLLCQCLGFGSGHFRCD SSRNCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE 5366 703 RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGFGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYGGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKCDNRGNLLQCICTGNGRG EWKCRPHTSVOTTSSGSGPFTDVRAAVYQPPPPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKCML\CTCLGNGSCCGTAVTQTYG	1 1			SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
NLRFLATTPNSLLVSWQFPRARITGYIIKYEKPGSPPREVVPRP RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP QLVVTLPHPNLHGPEILDVPSTVQKTPFVTHRGYDTGRGIQLPGT SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVMEGLNQPT DDSCFDPYTVSHYAVGDEWERMSESGPKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE 703 RLCCTGGGGGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGE EWKCERTISVQTTSSGSGPFTDVRAAVYQPQPPPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNCML\CTCLGNGVSCQETAVTQTYG	; I			AKVIDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVGQQMIFEEHGFRRTTPFTTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVFGTSTSAT LTGLTRGATNNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE 703 RLCCTGGGGGTPGASGKRGPAATTSLVLCIPSVPPPVFFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYGGWMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERTISVQTTSSGSGPFTDVRAAVYQPQPPPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNCML\CTCLGNGVSCQETAVTQTYG	1 [DVKSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVGQQMIFEEHGFRRTTPFTTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVFGTSTSAT LTGLTRGATNNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE 703 RLCCTGGGGGTPGASGKRGPAATTSLVLCIPSVPPPVFFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYGGWMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERTISVQTTSSGSGPFTDVRAAVYQPQPPPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNCML\CTCLGNGVSCQETAVTQTYG	1			NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
OLVTIPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQOPSVGQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVFGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE 5366 703 RLCCTGGGGGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPGPVAVS QSKPGCYDNGKHYQINQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCLGGAGRGIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYGGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKCDMRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNCML\CTCLGNGVSCQETAVTQTYG	1 [RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVMEGLNQPT DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE 5366 703 RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGFGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKCDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVSKADNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPPPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKCML\CTCLGNGVSCQETAVTQTYG	[]		l	QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIOLPGT
ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVMEGLNQPT DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD SSRRCHDMGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGGRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE 5366 8066 703 RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLMML RGFGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYGGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKCNMRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPPPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG	1	ł	ļ	SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGOE
LTGLTRGATYNI IVEALKDQQRHKVREEVVTVGNSVNEGLNQPT DDSCFDPYTVSHYAVGDBWERMSESGFKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE 5366 8066 703 RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERITSVOTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG	j			ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT
DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHPRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE 5366 8066 703 RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGIRRDFSRRLREANLVATCLPVRASLPHRLMML RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFPKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERITSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG]	1		LTGLTRGATYNI IVEALKDOORHKVRREVVTVGNSVNEGI NODT
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HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPETTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE 703 RLCCTGGGGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYCGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG]	!		SSRWCHDNGVNYKIGEKWDROGENGOMMSCTCLCNGKGEEKGDD
RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE 8066 703 RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGFGPGGLLLLAVLCLGTAVPSTGASKSKQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYGGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG	[]	1		HEATCYDDGKTYHVGEOWOKEYLGATCGCTCFGCODGWDGDYGD
ADREDSRE 5366 RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLMML RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYGGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPPPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG		1		RPGGEPSPEGTTGOGYNOVGODYNODTNOTTROTTES
RLCCIGGGETPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLMML RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERITSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG	1	Ì		ADREDSRE
PPSWRRQPPGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYGGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGGG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG	5366	8066	703	
RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGRTWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG			, 53	PROUDDOCCIDED DOCCIDOCCIDED DOCCIDED DOCCIDED DOCCIDED DOCCIDED DOCCIDED DOCCIDED DO
QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG			1	PEDERGUILLIANS
PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGGG EWKCERHTSVOTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG	1			ROPORGIANTE TO THE ROPORT OF THE PROPERTY OF T
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CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYGGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVOTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG] !	İ	ļ	PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG	[į.	CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG	{		Ì	CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG	1 1			ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG			1	EWKCERHTSVQTTSSGSGPFTDVRAAVYOPOPHPOPPPYGHCUT
GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ	[į.	DSGVVYSVGMQLA*KTOGNKOML\CTCLGNGVSCORTAVTOTVC
TANGET I SCI I BORQUOIDA COI I SAI EQUO	<u> </u>		1	GNSNGEPCVLPFTYNGRTFYSCTTEGPODGHLWCSTTSNVFODO
			<u>-</u>	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
.NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	Indicate, isisoleucine, kalysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of		S=Serine, T=Threonine, V=Valine,
l	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ		sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
	1		DNMKWCGTTQNYDADQKFGFCPMAAHEBICTTNEGVMYRIGDOW
1	1	,	DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDOCIVDDITYNVN
	1		DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
ľ			GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
ì			TETPSQPNSHPIQWNAPQPSHISKYLLRWRPKNSVGRWKEATIP
i			GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
1	1		PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
1			SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
}	1		VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
}	1		PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
		•	ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
	ĺ		KVTIMUTEDEGA WYCYDIDUI DIAU DCHUGODI DI GONTO
1	[KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
			TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
1			ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
	f		PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
İ			TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
			VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
			LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
1			HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
			PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
1 .			GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
) .			\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
			TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
			SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
1 1			APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
!			YTITVYAVTGRGDSPASSKPISINYRTEIDKPSOMOVTDVODNS
) [ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDOTEMTI
	- 2:		EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
			DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
	1		ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
			QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
1 1	i		SVVVSGLMVATKYEVSVYALKDTLTSRPAOGVVTTLENVSPPRR
			ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
]		J	DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
	į		NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
			RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
1 1	Ì	ł	QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
]		SGOOPSVGOOMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGOE
			ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT
		,	LTGLTRGATYNI IVEALKDQQRHKVREEVVTVGNSVNEGLNQPT
			DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
			SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
		!	HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
			RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
1 1		1	ADREDSRE
5367	235	3591	KKILNMLCKKNIVIEYLADILYEYLYGFCFSGIKKYLIIHVLRL
]]			ILELWMTRLLLEKSVSLQTQYLLLIVKILSWFPGKEMRHHLQIM
			EVMMRKQDS/RIVGNGSEQQLQKELADVLMDPPMDDQPGEKELV
		1	KRSQLDGEGDGPLSNQLSASSTINPVPLVGLQKPEMSLPVKPGQ
101	1	1	GDSEASSPETDVADED CIGIDON TIME VOLUME TO COMPANY TO COMP
	-		GDSEASSPFTPVADEDSVVFSKLTYLGCASVNAPRSEVEALRMM SILPSOCOLSLDUTI SVDNVSEGIVEL L DOOTSTELL NOT THE STATE OF THE ST
	1	}	SILRSQCQISLDVTLSVPNVSEGIVRLLDPQTNTEIANYPIYKI
	1	1	LFCVRGHDGTPESDCFAFTESHYNAELFRIHVFRCEIQEAVSRI
	1		LYSFATAFRRSAKQTPLSATAAPQTPDSDIFTFSVSLEIKEDDG
ſ		1	KGYFSAVPKDKDRQCFKLRQGIDKKIVIYVQQTTNKELAIERCF
	1		GLLLSPGKDVRNSDMHLLDLESMGKSSDGKSYVITGSWNPKSPH
1			FQVVNEETPKDKVLFMTTAVDLVITEVQEPVRFLLETKVRVCSP
		ł	NERLFWPFSKRSTTENFFLKLKQIKQRERKNNTDTLYEVVCLES
1		j	ESERERRKTTASPSVRLPQSGSQSSVIPSPPEDDEEEDNDEPLL
	+	1	SGSGDVSKECAEKILETWGELLSKWHLNLNVRPKQLSSLVRNGV
ı			
			PEALRGEVWOLLAGCHNNDHLVEKYRILITKESPODSAITRDIN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l .	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
,	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence	aequence	\=possible nucleotide insertion)
<u> </u>	sequence		<u> </u>
1	ì		RTFPAHDYFKDTGGDGQDSLYKICKAYSVYDEEIGYCQGQSFLA
1			AVLLHMPEEQAFSVLVKIMFDYGLRELFKONFEDLHCKFYOLE
I	į.	1	RLMQEYIPDLYNHFLDISLEAHMYASQWFLTLFTAKFPLYMVFH
ł	l	1	IIDLLLCEGISVIFNVALGLLKTSKDDLLLTDFEGALKFFRVQL
			PKRYRSEENAKKLMELACNMKISQKKLKKYEKEYHTMREQQAQQ
l			EDPIERFERENRRLQEANMRLEQENDDLAHELVTSKIALRKDLD
į.	1		NAEEKADALNKELLMTKQKLIDAEEEKRRLEEESAHLKKMCRRE
1		ł	LDKAESEIKKNSSIIGDYKQICSQLSERLEKQQTANKVEIEKIR
1	1		QKVDDCERCREFFNKEGRVKGISSTKEVLDEDTDEEKETLKNOL
1	l	1	REMELELAQTKL\QLVEAECKIQD\LEHPF*GLPFNE\VQAA\K
1	1	İ	KTWFNRTLSSIKTATGVQGKETC
5368	573	2014	GAAAGAADPRRGSLGGRTMLDFAIFAVTFLLALVGAVLYLYPAS
2308	2/3	2014	
1			RQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLHERYGPVVS
1		1	FWFGRRLVVSLGTVDVLKQHINPNKTLD/LF*NHAEVIIKVSIW
1	1	{	wwqce*kp\qrkklyengvtdslksnfalllklpeelldkwlsy
	1		PETQH\VPLSQHMLGFAMKSVTQMVMGSTFEDDQEVIRFQKNHG
			TVWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERK
İ			GRNFSQHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTW
			AIWFLTTSEEVQKKLYEEINQVFGNGPVTPEKIEQLRYCQHVLC
			ETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVLQDP
\	i	1	NTWPSPHKFDPDRFDDELVMKTFSSLGFSGTQECPELRFAYMVT
	ł		TVLLSVLVKRLHLLSVEGQVIETKYELVTSSREEAWITVSKRY
5369	1	6622	PRSLCFSLWAEAAVLADGGLRRRRRLLRGTMSASFVPNGASLED
	_		CHCNLFCLADLTGIKWKKYVWQGPTSAPILFPVTEEDPILSSFS
1			RCLKADVLG/VWRRDQRPERRE\L+IFWGGEDP\VLLTLFTMTY
		1	OKKKMECGRMDFPMNAVLCFSKAVHNLLERCLMNRNFVRIGKWF
	ļ	}	VKPYEKDEKPINKSEHLSCSFTFFLHGDSNVCTSVEINQHOPVY
j		1	
1			LLSEEHITLAQQSNSPFQVILCPFGLNGTLTGQAFKMSDSATKK
			LIGEWKQFYPISCCLKEMSEEKQEDMDWEDDSLAAVEVLVAGVR
	•		MIYPACFVLVPQSDIPTPSPVGSTHCSSSCLGVHQVPASTRDPA
j	J	1	MSSVTLTPPTSPEEVQTVDPQSVQKWVKFSSVSDGFNSDSTSHH
1	ŀ		GGKIPRKLANHVVDRVWQECNMNRAQNKRKYSASSGGLCEEATA
1	1		AKVASWDFVEATQRTNCSCLRHKNLKSRNAGQQGQAPSLGQQQQ
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A
l	1	}	SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ
ļ			PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM
		1	EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLREDEANIAWKYYK
1			FPKKKDVEFLPPQLPSDKFKDDPVGPFGOESVTSVTELMVOCKK
			PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF
1	İ	1	LFPDKKDRONSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS
]	IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT
			PGSKRSANGSDDKASCKRSKTGNLDPLSCISTADLHKMYPTPPS
		1	LEQHIMGFSPMNMNNKEYGSMDTTPGGTVLEGNSSSIGAOFKIE
		l	VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSOY
		!	LPLIKLPEECIYROSWTVGKLELLSSGPSMPFIKEGDGSNMDOE
		1	YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP
		ł	RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP
			ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDSCCICVCNMNIK
1 .			GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDELD
	1	ł	IIGRNTDCGKEAEKRFEALRATSAEHVNGGLKESEKLSDDLILL
1	}	ł	LQDQCTNLFSPFGAADQDPFPKSGVISNWVRVEERDCCNDCYLA
		1	LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL
			RMLLSLQPVLQDAIQKKRTVRPWGVQGPLTWQQFHKMAGRGSYG
1		1	TDESPEPLPIPTFLLGYDYDYLVLSPFALPYWERLMLEPYGSQR
	1		DIAYVVLCPENEALLNGAKSFFRDLTAIYESCRLGQHRPVSRLL
1		1	TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV
	1	1	CRYDLGPYLASLPLDSSLLSOPNLVAPTSOSLITPPOMTNTGNA
	1	ľ	NTPSATLASASSTMTVTSGVAISTSVATANSTLTTASTSSSSS
1.	1		SNLNSGVSSNKLPSFPPFGSMNSNAAGSMSTQANTVQSGQLGGQ
1		(QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH
L		L	AVTYPPAIVVYIIDPFTYENTDESTNSSSVWTLGLLRCFLEMVQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1 [to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
] }	sequence		\=possible nucleotide insertion)
			TLPPHIKSTVSVQIIPCQYLLQPVKHEDREIYPQHLKSLAFSAF
			TQCRRPLPTSTNVKTLTGFGPGLAMETALRSPDRPECIRLYAPP
ł			FILAPVKDKQTELGETFGEAGQKYNVLFVGYCLSHDQRWILASC
1		1	TDLYGELLETCIINIDVPNRARRKKSSARKFGLQKLWEWCLGLV
\			QMSSLPWRVVIGRLGRIGHGELKDWSCLLSRRNLQSLSKRLKDM
<u> </u>			CRMCGISAADSPSILSACLVAMEPQGSFVIMPDSVSTGSVFGRS
! !		{	TTLNMQTSQLNTPQDTSCTHILVFPTSASVQVASATYTTENLDL
ĺ			AFNPNNDGADGMGIFDLLDTGDDLDPDIINILPASPTGSPVHSP
			GSHYPHGGDAGKGQSTDRLLSTEPHEEVPNILQQPLALGYFVST
			AKAGPLPDWFWSACPQAQYQCPLFLKASLHLHVPSVQSDELLHS
1		1	KHSHPLDSNQTSDVLRFVLEQYNALSWLTCDPATQDRRSCLPIH
			FVVLNQLYNFIMNML
5370	1226	716	RWSRKLELRRAAQATESRPPQSQEMHPPTGKEVHALKRLRDSAN
		[ANDVETVQQLLEDGADPCAADDKGRTALHFASCNGNDQIVQLLL
		1	DHGADPNQRDGLGNTPLHLAACTNHVPVITTLLRGGARVDALDR
			AGRTPLHLAKSKLNILQEGHAQCLKAVR/HGGEADHPYAEGVSG
]]	APRAT*AARCSGVFPSPSRWLGSAPWSRSSCTIWSLPLHEAKCR
			AVRPLSSAAQGSAPSSSSCCTVSTSLALAESLSLFRACTSLPVG
		<u> </u>	GCISWL
5371	1331	167	IAAMLWKLLLRSQSCRLCSFRKMRSPPKYRPFLACFTYTTDKQS
1			SKENTRTVEKLYKCSVDIRKIRR*KDGYF*RMKPMLKKLRI/F
)			LQELGADETAVASILERCPEAIVCSPTAVNTQRKLWQLVCKNEE ELIKLIEQFPESFFTIKDQENQKLNVOFFQELGLKNVVISRLLT
i I			AAPNVFHNPVEKNKQMVRILQESYLDVGGSEANMKVWLLKLLSQ
ļ			NPFILLNSPTAIKETLEFLQEQGFTSFEILQLLSKLKGFLFQLC
ì			PRSIQNSISFSKNAFKCTDHDLKQLVLKCPALLYYSVPVLEERM
			QGLLREGISIAQIRETPMVLELTPQIVQYRIRKLNSSGYRIKDG
1			HLANLNGSKKEFEANFGKIQAKKVRPLFNPVAPLNVEE
5372	51	857	SPGAQFLWAAPDMPDPLFSAVQGKDEILHKALCFCPWLGKGGME
}	1		PLRLLILLFVTELSGAHNTTVFQGVAGQSLQVSCPYDSMKHWGR
	ļ		RKAWCRQLGEKGPCQRVVSTHNLWLLSFLRRWNGSTAITDDTLG
			GTLTITLRNLQPHDAGLYQCQSLHGSEADTLRKVLVEVLADPLD
Ĭ	}		HRDAGDLWFPG\DLRASRMPMWSTASPGASWKEKSPSHPLPSFS
1			SWPASFSSRF*QPAPSGLQPGMDRSQGHIHPVNWTVAMTQGISS
			KLCQG
5373	2814	346	VKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSPFRTPYTPNSQY
1	\		QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG
	1		TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE
	1		ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD
	i		KTSTTGSILNLNLDRSKAEMDLKELSESVQQQSTPVPLISPKRQ
		1	IRSRFQLNLDKTIESCKAQLGINEISEDVYTAVEHSDSEDSEKS
			DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKKPKP
			TNPVEIKEELKSTSPASEKADPGAVKDKASPEPEKDFSGKAKPS
	1		PHPIKDKLKGKDETDSPTVHLGLDSDSE\NBLVIDLGEDHSGRE
		1	GRKNKKEPKEPSPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAQ
}	1		TSAAGATATTSTSSTVTVTAPAPAATGSPVKKQRPLLPKE\TAP
		}	AVQRSCGTSSTVQQKEITQSPSTSTITLVTSTQSSPLVTSSGSM
		1	STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDAIKGTM\TEI
		}	YNDLSKN\TTWKAQLAEDSQGLRIEIEKLQWLHQQEL\SEMKHN
1		1	LELTMAEMRQSWEQERDRLIAEVKKQLELEKQQAVDETKKKQWC
1	1	1	ANFKKEAIFYCCWNTSYCDYPCQ\QAHWPEH\MKSCTQSATAPQ
	1		\QEADAE\VNTETLNKSSQGSSSSTQSAPSETASA\SKEKETSA
		1	EVENEGRATION COORDINATE VACUOSPILLE CONTROLL
P382			EKSKESGSTLDLSGSRETPSSILLGSNQGSDHSR\SNKSSWSSS
5374			DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPFLGTSK
	2814	346	DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPFLGTSK VKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSPFRTPYTPNSQY
	2814	346	DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPFLGTSK VKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSPFRTPYTPNSQY QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG
	2814	346	DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPFLGTSK VKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSPFRTPYTPNSQY QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE
	2814	346	DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPFLGTSK VKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSPFRTPYTPNSQY QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD
	2814	346	DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPFLGTSK VKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSPFRTPYTPNSQY QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD KTSTTGSILNLNLDRSKAEMDLKELSESVQQQSTPVPLISPKRQ
	2614	346	DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPFLGTSK VKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSPFRTPYTPNSQY QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	1	Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence		\=possible nucleotide insertion/
			TNPVEIKEELKSTSPASEKADPGAVKDKASPEPEKDPSGKAKPS
	i		PHPIKDKLKGKDETDSPTVHLGLDSDSE\NELVIDLGEDHSGRB
		l .	GRKNKKEPKEPSPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAQ
		Į.	TSAAGATATTSTSSTVTVTAPAPAATGSPVKKQRPLLPKE\TAP
		Į.	AVQRSCGTSSTVQQKEITQSPSTSTITLVTSTQSSPLVTSSGSM
	1	(STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDAIKGTM\TEI
			YNDLSKN/TTWKAQLAEDSQGLRIEIEKLQWLHQQEL/SEMKHN
	1	j	LELTMAEMRQSWEQERDRLIAEVKKQLELEKQQAVDETKKKQWC
	i	1	ANFKKEAIFYCCWNTSYCDYPCQ\QAHWPBH\MKSCTQSATAPQ
	}	1	\QEADAE\VNTETLNKSSQGSSSTQSAPSETASA\SKEKETSA
		1	/Annuar / Aut at managed and a state of the critical
			EKSKESGSTLDLSGSRETPSSILLGSNQGSDHSR\SNKSSWSSS
			DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPFLGTSK
5375	2907	1116	HIFLAEEEPMLERRCRGPLAMGPAQPRLLSGPSQESPQTLGKES
	1	1	RGLRQQGTSVA\QSGAQAPGRAHRCAHCRRHFPGWVA\LWLHTR
		1	RCQA/RGLPLPCPECGRRFRHAPFLALHRQVHAAATPDWGFACH
		1	LCGQSFRGWVALVLHLRAHSAAKAGPFACPKMARDAFWRRKAAS
			SSILRRCHPSRPRGPRPFICGNCGRSILPTWDQ/LKVAHKRVHV
	Į		SRRP*ERGPPAKVFWGPRPRGPPTGDTPPGPGGDAVDRPF\QCA
	1		CCGKRFRHK\PNLIRSHAACTSGERPHQ/CSRECG\KRFTNKPY
			LTS\HRRITHTARQPYPCKECGRRFRHKPNLLSHSKIHKRSEGS
		1	AQAAPGPGSPQLPAGPQESAAEPTPAVPLKPAQEPPPGAPPEHP
			QDPIEAPPSLYSCDDCGRSFRLERFLRAHQRQHTGERPFTCAEC
			GKNFGKKTHLVAHSRVHSGERPFRLARKCGRRFLPRASQSGGRN
	}	}	SAEPNAPRFGPFVCPDCGKAFRHKPYLAAHRPIATPAEKPYVCP
	Į	}	DCRKAFSQKSNL\VSHRRIHTGERPYACPDCDRSFSQKSNLITH
			RKSHIRDGAFCCAICGQTFDDEERLLAHQKKHDV
5376	4504	591	VSTFSLCLWPAGGGGRGRVSNMAQSKRHVYSRTPSGSRMSAEAS
			ARPLRVGSRVEVIGKGHRGTVAYVGATLFATGKWVGVILDEAKG
	1	1	KNDGTVQGRKYFTCDEGHGIFVRQSQIQVFEDGADTTSPETPDS
	1	1	SASKVLKREGTDTTAKTSKLRGLKPKKAPTARKTTTRRPKPTRP
			ASTGVAGASSSLGPSGSASAGELSSSEPSTPAQTPLAAPIIPTP
	1	1	VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA
		ł	KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKBAKEAL
	į		EAKERYMEEMADTADAIEMATLDKEMAEERABSLQQEVEALKER
	1		VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV
		i	RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ
		i	AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG
			DLEAMNEMNDELQENARETELELREQLDMAGARVREAQKRVEAA
	1	l l	QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP
			ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD
		İ	SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE
			RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR
	1		LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT
			LD\VYKKVGSLYPEMSAHEKSLDFLTELLIAKIQLDEIVNVEFBI KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG
	Į.	(KATKI I ÖHLI DI HITARÜYENÇI INDANDARKI I ÖSAMACASARA
]		RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRRMPGT
			DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI
		\	APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL
			ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA
		1	EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS
	1	1	AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL
)	}	EAEKAELKORLNSOSKRTIEGLRGPPPSGIATLVSGIAGEEQQR
			GAIPGOAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL
}			KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET
			LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL
			KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG
1	1	[
			KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS
5377	762	1106	DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES*
		1	/WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK
	1 .	1	SS*WPGYDGWWGGQYIFIFRGMRWEBQP
5378	2009	664	QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL RFIATPRLSAMPHIDNDVKLDFKDVLLRPKRSTLKSRSEVDLTR

ID b	Predicted Deginning Ducleotide Location Corresponding Lo first	Predicted end nucleotide location corresponding	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
NO: n	nucleotide location corresponding	location corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
l c t a r	location corresponding	corresponding	u_utetidine Teleplancine Kelweine
t a r	corresponding		
t a r			L=Leucine, M=Methionine, N=Asparagine,
a r a	to first	to first	D=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
a		amino acid	
a	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
S	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			SFSFRNSKQTYSGVPIIAANMDTVGTFKMAKVLCKS*VPGSFWD
			VPQMGCVFLIYKLFTLKWKMLLLSVLLPASILVAEKFSLFTAVH
			KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP
)		QVKYICLDVANGYSEHFVEFVKDVRKRFPQHTIMAGNVVTGEMV
		1	EELILSGADIIKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA
	·	,	HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG
,)			ELIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV
	'		PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ
			VNPIFSEAC
			QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL
5379	2009	664	
			RFIATPRLSAMPHIDNDVKLDFKDVLLRPKRSTLKSRSEVDLTR
1			SFSFRNSKQTYSGVPIIAANMDTVGTFEMAKVLCKS*VPGSFWD
			VPQMGCVFLIYKLFTLKWKMLLLSVLLPASILVAEKFSLFTAVH
			KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP
		Ì	QVKYICLDVANGYSEHFVEFVKDVRKRFPQHTIMAGNVVTGEMV
j			EELILSGADIIKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA
į į			HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG
1			ELIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV
1			PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ
1			VNPIFSEAC
5380	2	2050	PSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS
""			SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGME
[SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL
()		1	SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP
1 1			RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA
1			YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP
1		1	RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV
1		\	F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII
1		I	H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA
1		1	FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM
1			CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI
j			KLHPWVTRHGAEPLPSEDENCTLVEVTEEBVENSVKHIPSLATV
			ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL
1			SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR
} }			*PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL
1 1			
<u></u>		<u> </u>	PDLVGAPGSHFCFLNIALLRYNSHTM PSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS
5381	2	2050	PSKAGGAERGKAAAAKS YOOSAAGWECYS VUULAGA CTUT CMP
1			SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGME
1 -1			SPIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL
1			SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP
1 1)	RLPRRPTVBSHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA
1			YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP
1			RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV
1			F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII
1			H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA
1 (FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM
j }		1	CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI
1			KLHPWVTRHGAEPLPSBDENCTLVEVTEEEVENSVKHIPSLATV
1			ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL
, 1		ł	SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR
1 1			*PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL
1			PDLVGAPGSHFCFLNIALLRYNSHTM.
1		100	GARGSQQDAPALQEAEVRGPERAQPARGRMTKARLFRLWLVLGS
5382	1536	203	VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE
1			LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMESVRG
] }			ETAUSDVDEFEDKFESAGVKQSDEPKKETEQFFAFGSNBESVKG
1			YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD
1			DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH
1	1		RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL
		1	KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV
1 1	1		RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH
1 1			WRQVYRLCHPCQIDYDFVGKLETLDEDAAQLLQLLQVDLAAPLP

	T Dec 23 and 2	1 W. 2 3 7 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3	
SEQ ID	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
1	sequence	ł	\=possible nucleotide insertion)
	 		PELPGTGPPSSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKP
			ENLLRD
5383	45	5250	VERLLGCRNSKRTWRMLISKNMPWRRLQGISFGMYSAEELKKLS
ł			VKSITNPRYLDSLGNPSANGLYDLALGPADSKEVCSTCVQDFSN
} .	1	,	CCCUI CUTEL DI TERRIPI I PRIVI MILITARE PROGRESSIONI
1	1	ļ	CSGHLGHIELPLTVYNPLLFDKLYLLLRGSCLNCHMLTCPRAVI
	1	j	HLLLCQLRVLEVGALQAVYELERILSRFLEENADPSASEIREEL
1	ì]	EQYTTEIVQNNLLGSQGAHVKNVCESKSKLIALFWKAHMNAKRC
			PHCKTGRSVVRKEHNSKLTITFPAMVHRTAGQKDSEPLGIEEAQ
ſ	[IGKRGYLTPTSAREHLSALWKNEGFFLNYLFSGMDDDGMESRFN
	1		PSVFFLDFLVVPPSRSRPVSRLGDQMFTNGQTVNLOAVMKDVVL
!			IRKLLALMAQEQKLPEEVATPTTDEEKDSLIAIDRSFLSTLPGQ
			SLIDKLYNIWIRLQSHVNIVFDSEMDKLMMDKYPGIRQILEKKE
1			GLFRKHMMGKRVDYAARSVICPDMYINTNEIGIPMVPATKLTYP
1	1	i	QPVTPWNVQELRQAVINGPNVHPGASMVINEDGSRTALSAVDMT
			QREAVAKQLLTPATGAPKPQGTKIVCRHVKNGDILLLNRQPTLH
1			RPSIQAHRARILPEEKVLRLHYANCKAYNADFDGDEMNAHFPQS
İ	1		ELGRAEAYVLACTDQQYLVPKDGQPLAGLIQDHMVSGASMTTRG
			CFFTREHYMELVYRGLTDKVGRVKLLSPSILKPFPLWTGKQVVS
1	ļ		TIT THIS DEPTH OF THE CONTROL OF THE PROPERTY
1			TLLINIIPEDHIPLNLSGKAKITGKAWVKETPRSVPGFNPDSMC
1			ESQVIIREGELLCGVLDXAHYGSSAYGLVHCCYEIYGGETSGKV
1			LTCLARLFTAYLQLYRGFTLGVEDILVKPKADVKRQRIIEESTH
!			CGPQAVRAALNLPEAASYDEVRGKWQDAHLGKDQRDFNMIDLKF
1			KEEVNHYSNBINKACMPFGLHRQFPENTLQLMVQSGAKGSTVNT
			MQISCLLGQIELEGRSTPLMASGKSLPCFEPYEFTPRAGGFVTG
			RFLTGIKPPEFFFHCMAGREGLVDTAVKTSRSGYLQRCIIKHLE
			GLVVQYDLTVRDSDGSVVQFLYGEDGLDIPKTQFLQPKQFPFLA
			SNYEVIMKSQHLHEVLSRADPKKALHHFRAIKKWQSKHPNTLLR
			RGAFLSYSQKIQEAVKALKLESENRNGR/RPWDS/G/RMLRMWY
			ELDEESRRKYQKKAAACPDPSLSVWRPDIYFASVSETFETKVDD
	<u> </u>		YSQEWAAQTEKSYEKSELSLDRLRTLLQL\KWQRSLCEPGEAVG
Į l			LLAAQSIGEPSTQMTLNTFHFAGRGEMNVTLGIPRLREILMVAS
			ANIKTPMMSVPVLNTKKALKRVKSLKKQLTRVCLGEVLQKIDVQ
			ESFCMEEKQNKFQVYQLRFQFLPHAYYQQEKCLRPEDILRFMET
l	i i		DEEAL I MEGTANISHING OF DEPHAL LOOK CORNED TO WARREN
}			RFFKLLMESIKKKNNKASAFRNVNTRRATQRDLDNAGELGRSRG
			EQEGDEEEEGHIVDAEABEGDADASDAKRKEKQEEEVDYESEEE
1			EEREGEENDDEDMQEERNPHREGARKTQEQDEEVGL/GH*GGPV
1			PSRPPDAAPETHPQPGAPGA\EAMERRVQAVREIHPFIDDYQYD
}	,		TEESLWCQVTVKLPLMKINFDMSSLVVSLAHGAVIYATKGITRC
} I			LLNETTNNKNEKELVLNTEGINLPELFKYAEVLDLRRLYSNDIH
			AIANTYGIEAALRVIEKEIKDVFAVYGIAVDPRHLSLVADYMCF
			EGVYKPLNRFGIRSNSSPLQQMTFETSFQFLKQATMLGSHDELR
	·		SPSACLVVGKVVRGGTGLFELKQPLR
5384	196	886	QSCGQRLPTVL*L*GPPGSCPCILSLF\PGRPHALPEIRPYINI
j			TILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG
į l			APCOKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT
į l			GQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS
j			ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF
; I			SGHLIKAEDD
5385	326	799	LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKVKIHM
			SDTFDD DYTL 1 DD OD VVDWYCHDDDWYD DOWN DOWN DOWN DOWN DOWN DOWN DOWN DOW
			SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A
(I		ĺ	VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ
1-E322-1			SDGERKAYVRLAPDYDALVVATKIGIT
5386	326	799	LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM
ł l	j	Į	SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A
	Į		VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ
L 1			SDGERKAYVRLAPDYDALVVATKIGIT
5387	2	2117	FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA
			SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY
1 1	ŀ	,	LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL
			ALFEDEMUMA CLOS ALTICA DOMOGRAPIO TERRETORIES CONTRACTORIO DE CARLO DO CONTRACTORIO DE CARLO
İ			ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA
			TVVSIIIVFDPLGGKMAPYSSAGPSHLDSHDSSQLLNGLKTAAT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO.	location		H=Histidine, I=Isoleucine, K=Lysine,
l	l .	corresponding	
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
)	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
<u> </u>			SVWETRIKLLCCCIGKDDHTRVAFSSTAELFSTYFSDTDLVPSD
	}		IAAGLALLHQQQDNIRNNQEPAOVVCHAPGSSOEADLDAELKNC
ļ	t		HHYMQFAAAAYGWPLYIYRNPLTGLCRIGGDCCRSKNPQTMT/M
ì			I =
	i	}	VGGDQLQL/CTSAPILHTHRAAVQGLHPRQLPWTRFTELPFLVA
ľ	l	1 .	LDHRKESVVVAVRGTMSLQDVLTDLSAESEVLDVECEVQDRLAH
j]	KGISQAARYVYQRLINDGILSQAFSIAPEYRLVIVGHSLGGGAA
		1	ALLATMVRAAYPQVRCYAFSPPRGLWSKALQEYSQSFIVSLVLG
{	į	1	KDVIPRLSVTNLEDLKRRILRVVAHCNKPKYKILLHGLWYELFG
1		Į	GNPNNLPTELDGGDQEVLTQPLLGEQSLLTRWSPAYSFSSDSPL
1	İ		DSSPKYPPLYPPGRIIHLQEEGASGRFGCCSAAHYSAKWSHEAE
1		(FSKILIGPKMLTDHMPDILMRALDSVVSDRAACVSCPAOGVSSV
l	1	Ì	DVA
5388	1569	753	TADGGAGGGGRQAGVRRHYLYPFTGGYRRRAACQAERPAARS
5300	1309	1 ,33	KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMLCSTGCGFYGNPR
i		1	TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQSALDST
1	1		1
I	}	1	SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS
l			DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMF
	1		TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK
		l	ILEHLQTKN
5389	1569	753	TADGGAGGGGRRQAGVRRHYLYPFTGGYRRRAACQAERPAARS
ľ	[ł	KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMLCSTGCGFYGNPR
	1	i	TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQSALDST
1	1	Į.	SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS
i			DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMF
	1	1	TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK
			ILEHLOTKN
5390	217	1332	EDPRKLMEDKMWSECEGPEMSLVCLTDFQAHAREQLSKSTRDFI
3330	/	1332	EGGADDSITRDDNIAAFKRIRLRPRYLRDVSEVDTRTTIQGEEI
ł	}		SAPICIAPTGFHCLVWPDGEMSTARAAQAA\GICYITSTFASCS
		1	LEDIVIAAPEGLRWFQLYVHPDLQLNKQLIQRVESLGFKALVIT
ľ		}	
1	1		LDTPVCGNRRHDIRNQLRRNLTLTDLQSPKKGNAIPYFQMTPIS
			TSLCWNDLSWFQSITRLPIILKGILTKEDAELAVKHNVQGIIVS
1.	ļ		NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK
•	1		ALALGAKCIFLGDAILWALASKGEHGVKEVLNILTNEFHTSMA\
		<u></u>	LTGCRSVAEINRNLVQFSRL
5391	1	1292	VKKAAGRSRGPPTAGGQRCEEAPGTVMERRLGVRAWVKENRGSF
		1	QPPVCNKLMHQBQLKVMFVGGPNTRKDYHIEEGEEVFYQLEGDM
			VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVER
Ì			RRLETELDGLRYYVGDTMDVLFEKWFYCKDLGTQLAPIIQEFFS
	1	1	SEQYRTGKPIPDQLLKEPPFPLSTRSIMEPMSLDAWLDSHHREL
	1	1	QAGTPLSLFGDTYETQVIAYGQGSSEGLRQNVDVWLWQLEGSSV
		1	VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q
		{	DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV
1		J	YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL
1			PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS
5392	 	1623	IRGSNAQKVVGASGSGGAGPQPDPAGPGGVPALAAAVLGACEPR
3372	1	1323.	CAAPCPLPALSRCRGAGSRGSRGGRGAAGSGDAAAAAEWIRKGS
1			1
1			FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT
1		1	RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA
1		1	GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD
			YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY
		· ·	LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL
1			GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP
1	}		PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR
			PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ
1			LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH
			AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE
		1	SELHLRGVVSREP
5393	2	982	GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP
1	1		PKAVLKLEPPWINVLQ\EDSVTLTCQGAPQP/ERSDSIQWFHNG
			· · · · · · · · · · · · · · · · · · ·

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
, -	1	nucleotide	
ID	beginning		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	-	\=possible nucleotide insertion)
	1		\NLIPTHTQPS\YRFKANNN\DSGEYTCQTGQTSL\SDPVHLTV
1	1	}	LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFONGK
1]	1	1
			SQKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITV
{	1		QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN
ļ	j	1	STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP
L	<u> </u>		RAPTDDDKNIYLTLPPNDHVNSNN
5394	2	982	GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP
1	1		PKAVLKLEPPWINVLQ\EDSVTLTCQGAPQP/ERSDSIQWFHNG
1			\NLIPTHTQPS\YRFKANNN\DSGEYTCQTGQTSL\SDPVHLTV
1 .	ł	Į.	LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFQNGK
1	j	1	SQKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITV
1		1	QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN
1	1	1	
J	J.	1	STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP
		ļ	RAPTDDDKNIYLTLPPNDHVNSNN
5395	3135	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS
	1	1	SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK
1		1	KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
	1		LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
1		1	RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
			SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP
l	}		PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL
]		1	PQQSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
	1		ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSODP
ļ	1	i	TPAATPETPPVISAVVHATDEEKLAVTNOKWTCMTVDLEADKOD
	1	}	YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD
l .	1		DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE
ļ	1	Į	ALVNTAAKNOHPVPRGLAPNQESHLQVPEKSSQKELEAMGLGTP
1			
[SEATEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
j			PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ
Į.			PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
1			YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
1	1	1	\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR
1			YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
ĺ	i	1	CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS
5396	3135	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS
	1	l	SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKOTTK
	1	ſ	KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
	1	1	LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVONSPPVG
l.	[1	RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
1	Í		1
	J	1	SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP
	}	1	PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL
	1		PQQSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
		1	ANGVDGDGLNKPAKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP
	1		TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD
	1	}	YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD
1	}		DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFRETE
	1		ALVNTAAKNOHPVPRGLAPNOESHLOVPEKSSOKELEAMGLGTP
			SEATEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
]	1]	PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ
1			PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
1	1		YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
]	ļ	\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAOEYLSRVKKEEOR
l			1 '
			YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
L			CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS
5397	3135	531	RASDAKNOEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS
	1	1	SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK
		j	KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
1	[LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
	1		RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
1	1	1	SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPBKLDNTPASP
({		PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL
		<u> </u>	

Deginning	- 050	1 5 37 1	Predicted end	Amino acid segment containing signal peptide
No: nucleotide corresponding to first amino acid residue of saino acid residue of saino acid residue of saino acid residue of saino acid sequence solvente, control of the saino acid sequence solvente, control of the saino acid sequence solvente, control of the saino acid sequence solvente, control of the saino acid sequence solvente, control of the sequence solvente, control of	SEQ	Predicted		
Cocresponding Corresponding Corresponding Cofirst Samina acid Lieucine, Machinoline, Na-Apparagine, Proline, Orditamine, Na-Apparine, Seserine, Machinoline, Na-Apparagine, Proline, Orditamine, Na-Apparine, Seserine, T-Threchine, V-Valine, V-Scote Amina acid Sequence Codon, Y-possible nuclectide deletion, Y-possible nuclectide dele			1	
to first amino acid amino acid amino acid amino acid sequence sequence sequence sequence sequence sequ	NO:			
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid sequence Person acid amino acid am				
amino acid residue of amino acid sequence Sequence Sequence Codon, /=possible nuclectide delection, ->possible nuclectide insertion) FOGSYMPEPTORESVDPFKTSKRFESPSKPASASFEIRASAME ANGYDDOLINKRAKKKEYRLFKETTERVKSKRSESLEDPSKPAS ANGYDDOLINKRAKKKEYRLFKETTERVKSKRSESLEDPSKPASFEIRASAME ANGYDDOLINKRAKKKEYRLFKETTERVKSKRSESLEDPSKPASFEIRASAME ANGYDDOLINKRAKKKEYRLFKETTERVKSKRSESLEDPSKPASFEIRASAME ANGYDDOLINKRAKKEYRLFKETTERVKSKRSKRSESLEDPSKPASFEIRASAME ANGYDDOLINKRAKKEYRLFKETTERVKSKRSKRSESLEDPSKPASFEIRASAME ANGYDDOLINKRAKKEYRLFKETTERVKSKRSKRSKRSESPETED ALVITAARNOHEVPRELAPNOSEINLOPPECSGSSFEETE ALVITAARNOHEVPRELAPNOSEINLOPPECSGSSFEETE SEALETTAPEGSFASAAALISRIAAFVSLCAALDYLEPOLAEKN PELFAQUEREAAMPTOVISITARVAKSTAGABETIAKERASAME SEKTIAAMOHERDROERSKRSVAMERSSKSKLKKRSESRESCVA ALADLFRRYERMKEVLEGFRANGEVLKRCAGETLSKVKKEER ALADLFRRYERMKEVLEGFRANGEVLKRCAGETLSKVKKEER ALADLFRRYERMKEVLEGFRANGEVLKRCAGETLSKVKKEER ANGYLAAMEN SEKTIAAMOHERDROERSKSSSSOMAMOHARDATE ANGYLAAMEN SEKTIAAMOHARDATIAA				
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MURILSODVKSYSTIKOLOMIOVSDSKEAVRLIKUGIKHQSVAFT KINNASSRSHSIPTVKILQIEDSEMSRVIRVSELSLODLAGSER THKTQNEGERLRETGNINTSLITLEKCINVLKNESKSKFQOHVS FRESKLTHYF/GSFFNSKKICMIVNISQCYLAYDETINVLKPS ALAQKVCVPDTIANSGOEKLGPVKSQDVSLDSNSKSKILDVKNA ATISWENSLEDLMEDEDLVEELENAEETED/VGETKLLDEDLDK TLEENKAFISHEEKRKLLDLIEDLKKKLINSKKEKLTLEFKIRE ETVOEFTGYNAQREADFKETLLQESELIEENAERLAIFKDLVC KCDTREBAAKDICATKVETERATACLELKFNOIKAELAKTKGEL IKTKEELKKRENESDSLIQELETSNKKI ITQNQRIKELINIDQ KEDTINBFQNLKSHMENTFKCNDKADTSSLIINKKLICNSTVEV FKDSKSKICSSRKKVUENELQODEPPAKKSGIHVSSAITEDQKK SEEVEPNIABIEDIRVLQENNSGLAFLLITENELKEKEKKAE LNKQIVHPOQELSLSEKKNLTLSKEVQQIQSNYDIALAELHVOK SKNOEQEEKIMKLSNSIETARSITNNVSQIKLMHTKIDELRIL DSVSQISNIDLLAURDLSNSSSEDDLFATQLLGENDYLVSKSKQ KEYRIQBPNENSFHSSIESITARSITNNVSQIKLMHTKIDELRIL DSVSQISNIDLLAURDLSNSSSEDDLFATQLDLIKEETILQLKKE (ALEKLAPVKSYKOENNIKLKEEHANDODLLKEEKETILQQLKKE QUEKLAPVKSYKOENNIKLKEEHANDODLLKEEKTILQQLKKE LQEKNVTLDVQIQHVVEGKRALSELTQGVTCYKAKIKELETILE TOKVERSHSAKLEQDILEKESIILKLERILLEFCEHLQOSVKAT KOLNIVKELKLEETITQTINNLQMHLQDLKEEETINGCTSKK LKEELSASSAATON LNADLQRKEEDYADLKEKLTDAKKQIKOV QKEVSVMRDEDKLLRIKINDLEKKKINQCSQBLDMKOR\TIOQLK EQLUNKELKLEGITOLTNNLQMAKKMLEEKMILTQAKKE LKEELSASSAATON LNADLQRKEEDYADLKEKLTDAKKQIKOV QKEVSVMRDEDKLLRIKINDLEKKKINQCSQBLDMKOR\TIOQLK EQLUNCKELKLEGITOLTSTEISRNKLEDGSOTVUDSCEV EQDQVIL\BAKLEEVERLATTLDRWRVKCNDLETKNNQRSNKEHE NITDULGKLTHLQDELQESSGVANKKKULEKMILTQAKKE ENIRNKEMKKYABDREFFFKQNEMEILTAQLTEKDSDLQKWRB ERDQLVAALEIQLKALISSINVQKDMEIEQLAKRIISTSTEKTTO MOKFKRISSADDENLATFKKRGGTLQKFGDFLQHS STENDOSTRFFKPELBIQFTPLQFNKMAVKHBGCTTPVTVKIFK ARKKNEMEEDLVKCENKKNATPRTNLKPPISDDRNSSVKKED KVAIRPSSKKTYSLRSQASIIGVNLATKKKRGGTLQKFGDFLQHS FSILQSKAKKIIETMSSKILSNVRASKENVSQPKRAKKLYTSE ISSPILDIGGQVILNDOKMESDBOTIATKKRGGTLQKFGDFLQHS FSILQSKAKKIIETMSSSKILSNVRASKENVSQPKRAKKLYTSE ISSPILDIGGVILNDOKMESDBOTIATKKRKGGTLQKFGDFLQHS FSILQSKAKKIITDAGKGVVMASDLAKKVINSGVKNYQPKRAKKLYTSE ISSPILDIGGVILNDOKMESDBOTITTITIMMQIRQEDFKE LILAMMVNDKEKKGVVMASDLAKKUTSGEKLITHKVVDDLFFEVGU VADIPPNGKVKYDETHKITSYLDGTY FSHOOD				T =
KLMNASSRSHIPTVKILQIEDBEMSRVIRVSELSLCLDAGSER TMKTQNEGERLRETGNINTSLLTLKKKINSEKSKFQONYS PRESKLTHYP/G9FFNGKGKICMIVNISQCYLAYDETINVIKRS ATAGKVCVPDTIMSSQEKLFGPVKSGDVSLDSNSNSKILNVKR ATISWENSLEDLMEDEDLVEBLENAEETED/VGBTKLLDEDLDK TLEENKAFISHEEKRKLLDLIEDLKKKLINSKKKKLTLEKKIR ETTGEFTGYNAQREADFKETLLQEREILERAERRLAIFKDLVG KCDTREBAAKDICATKVETTERATGLLEKFNGIKAELAKTKGEL IKTKEELKKRENESDSLIQELETSNKKIITQNQRIKELINIID KEDTINFFQNLKSHMENTFKCNDKADTSSLIINNKLICNSTVEV PROSKSKICSSRKVENENELQODEPPAKKGIHVSSAITEDGKK SEEVRPNIABIEDIRVLQENNEGLRAFDLLTIENELKEKEKEKAE LNKQIVHFQQELSLSEKKNLTLSKEVQQIQSNYDIAIAELHVQK SENGEGEKIMKLSNEIETATRSITINNVGIKLHHTRIDBLRTI DSVSGISNIDLLNIRDLSNSSEEDNLPNTGLDLLGNDYLVSKQV KYRIGDBONENSPHSSIEAIHESTINNVGIKLHHTRIDBLRTI DSVSGISNIDLLNIRDLSNSSEEDNLPNTGLDLLGNDYLVSKQV KYRIGDBONENSPHSSIEAIHESTIVANGTKAKKEETLIQLKEE LOEKNVTLDVGIQHVVEGRAILSLICGVTYKAKIKELETILE TQXVERSHSAKLEGDILEKESIILKLERNLEFSEHLQDSVKNTI KDLNVKELKLKEEITQLTNNLQDMKHLLQLKEEEEETNRQETEK LKEELSASSARTQN\LNADLQRKEBDYADLKEKLTDARKGIKOV QKEVSVMADEDKLIKIKINELKENGCSGLIMMKQN\TTGOKKE BLANGKVERAIQQYERACKDLNVKEKIIEDMRWTLEEGECTOV EQDQVL\RAKLEEVERLATELDRWKVKONDLETKNNORSNKEHB NNTDVLGKLINLQDELQESEGKYNADRKKWEEEMMI.TQAKEA ENIRKEMKKVAGDREFFFKQONEMEILTAGLTEKDGDLQKMRB ERDQLVAALETQLKALISSNNVGMEEGLIKITGTETSKITGTI MDIKKPKRISSADPDKLQTEPLSTSFEISRNKIEDGSVVLDSCEV STENDGSTRFFKEDELIQFTPLQPNMAVKHPGCTTEVTVXIFK ARKRENBEMEDLVKCENKKANTPBLEFOLKRIITSTSTSKITGTU MDIKKPKRISSADPDKLQTEPLSTSFEISRNKIEDGSVVLDSCEV STENDGSTRFFKEDELIQFTPLQPNMAVKHPGCTTEVTVXIFK ARKRENBEMEDLVKCENKKANTPBLEFOLKRIITSTSTSKITGTU ARRKENKENSEMEDLVKCENKKANTPUKLFGISTORNSVKKEG KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTLQKFGDFLQHS FEILQSKAKKIETMSSSKLISNVASKENSOPKRARKKLYTSE ISSPIDIGGQVILMDQKMESDPLGIIKRINKOPKRORNSVKKEG KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTLQKFGDFLQHS FEILQSKAKKIETMSSKLISTLGEKLTHKEV\DDLFFRE ARPTGEVQRHLQTHDIDGDELDFTFTLTHMMQIKGEDPKKE JLLAMMWDKEKKGYVMASDLLASKLTSLGEKLTHKEV\DDLFRE \ADIEPNGKVKYDEFTHKITSYLDGTY SHOOSMEDIFCHGHKVYRLKFPAVEEIIQKQVKVNCTAEVLYPSTGGB SHOOSMEDIFCHGHKVYRLKFPAVEEIIQKQVKVNCTAEVLYPSTGGB				1
TMKTQNEGER.RETGNINTSLLTLGKCINVLKNSEKSKCQOHVE PRESKLTHYE/QSFPKOKKICMIVNISQCYLAYDETIANULKPS ATAGKCVCYPDTIASGCKLGEVYKSGOVSLDSNSNSKLINVKR ATISMENSLBOLMEDDEDLVEBLENABETED/VGETKLLDEBLDK TLEENKAFISHEEKRKLLDLIEDLKKKLINBKKEKLTLEKFKIRE EVTOEFTQYMAQRADFKETLLOEREILEENABERLAIFKDLVG KCDTREBAAKDICATKVETERATACLELKFRQIKAELAKTKGEL INTKEELKKRRNESDSLIGBLETKKITJONGKIKELINITJON KEDTINBFONLKSHIMENTFKCHDKADTSSLIINKLICHTEVEV PKDSKSKICSERKRVNENELQQDEPPAKKGSIHVSSAITEDQKK SEEVERPIABIEDIRVLQENNEGLRAFLLITENELKMEKEEKAE LNKGIVHFOGELSLSEKKNLTLSKEVQQIGSNYDIATAELHVOK SKNQEBEKINKLNBIETATRINVOGIKLHHTIDELRTI DSVSQISNIDLLNLRDLSNGSBEDNLPNTQLDLLGNDYLVSKQV KEYRIGBENENSHSIETATRINVOGIKLHHTIDELRTI DSVSQISNIDLLNRDLSNGSBEDNLPNTQLDLLGNDYLVSKQV KEYRIGBRNENSFHSSIEAIWEECKEIVKASSKKSKQIEELEK QIEKLAAPKVSKYNDENNIKLKEHRODDLLKEKETILQQLKWE LQEKNVTLDVQIQHVVEGKRALSELTQGVTCYKARIKELETILE TQKVERSHSAKLEQDILEKESIILKLERNLKEFQEHLQDSVKNT KOLNVKCIKLKEEITQLINNLQDMKHLLQLKEEBEETNRGETEK LKEELSASSARTON\LNADLQRKEBEDYADLKEKLTDARKQIKOV QKEVSWAMDEDKLIKIRINIENEKKOCOSGLDMKQNT\TOQUK EQLINQKVEBAIQOYERACKDLNVKKIIEDMRMTLBEQECTOV EQDQVL\BAKLEBVERLATELDRAWKKCODLETKNNQRSNKEHE NNTDVLGKITHLQBLQESEGVANDKKWLEEKMITTQAKER ENIRMKEMKKVABDREFFFKQNEMEILTAQLTEKBGDLQKWRB ERDQLVAALBIQLAGESGVANDRKWHEETMAMITTQAKER ENIRMKEMKKVABDREFFFKQNEMEILTAQLTEKBGDLQKWRB ERDQLVAALBIQLALESSNVQKDNEIEQLKRIISTSKETGTI MDIKKRRISSADDPKLQTEPLETSFEISRNKIEDGSVVLDSCEV STENDQSTRFPKPELBIQTFPLQPNRMAVKHGCTTEVTVKIFK ARKRSNEMEEDLVKCENKKANTPRTUKKPGSDNRSVKKEG STENDQSTRFPKPELBIQTFPLQPNRMAVKHGCTTEVTVKIFK ARKRSNEMEEDLVKCENKKANTPRTUKKPGSDNRSVKKEG KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTLQKFGDFLQHS FSILGSKAKKIIETMSSSKLSNVRASKENVOPKRAKKLYTSE SSPIDIGGOVILMDROMMESDOPQIIKRRLSTGERLTHMHQIKGEDFKGE TILAMMVOKEKKGVVANSDLEKSTLSGEKLTHIMHQIKGEDFKGE VADIEPNGKVKYDEPTHKITSJEGGTVHAMPGVEVOVCVK ADIEPNGKVKYDEPTHKTTSJEGTYNYQGGTPHRVFEVQKVK ADIEPNGKVKYDEPTHKYTSJEGTYNYQGGTPHRVFEVQKVK ADIEPNGKVKYDEPTHKYTSJEGTYNYQGGTPHRVFEVQKVK		1	į.	
FRESKLTYP/OSFFNGKKICMINISQCYLAYDETLNILKES ATAGKVCYPDTINISQEKLFGPYKSQDVSLDSNSNSKLINVKR ATISMENSLEDLMEDELUVEELENABETED/VGETKLLDEDLDK TLEENKAFISHEEKRKLIDLIEDLKKKLINEKKEKLTLEKTIKE EVTQEFTQYMAQREADFKETLLQEEILEENABERLAIFKDLVG KCDTREBAAKDICATKVETERATACLELKENQIKAELAKTKGEL IKTKEELKKRENESDSJJQELETSNKKITYNORIKELINITOQ KEDTINBFONLKSHMENTFKCNDKADTSSLIINIKLICNSTVEV PKDSKSKICSERKRVNENELQQDEPPAKKGSIHVSSAITEDQKK SEEVERNIABTEDIRVIQENNEGLRAFLLTIENELKNEKEKEKAE LNKQTVHFOQELSISEKKNITEKVOQIQGNYDIATAELHVOK SKNQEGEKIMKLSNEIETATRSITNNVSQIKLMHTKIDELRTL DSVSGISNIDLLNIRDLSNGSBEDNLENTQLDLLGKNYLVSKGV KEYRIQBPNERNSFHSSIEALWECKEIVKASSKKSHQIEELEK QIEKLQABVKGYKDENNRLKEKEHKNQDDLLKEKETLIQLKEE LQEKNVTLDVQIQHVVEGKRALSETTQSUTCYKAKIKELETILE TQKVERSHSAKLEQDILEKESIILKLERNLKEFCBHLQDSVKNT KOLNVERLKLKEETTQLTNNLQDMKHLLQLKEEEEETNRGETEK LKEELSASSARTON\LNADLQRKEEEETNRGETEK LKEELSASSARTON\LNADLQRKEEEETNRGETEK LKEELSASSARTON\LNADLQRKEKLIEDRRVKCNDLETENNGSTSK LKEELSASSARTON\LNADLQRKEEEEDYADLKEKLITDAKKQIKOV QKEVSVMEDEDKLLRIKINELEKKKNQCSGELDMKGR\TIQQLK BQLINGKVERAIQQYERACKOLNYKERIIBMMMTLEBORGTOV DGDQVIL\RAKLESVEVERLATELDRRVKCNDLETENNORSNKEHE NNTDVLGKLTNLQDELQESEQKYNADRKKMLEEKMMLITQAKEA ENIRKEMKKVAEDRERFFKQQNEMEILTAQLTEKDODLQKMER ERDQLVAALEIQLKALISSNOOMEIGLGKRIISETSKIETGI MDIKPKRISSADPDKLQTEPLSTSFEISRNKIEDGSVVLDSCEV STENDOSTRFFKPELBIQFTPLOPINMAVKHPGCTTFVVTKIFK ARKRNEMEEDLVKCENKNATPRTALKFPISDDRNSSVKEO KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTLQKFGDFLQHS STENDOSTRFFKPELBIQFTPLOPINMAVKHPGCTTFVVTKIFK ARKRNEMEEDLVKCENKNATPRTALKFPISDDRNSSVKKOO KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTLQKFGDFLQHS STENDGSTRFFKPELBIGFTFLORMONSQPKRAKKRLYTSE ISSPIDISGOVILMDQKNKESDHOIIRRRLTKTTAK GPPMAKFLSQDOINSYKECFSLYDKOORGKIKATDLMVANRCLG ASPTPGEVQRILQTHGIGNGELDFSTFLIIMMQIKQEDPKKE LLAMMYDKEKKGYVAASDLRSKLTSLGEKLTHKEV\DDLFRE \ADIEPNGKVKYDEFIKKITSYLDGTY SHCSSGMEIPPTNYPASRAALVAONYINYQQGTPHRVFBVOKVK DASMEDIFORGHKYNLKFAVBEIIQKQVKVCTAEVLVPSTGGE		}	1	
ALAQKVCVPDTLNSSQEKLPGPVKSSQDVSLDSNSNSKILNVKR ATISMENSLEDLMEDEDLVEELENAEPTED/VGETKLLDEDLDK TLEENKAFISHEERK KLIDLIEDLKKKLINEKKEKLTLEFKIRE EVTQEFTOYWAQREADYKETLLQEREILENAERRALAIPKOLVG KCDTREBAAKDICATKVETEEATACLELKFNQIKAELAKTKGEI INTKEELKKRENGSSLIQELETSNKKIITONORIKELINIID KEDTINBFONLKSIMENTPKCNDKADTSSLIINNKLICONTVEV PKDSKSKICSERKRVNENELQQDEPPAKKGSIHVSSAITEDQKK SEEVERPATAEIEDIRVLQENNEGLRAFILLTEENELKNEKEKEEKAE LMKQIVHFOQELSJESKENLTISKEVQOIGSNYDIATAELHVOK SKNQEGEKIMKLINEIBTATRSITNNVSQIKLMHTKIDELRTI DSVSGISNIDLLINLRDLSNGSBEDNLENTOLDLLGRDYLLVSKOV KEYRIQBPNRENSPHSSIEATWEECKBIVKASSKKSHQIEELKG QIEKLQAEVKGYKODENNRLKEKEHKNQDDLLKEKETLIQQLKEE LQEKNVTLDVQIQHVVBGKRALSELTGGVTCYKAKIKELETILE TOKVERSHSAKLEQDILEKESIILKLERNLKEFQEHLQDSVKNY KDLNVVELKLKEEITQLTUNNLQDMKHLLQLKEEBEETNRQETEK LKEELSASSARTQN\LNADLQRKEEDYADLKEKLITDAKKQIKOV QKEVSVMRDEDKLLRIKINELEKKKNOCSGELDMKOR\TTOQIK BOLDINGKVERAIQQYERACKONKEKI IBBMRHILEEGETOV GEOGOVIL\BAKLEEVERIATELDRWRVKCNDLETKNNQRSNKEHE NNTDVLGKILTNLQDELQESEGKYNADRKMILEERMMLITQAKBA ENIRNEMKKYAEDERFFKQONEMEILTAQLIEKEBEDOTOV BODQVIL\BAKLEEVERIATELDRWRVKCNDLETKNNQRSNKEHE NNTDVLGKILTNLODELQESEGKYNADRKMILEERMMLITQAKBA ENIRNEMKKYAEDERFFKGONEMEILTAQLIEKEBDLOKKHE BERDQLVAALEIQLKALISSNVQKDNEIEQLKRIISETSKIETQI MDIKPKRISSADPDKLQTEPLSTFFISRNKIEDGSVVLDSCEV STENDQSTRFPKPELIQFTPUTKIEK ARKRSNEMEEDLLVKCENKKNATPRTNLKFFISDDRNSSVKKEQ KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTIQKFGDFLOKIS PSILQSKAKKIIETNSSKLSNVARSKENNSGPKGTPLOKIS PSILQSKAKKIIETNSSKLSNVARSKENNSGPKRAFKLYTSE SSPIDISGQVILMDQKMKESDHQIIKRRETTRYTAK 5399 705 230 GPRMAKFLSODOINSYKECFSLYDKOGKSKATDLMVANKCLG SPPIDLSGOVILMDQKKKESDHOJIKRRLTTAKEVLYDDLFRE \ADIEPNGKVKYDEFIKKITSYLDGTY \ADIEPNGKVYXDEFIKKITSYLDGTY \ADIEPNGKVYXDEFIKKITSYLDGTY \ADIEPNGKVYXDEFIKKITSYLDGTY \ADIEPNGKVYXDEFIKKITSYLDGTY \ADIEPNGKVYXDEFIKKITSYLDGTY		1		TMKTQNEGERLRETGNINTSLLTLGKCINVLKNSEKSKFQQHVP
ATISWENSLEDLMEDEDLVEBLENABETED/VOETKILDEDLUK TLEENKAFISHEEKRKLLDLIEDLKKKLINEKKEKLTLEFKIRE EVTOEFTOYWAGGRADFKETLLQEREILEENABRRIAIFKOLVG KCDTREBAAKDICATRVETEBATACLELKFNOIKABLAKTKGEL IKTKEELKKRENESDSLIQELETSNKKIITONORIKELINIID KEDTINBFONLKSHMENTFKCNDKADTSSLIINNKLICNETVEV PKOSKSKICSBERGVNENBLQQDEPPAKKSIHVSSAITEDQKK SEEVRPNIABIEDIRVLQENNEGLRAPLLTIENELKNEKSEKAB LIKKQIVHFQQELSLSEKKNILTISKEVQQIQSNYDIALABLHVQK SKNQEQBERIMKLSHEIBTATRSITINVSQIKLMHTKIDELRTI DSVSQISNIDLIANDROISBERDNIPNTOLDLLGHDYLVSKQV KEYRIQBPNRENSFHSSIBAIWEECKEIVKASSKKSHQIEELBQ QIEKLQAEVKGYKDBNNRLKEKEHNKQDDLLKEKETLIQQLKBE LQEKNVTLDVQIQTOVVEGKRABEENLOPTVYRAKIKELETILE TQKVERSHSAKLEQDILEKESIILKLERNLKEFQEHLQDSVKNT KOLNVKELKLKEEITQLTINNLQDMKHLLQLKEEBEETNRQETEK LKEELSASSARTON\LNADALQRKEBDYADLKEKLTDAKKQIKQV QKEVSVMRDEDKLAIKINLOLGKEEBETNRQETEK LKEELSASSARTON\LNADALQRKEBDYADLKEKLTDAKKQIKQV QKEVSVMRDEDKLAIKINLOLGKEELDRAWKKCNDLETKINNQGSNKEHE NNTDVLGKLTNLQDELQESEQXYNADRKKHLEEKMMLITQAKRA EGLINGKVEEAIQGYURACKODLETKINNQGSNKEHE NNTDVLGKLTNLQDELQESEQXYNADRKKKLEEKMLITQAKRA ENIRNKEMKKYAEDRERFFFKQONEMEILTAQLTEKDSDLQKWRB ERDQUVAALEIQLKALISSNVQKDMEIELDARITSSTSKIETQI MDIKPKRISSADPDKLQTEPLSTSFEISRNKIEDGSVVLDSCEV STENDQSTRFPKPELBIQFTPLQPNKMAVKHDEGTTPVTVKIPK ARKRSNEMEEDLVKCENKKNATPETNLKPPISDDRNSSVKKEQ KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTLQKFGDFLQHS STENDQSTRFPKPELBIQFTPLQPNKMAVKHPGCTTPVTVKIPK ARKRSNEMEEDLVKCENKKNATPETNLKPPISDDRNSSVKKEQ KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTLQKFGDFLQHS SSIDISGQVILMDQKMKESDHQIIKRRLRTKTAK TSPPIDISGQVILMDQKMKESDHQIIKRRLRTKTAK ASPTPGEVQRHLQTHGIDGNGELDFSTFTITIMMQIKQEDPKKE ILLAMLMVDKEKKGYVMASDLRSKLTSLGGKLTHKEV\DDLFKE VADIEPRGKVKYDEFIHKITSYLDGTY SHOOG		l	1	FRESKLTHYF/QSFFNGKGKICMIVNISQCYLAYDETLNVLKFS
TLEENKAFISHEEKRKLLDLIEDLKKKLIMEKEKUTLEEKIRE EYTOEFTOYMAGREADFKETTLLGEREILEENAERRIAIFKDLYG KCDTREBARAKDICATKVETERATACLELKFNOIKAELAKTKGEL IKTKEELKKRENESDSLIGELETSNKKIITOORGIKELINIIDL KEDTINBFONLKAHENTFKCHDKAADTSSLIINNKLICNETYDV PKDSKSKIGSERKRVNENELQODEPPAKKSIHVSSAITEDQKK SEEVRPIAEIEDIRVLQENNEGLRAFLLTIENELKNEKEEKAE LINKQIVHFQQELSLSEKKRITISKEVQQIQSNYDIAIAELHVOK SKNOEGBERIMKLISHEITATASITNNVSQIKLMHTKIDELRTI DSVSQISNIDLLINLRDLSNGSBEDNLPNTOLDLLGNDYLVSKOV KEYRIQBPNRENSFHSSIEAIWEECKEIVKASSKKSHQIEELEG QIEKLQAEVVGKYKDRINNLKEKEHKNQDDLLKEKETLIQQIVCYKAKIKELETILE TOKVERSHSAKLEQDILEKESIILKLERNLKEFQEHLQDSVKTH KOLLNVKELKIKESITOLTINLQDMKHLLQLKEEEBETINRGETEK LKEELSASSARTON\LINADLQRKEEDYADLKEKLTDAKKQIKOV QREVSVMRDEDKLIRIKINLEKKKONGCSGLADMKGR\TIQQKE EQQUVL\RAKLEEVERLATELDRWRVKCNDLETKKNQRSNKEHE NNTDVIGKLTNLQDELQESEGXYNADRKKWLEEKMLITQAKEA ENIRKEMKKYADERSFFKQONEMEILTAQITEENDSDLQKNRB ERDQLVAALEIQLKALISSNVQKDNEIELTAQITEENDSDLQKNRB ERDQLVAALEIQLKALISSNVQKDNEIELTAGITEENDSDLQKNRB ERDQLVAALEIQLKALISSNVQKDNEIELTAGITEENDSDLQKNRB ERDGLVAALEIQLKALISSNVQKDNEIELTAGITEENDSDLQKNRB ERDDLSAKAKILIETMSSSKISNVBASKENVSOPKRAKRKLYTSE STENDQSTRFPKPELBIGTFFLQPNRMAVKHPGCTTPVTVKIKK ARKRKSNEMEEDLVKCENKKNATPRTNLKFPISDDRNSSVKKEQ KVAIRPSSKKTISLBSQASIIGVNLATKKKEGTLQKFGOFDLOHS SEJOLSGAKKILTETMSSSKLISNVBASKENVSOPKRAKRKLYTSE ISSPIDISGQVILMDQKMKESDHQIIKRRLKTKTAK 5399 705 230 GFRMAKFLSQDQINEYKECFSLYDKOQRGKIKATDLMVAMRCLG SPENGKYKTILTENSKLISTYSSKLISNVBASKENVSOPKRAKRKLYTSE ISSPIDISGQVILMDQKMKESDHQIIKRRLRTKTAK SSPPIGEVORMILTETHSSILISTISTINTNAGVORTHRVFEVOKVK ALPEPSKKTISLSGASIIGVNIATKKECTILDKORDFDLOHSFI ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFFRE \ADIEBROKVKYDEFIHKITSYLDGTY SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFEVOKVK QASMEDIPORGKKYRLBFTASRALVAQONYINYQQGTPHRVFEVOKVK QASMEDIPORGKKYRLBFTASRALVAQONYINYQQGTPHRVFEVOKVK QASMEDIPORGKKYRLBFRARALVAGNYINYQQGTPHRVFEVOKVK				AIAQKVCVPDTLNSSQEKLFGPVKSSQDVSLDSNSNSKILNVKR
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MDIKPKRISSADPDKLQTEPLSTSFEISRNKIEDGSVVLDSCEV STENDQSTRFPKPELBIQFTPLQPNKMAVKHPGCTTPVTVKIPK ARKRKSNEMEEDLVKCENKKNATPRTNLKFPISDDRNSSVKKEQ KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTLQKFGDFLQHS PSILQSKAKKIIETMSSSKLSNVEASKENVSQPKRAKRKLYTSE ISSPIDISGQVILMDQKMKESDHQIIKRRLRTKTAK S399 705 230 GPRMAKFLSQDQINEYKECFSLYDKQQRGKIKATDLMVAMRCLG ASPTPGEVQRHLQTHGIDGNGELDFSTFLTIMHMQIKQEDPKKE ILLAMLMVDKEKKGYVVASDLRSKLTSLGEKLTHKEV\DDLFRE \ADIEPNGKVKYDEFIHKITSYLDGTY S400 931 248 SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFEVQKVK QASMEDIPGRGHKYRLKFAVEEIIQKQVKVNCTAEVLYPSTGQE	1			12.72
STENDQSTRFPKPELBIQFTPLQPNKMAVKHPGCTTPVTVKIPK ARKRKSNEMEEDLVKCENKKNATPRTNLKFPISDDRNSSVKKEQ KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTLQKFGDFLQHS PSILQSKAKKIIETMSSSKLSNVBASKENVSQPKRAKRKLYTSE ISSPIDISGQVILMDQKMKESDHQIIKRRLRTKTAK 5399 705 230 GPRMAKFLSQDQINEYKECFSLYDKQQRGKIKATDLMVAMRCLG ASPTPGEVQRHLQTHGIDGNGELDFSTFLTIMHMQIKQEDPKKE ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRE \ADIEPNGKVKYDEFIHKITSYLDGTY 5400 931 248 SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFEVQKVK QASMEDIPGRGHKYRLKFAVEEIIQKQVKVNCTAEVLYPSTGQE				
ARKRKSNEMEEDLVKCENKKNATPRTNLKFPISDDRNSSVKKEQ KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTLQKFGDFLQHS PSILQSKAKKIIETMSSSKLSNVRASKENVSQPKRAKRKLYTSE ISSPIDISGQVILMDQKMKESDHQIIKRRLRTKTAK 5399 705 230 GPRMAKFLSQDQINEYKECFSLYDKQQRGKIKATDLMVAMRCLG ASPTPGEVQRHLQTHGIDGNGELDFSTFLTIMHMQIKQEDPKKE ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRE \ADIEPNGKVKYDEFIHKITSYLDGTY 5400 931 248 SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFEVQKVK QASMEDIPGRGHKYRLKFAVEEIIQKQVKVNCTAEVLYPSTGQE	1		1	
KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTLQKFGDFLQHS PSILQSKAKKIIETMSSSKLSNVEASKENVSQPKRAKRKLYTSE ISSPIDISGQVILMDQKMKESDHQIIKRRLRTKTAK 5399 705 230 GPRMAKFLSQDQINEYKECFSLYDKQQRGKIKATDLMVAMRCLG ASPTPGEVQRHLQTHGIDGNGELDFSTFLTIMHMQIKQEDPKKE ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRE \ADIEPNGKVKYDEFIHKITSYLDGTY 5400 931 248 SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFEVQKVK QASMEDIPGRGHKYRLKFAVEEIIQKQVKVNCTAEVLYPSTGQE				
PSILQSKAKKIIETMSSSKLSNVBASKENVSQPKRAKRKLYTSE ISSPIDISGQVILMDQKMKESDHQIIKRRLRTKTAK 5399 705 230 GPRMAKFLSQDQINEYRECFSLYDKQQRGKIKATDLMVAMRCLG ASPTPGEVQRHLQTHGIDGNGELDFSTFLTIMHMQIKQEDPKKE ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRE \ADIEPNGKVKYDEFIHKITSYLDGTY 5400 931 248 SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFEVQKVK QASMEDIPGRGHKYRLKFAVBEIIQKQVKVNCTAEVLYPSTGQE	l			
ISSPIDISGQVILMDQKMKESDHQIIKRRLRTKTAK 5399 705 230 GPRMAKFLSQDQINEYKECFSLYDKQQRGKIKATDLMVAMRCLG ASPTPGEVQRHLQTHGIDGNGELDFSTFLTIMHMQIKQEDPKKE ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRE \ADIEPNGKVKYDEFIHKITSYLDGTY 5400 931 248 SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFEVQKVK QASMEDIPGRGHKYRLKFAVEBIIQKQVKVNCTAEVLYPSTGQB	1		1	
5399 705 230 GPRMAKFLSQDQINEYKECFSLYDKQQRGKIKATDLMVAMRCLG ASPTPGEVQRHLQTHGIDGNGELDFSTFLTIMHMQIKQEDPKKE ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRE \ADIEPNGKVKYDEFIHKITSYLDGTY 5400 931 248 SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFEVQKVK QASMEDIPGRGHKYRLKFAVEEIIQKQVKVNCTAEVLYPSTGQE	1			
ASPTPGEVQRHLQTHGIDGNGELDFSTFLTIMHMQIKQEDPKKE ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRE \ADIEPNGKVKYDEFIHKITSYLDGTY 5400 931 248 SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFEVQKVK QASMEDIPGRGHKYRLKFAVEEIIQKQVKVNCTAEVLYPSTGQE			<u> </u>	
ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRE \ADIEPNGKVKYDEFIHKITSYLDGTY 5400 931 248 SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFEVQKVK QASMEDIPGRGHKYRLKFAVEEIIQKQVKVNCTAEVLYPSTGQE	5399	705	230	
\ADIEPNGKVKYDEFIHKITSYLDGTY 5400 931 248 SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFEVQKVK QASMEDIPGRGHKYRLKFAVEEIIQKQVKVNCTAEVLYPSTGQE	1	1		ASPTPGEVQRHLQTHG1DGNGELDFSTFLT1MHMQ1KQEDPKKE
5400 931 248 SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFEVQKVK QASMEDIPGRGHKYRLKFAVEEIIQKQVKVNCTAEVLYPSTGQE]			ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRE
5400 931 248 SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFEVQKVK QASMEDIPGRGHKYRLKFAVEEIIQKQVKVNCTAEVLYPSTGQE	l	1		
QASMEDIPGRGHKYRLKPAVEEIIQKQVKVNCTAEVLYPSTGQE	5400	931	248	
1 1 1		1	"	
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SEC	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nuclcotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine.
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			FGNVSPEMTLVLHLAWVACGYIIWONSTEDTWYKMVKIOTVKOV
		ì	QRNDDFIELDYTILLHNIASQEIIPWQMQVLWHPQYGTKVKHNS
i			RLPKEVQLE
5401	3	1360	TGWSYGPTTSLAFLAPRDFPFPPKLLIHPQAVVRLSCGAGSMGS
	1		QAAAEWRNWASWEGSSSLSGCSMGCFKDDRIVFWTWMFSTYFME
		[KWAPRODDMLFYVRRKLAYSGSESGADGRKAAEPEVEVEVYRRD
			SKKLPGLGDPDIDWEESVCLNLILQKLDYMVTCAVCTRADGGDI
1			HIHKKKSQQVFASPSKHPMDSKGEESKISYPNIFFMIDSF\EE\
1			VFSDMTVGKGEMVCVELVASDKTNTFQGVIFQGSIRYEALKKVY
1			DNRVSVAARMAQK\MSFGFSKYSNMEF\VR\MKGPQGKGHAEMA
			VSRVSTGDTSPCGTEEDSSPASPMHERVTSFSTPPTPERNNRPA
		1	FFSPSLKRKVPRNRIAEMKKSHSANDSEEFFREDDGGADLHNAT
[NLRSRSLSGTGRSLVGSWLKLNRADGNFLLYAHLTYVTLPLHRI
	<u> </u>		LTDILEVRQKPILMT
5402	3445	1563	GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV
			PGADILNSYAGLACVEEPNDMITESSLDVAEEEIIDDDDDDDTL
l			TVEASCHDGDETIETIEAAEALLNMDSPGPMLDEKRINNNIFSS
1			PEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGASSPEQ
1			PKRKKGRKTKPPRPDSPATTPNISVKKKNKDGKGNTIYLWEFLL
			ALLQDKATCPKYIKWTQREKGIFKLVDSKPVSRLWRKHKNKP\D
			MNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDE
1			DPSSSIESSDPSLSSSATSNRNQTSRSRVSSSPGVKGGATTVLK
	•		PGNSKAAKPKDPVEVAQPSEVLRTVQPTQSPYPTQLFRTVHVVQ PVQAVPEGEAARTSTMQDETLNSSVQSIR\TIQAPTQVPVVVSP
			RNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPSSQP
1			MTVLKENVMLQSQKAGSPPSIVLGPARV\QQVLTSNVQTICNGT
			VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ
Ì			ETKTLTQEVEKKESEDHLKENTEKTEQQPQPYVMVVSSSNGFTS
1			QVAMKQNELLEPNSF
5403	3445	1563	GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV
			PGADILNSYAGLACVEBPNDMITESSLDVAREEIIDDDDDDDTL
}			TVEASCHDGDETIETIEAAEALLNMDSPGPMLDEKRINNNIFSS
			PEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGASSPEO
1			PKRKKGRKTKPPRPDSPATTPNISVKKKNKDGKGNTIYLWEFLL
1		l I	ALLQDKATCPKYIKWTQREKGIFKLVDSKPVSRLWRKHKNKP\D
İ			MNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDE
			DPSSSIESSDPSLSSSATSNRNQTSRSRVSSSPGVKGGATTVLK
			PGNSKAAKPKDPVEVAQPSEVLRTVQPTQSPYPTQLFRTVHVVQ
1			PVQAVPEGEAARTSTMQDETLNSSVQSIR\TIQAPTQVPVVVSP
			RNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPSSQP
1			MTVLKENVMLQSQKAGSPPSIVLGPARV\QQVLTSNVQTICNGT
			VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ
			ETKTLTQEVEKKESEDHLKENTEKTEQQPQPYVMVVSSSNGFTS
5404	100		QVAMKQNELLEPNSF
3404	187	1111	LPVTLIFAKMKTLQSTLLLLLLVPLIKPAPPTQQDSRIIYDYGT
			DNFEESIFSQDYEDKYLDGKNIKEKETVIIPNEKSLQLQKDEAI
			TPLPPKKENDEMPTCLLCVCLSGSVYCEEVDIDAVPPLPKESAY
1	1		LYARPNKIKKLT\AKDFADIPNLRRLDFTGNLIEDIEDGTFSKL SLVEELSLAENQLLKLPVLPPKLTLFNAKYNKIKSRGIKANAFK
			KLNNLTFLYLDHNALESVPLNLPESLRVIHLQFNNIASITDDTF
			CKANDTSYIRDRIEEIRLEGNPIVLGKHPNSFICLKRLPIGSYF
5405	2199	1220	QNSRSLHMDPQNQHGSGSSLVVIQQPSLDSRPRLDYEREIOPTA
			ILSLDQIKAIRGSNEYTEGPSVVKRPAPRTAPRQEKHERTHEII
			PINVNNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGS
1			NSSASSEQGLLGRSPPTRPVPGHRSERAIRTQPKQLIVDDLKGS
1			LKEDLTQHKFICEQCGKCKCGECTAPRTLPSCLACNROCLCSAE
			SMVEYGTCMCL\VKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR
			YLCMGAMSLFLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS
	1		NTVYCKLESCPSRGQGKPS
5406	279	2732	RWRTYNVEGPLTFMDVAIEFCLEEWOCLDTAQONLYRNVMLENY
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CEO Dradi	- Dredic	ted end Amin	no acid segment containing signal peptide
SEQ Predi			
ID begin	- 1		Alanine, C=Cysteine, D=Aspartic Acid, E=
NO: nucle			tamic Acid, F=Phenylalanine, G=Glycine,
locat			istidine, I=Isoleucine, K=Lysine,
corre	sponding to fir	st L=L	eucine, M=Methionine, N=Asparagine,
to fi	rst amino	acid P=P:	roline, Q=Glutamine, R=Arginine,
amino	acid residu	e of S=Se	erine, T=Threonine, V=Valine,
resid			ryptophan, Y=Tyrosine, X=Unknown, *=Stop
1			on, /=possible nucleotide deletion,
1 1			• • •
seque	nce		ossible nucleotide insertion)
			VFLG/IIAVSKPDLITCLEQEKEPWEPMRRHEMVAKPPVMC
		SHF	TQDFWPEQHIKDPFQKATLRRYKNCEHKNVHLKKDHKSVDE
1		CKV	HRGGYNGFNQCLPATQSKIFLFDKCVKAFHKFSNSNRHKIS
	i	HTE	KKLFKCKECGKSFCMLSHLAQHKIIHTRVNFCKCEKCGKAF
1 1	ì	- 1	SIITKHKRINTGEKPYTCERCGKVFNWSSRLTTHKKNYTRY
l 1	1		KCEECGKAFNKSSILTTHKIIRTGEKFYKCKECAKAFNQSS
1			
			EHKKIHPGEKPYKCEECGKAFNWPSTLTKHKRIHTGEKPYT
	ł	CEE	cgkafnqfsnltthkrihta\ekfykctecgeafsrs\snl
		TKH	KEIHTEKKPYKCBECGKAFKWSSKLTEHKLTHTGEKPYKCE
1		l KCG	KAFNCPSIITKHNRINTGEKPYTCEECGKVFNWSSRLTTHK
			TRYKLYKCEECGKAFNKSSILTTHKKIHIEKKFYKCEECGK
]			WSSKLTEHKITHTGEKPYKCEECGKAFNHFSILTKHKRIHT
			PYKCEECGKAFTQSSNLTTHKKIHTGEKFYKCEECGKAFTQ
]]			LTTHKKIHTGGKPYKCEECGKAFNQFSTLTKHKIIHTEEKP
		YKC	eecgkafkwsstltkhkiihtgekpykceecg\kafklsst
		LST	HKIIHTGEKPYKCEKCGKAFNRPSNLIEHKKIHTGEQPYKC
1		1	GKAFNYSSHLNTHKRIHTKEQPYKCKECGKAFNQYSNLTTH
]			HTGEKLYKPEDVTVILTTPOTFSNIK
			RROSSCCTGWLAGWLLRAAPRFCRRTETDMEQGKGLAVLIL
5407	3		
			LLQGTLAQSIKGNHLVKVYDYQEDGSVLLTCDAEAKNITWF
i i	ì	1	KMIGFLTEDKKKWNLGSNAKDPRGMYQCKGSQNKSKPLQVY
1 1	f	YRM	CONCIELNAATISGFLFAEIVSIFDLAVGVYFIAGTGMEFR
}		Qs\	RASDKQTLLP\NDPAPTQPLKDPRKMTQYSHLQGN\QLRRN
5408	2745	6128 QGS	KGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP
3400	2/33		OHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL
ł ł		1	PVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF
			-
		t t	CPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP
	ì		TDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE
	ł	VRN	kdmswpeemsfiansskidrhkvptekgatglsnlgntcfm
		NSS	IQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD
i	1	LVO	BLWSGTOKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL
	ł	, -	LHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS
]]	}		DLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL
1 1	1		VIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSBQIL
! i			
1 1)		VHGSNIKNFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP
	1	, -	DFSSSPSTNEMFTLTTNGDLPRPIFIPNGMPNTVVPCGTEK
1 1		NFT	NGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYFLSSQKNR
	İ	PSL	FGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPQEASNH
1		AOD	CDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE
1		ı –	FIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSRRAQ
1	[INLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR
1	1		ILIIHLKRPQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP
	l		
	1		QHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS
1	Ì		LSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS
1	ļ		LRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH
		VLG	GSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG
		NHS	EEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN
1 1			KWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK
1			KKMADTSSMDEDFESDY\EKYCVLQ
<u> </u>			
5409	2745		KGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP
			QHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL
		APR	PVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF
}		STP	CPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP
1			TDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE
			KDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM
1			
	}		IQCVSNTQPLTQYF1SGRHLYELNRTNPIGMKGHMAKCYGD
	}		ELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL
1		T.DG	LHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS
1 1			
1			DLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL
		IVV	DLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL VIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL
		IVV	DLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL VIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL VHGSNIKNFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP

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Notation corresponding to first amino acid residue of anino acid residue of anino acid sequence Notation Sequence	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Costion Coffee	ID	beginning	nucleotide	
corresponding to first damino acid m	NO.	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
corresponding to first amino acid amino acid residue of amino acid sequence and acid residue of amino acid sequence and acid sequence acid seq			corresponding	H=Histidine T=Isoleucine, K=Lysine.
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid sequence ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, (*possible nucleotide deletion, Tyrofssspringht/ThroGlernit ThroGle	ļ			
amino acid residue of amino acid sequence Sequence Sequence Codon, /=possible nucleotide deletion, _>possible nucleotide deletio				
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TGRANGERIKALGSFOKESPUTGLEAARRERTHESAPARPEGG GKRRESDAGAGGERASVKTOGCREGGRTMAGDSEQTLQNHQOPN GGEFFLIGVSGGTASGKSVCAKTVQLLGQNEVDYRQKQVVILS QDSFYRULTSEQKAKALKGQFNFDHPDAFDNELILKTLKEITEG KTVOJPVDFVSHSREETVTVYPAPOVLEGILAFYSOER/IR LNGGPS\NRTINGCLGNSTYDSRKRQASESSRRH TSQLAVAPAPEFCLPFR\KYADVIIPR\GADN\RVPINLIVOHIO\DI LNGGPS\NRTINGCLGNSTYDSRKRQASESSRRH LNGGPS\NRTINGCLGNSTYDSRKRQASESSRRH S412 3180 313 QGISNFPHKEANFWFEVSGYLISPLRSFFVDFALERSIMASFWN KMEGESSRFBIHTPVSDKKKKKCSINKERPQKHSHEIFRDSSLV NEQSGITRRKRKENFOHLISSPLKKSRICDETANATSTLKKRK KRRYSALEVDEBAGVTVVLVDKENINTPHFRKDVDVVCVDMS IEQKLPFR\PKTKFVQVLAKSH\AHKSEALHSKVRSKKNKKOJR KAASWESQRA\RDTLPQSEFPTQBESULSVGPGGEITELP\ASA HKNKSKKKKKSNRYET\LAMPEGSQAGERAGTUMGESQFTV GLDDETTQLLGPTHKKSKKKKKKSNNQEFSELAMPEGSQVGS EVGANMGES\RPAVGLHGETAGIPAFAYNKKGKKKKKKSNNQEF EAVAMPESLESAYPEGSQVGSEVGTVESGTALKGFKESNTKKK SKKRKLTSVKRARVSGDDFSVPSKNESTLFDSVEDDGAMMEG VKSRPRQKKTQACLASKHVQEAPRLEFANEENVETAEDSSIRY LSANSGDADDSDADLGSAVKQLGEFINIKDRATSTIKMTVRDD LERFKEFKAGGVAIKFGKFSVKENKQLEFNIKDATIKKMYSDD LERFKEFKAGGVAIKFGKFSVKENKQLEKAVEDFLALTGIESAD KLLYTDRYPEKSVITNLKRRYSFRLHIG\RNIARPWKLIYYRA KMFDVNNYKGRYSEGDTE KLKMYHSLLGNDMKTIGEMVARRSL SVALKFSGISSQRNRGAMSKETTRIL KAVEEVILKKMSPOBIK EDSKLOENPESCISLTVERKLYKGHVEVEVEAVOTRINMCKGS KWTEILTKRMTNGRIYYGMALRAKVSLIERLYEINVEDITNEI DWEDLASAIGDVPSTVOTKFSRLKAVYVPPMOKKTFPEIIDYL YETTLEJLLEKELKENMEKKGTTIGTPAAPRQVPFPMOKTFPEIIDYL YETTLEJLLEKELKENMEKKGTTIGTPAAPRQVPFPMOKTFPEIIDYL SEGGGHKKRKRRPRRHAMPTDYIPVLMEAKAGHIT TTEIKRWICALIGILTGLVACFIUTPALFROTHFATERGGG TPLLNGAGFOAARGSFRSALFRVGMSVLLDDELLEP\DMDP HPFPREIPHHEKLLSLKYESDJYDNSKOLJELEERRINHTAFR TTEIKRWICALIGILTGLVACFIUTPALFROTHSPUTSHAGGG IKCELNGVKIPHVVRIKKTLUIKVSGVILVVENIAGLKYRVIKKNID KFTEKGGLSFSLLLWATLNAAFVLVGSVIVAFIEPPVAAGSGIPQ IKCELNGVKIPHVVRIKKTLUIKVSGVILVVENIAGLKYRVIKKNID KFTEKGGLSFSLLLBATLNAAFVLVGSVIVAFIEPPVAAGSGIPQ IKCELNGVKIPHVVRIKKTLUIKVSGVILVVENIAGLKYRVIKKNID VISHAMGGGOAAFGAPRAMANVSKKVSMAYTHEIPVFIAMGVV VSAAFGAPVGGVLPSLEEGASFWNOFLTWEIFFASMISFFTLINF VISHYMOALDIGGGVLPSLEEGASFWNOFLTWEIFFASMISFFTLINF VISHYMOALDIGGROFHAANTATUVAAVAVATATVA		1	1	ENINIDEASRCLVKHILANECDLMESIEPDVVKPHLTSTKVASC
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SGSVIAAGISQGRSTSLKRDFKIFEYLRRDTEKRDFVSAGAAAG VSAAFGAPVGGVLFSLEEGASFWNQFLTWRIFFASMISTFTLNF VLSIYHGNMWDLSSPGLINFGRFDSEKMAYTIHEIPVFIAMGVV GGVLGAVFNALNYWLTMFRIRYIHRPCLQVIEAVLVAAVTATVA	1		1	
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FVLIYSSRDCQPLQGGSMSYPLQLFCADGEYNSMAAAFFNTPEK				

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
[residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ì	amino acid	sequence	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		SVVSLFHDPPGSYNPLTLGLFTLVYFFLACWTYGLTVSAGVFIP
1	1		SLLIGAAWGRLFGISLSYLTGAAIWADPGKYALMGAAAQLGGIV
			RMTLSLTVIMMEATSNVTYGFPIMLVLMTAKIVGDVFIEGLYDM
			HIQLQSVPFLHWEAPVTSHSLTAREVMSTPVTCLRRREKVGVIV
		}	DVLSDTASNHNGFPVVEHADDTQPARLQGLILRSQLIVLLKHKV
	ļ		FVERSNLGLVQRRLRLKDFRDAYPRFPPIQSIHVSQDERECTMD
	}		LSEFMNPSPYTVPQEASLPRVPKLFRALGLRHLVVVDNRNQVVG
)		LVTRKDLARYRLGKRGLEELSLAQT
5414	2130	390	GVASAWDRALFSPLLSPTSRVFRTSPPRCVSTETGRRDRARVPS
			QWCSVLQGKLPVSGRTSLACVRSILLSPASSPRKVGIVGGTGAR
1			AGAAPRDHGRVRHRRPSSARRMTRTTGQCLAPRGCQGPRGTRSP
	1		RSPRSRTRRGCSASPACLP/CRSALIVAVLCYINLLNYMDRFTV
	1	}	AGVLPDIEQFFNIGDSSSGLIQTVFISSYMVLAPVFGYLGDRYN
	1	}	RKYLMCGGIAFWSLVTLGSSFIPGEHFWLLLLTRGLVGVGEASY
			STIAPTLIADLFVADQRSRMLSIFYFAIPVGSGLGYIAGSKVKD MAGDWHWALRVTPGLGVVAVLLLFLVVREPPRGAVERHSDLPPL
	1		NPTSWWADLRALARNPSFVLSSLGFTAVAFVTGSLALWAPAFLL
	· ·	ļ	RSRVVLGETPPCLPGDSCSSSDSLIFGLITCLTGVLGVGLGVEI
			SRRLRHSNPRADPLVCATGLLGSAPFLFLSLACARGSIVATYIF
ļ			IFIGETLLSMNWAIVADILLYVVIPTRRSTAEAFQIVLSHLLGD
]			AGSPYLIGLISDRLRRNWPPSFLSEFRALQFSLMLCAFVGALGG
			AAFLGTAHLH
5415	693	2986	IPPKTKLELQKH\LTTLT\NQEQATIFEEVQKLRPRNEQRENEL
		}	IISFLRCLFEEKQKEHIHIGEMKQTSQMAAENIGSELPPSATRF
1			RLDMLKNKAKRSLTESLESILSRGNKARGLQBHSISVDLDSSLS
ļ			STLSNTSKEPSVCEKEALPISESSFKLLGSSEDLSSDSESHLPE
]			EPAPLSPQQAFRRRANTLSHFPIECQEPPQPARGSPGVSQRKLM
			RYHSVSTETPHERKDFESKANHLGDSGGTPVKTRRHSWRQQIFL RVATPQKACDSSSRYEDYSELGELPPRSPLEPVCEDGPPGPPPE
1			EKKRTSRELRELWQKAILQQILLLRMEKENQKLQASENDLLNKR
i			LKLDYEEITPCLKEVTTVWEKMLSTPGRSKIKFDMEKMHSAVGO
j			GVP\RHHRGEIWKFLAEQFHLKHQFPSKQQPKDVPYKELLKQLT
l		i	SQQHAILIDLGRTFPTHPYFSAQLGAGQLSLYNILKAYSLLDQE
			VGYCQGLSFVAGILLLHMSEEEAFKMLKFLMFDMGLRKQYRPDM
1			IILQIQMYQLSRLLHDYHRDLYNHLEEHEIGPSLYAAPWFLTMF
			ASQFPLGFVARVFDMIFLQGTEVIFKVALSLLGSHKPLILQHEN
	1		LETIVDFIKSTLPNLGLVQMEKTINQVFEMDIAKQLQAYEVEYH
			VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANG
			RIQSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRRS
EATE	27	4074	AKPSDREPECTOPEPTGD
5416	1 4/	40/4	KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES
	1		LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP
			ENROLPPPS POLPKHNLHVTKTLMETRRLEOERATMOMTPGEF
			RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG
			SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLOHIRBOM
			AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA
			SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME
			TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC
1			RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE
			AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT
			KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH
1			MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER
			VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT
			NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV
		}	MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ
1			TSTQTVETRTVAVGRGRVKDINSSTKTRSIGVGTLLSGHSGFDR
			PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ
}			TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAST
			EELRNPDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQPE
			

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RQELEEKIRRKEEEEAKTVSAAAAEKEPVPVPVQEIEIDSTTEL DGHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPR\EPPI LPRIQEQFQKWPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHBLKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF 5419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESBACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCCHHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG	5418	24	1133	
DGHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPR\EPPI LPRIQEQFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHBLKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF 5419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG				
LPRIQEQFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK GKQVSVALSSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EPGKCVLVNLSKVGEYWMNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTPDYHQKLQGKPQSHBLKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF 5419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRRKSEEEGGRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDBESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG	1		ľ	
GKQVSVALSSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTTPYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF 5419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDFASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDBESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVXNPQSKT YCKRLQVLCPPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG			1	1
EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF 5419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALKHMERCXAKYESQTSFGSMYPTRIEGATRLFCDVXNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG				
EEQAVLDRLTFDYHQKLQGKPQSHBLKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF 5419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESBACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPBRADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG	1			
GQRFDPAMFNISPGAVQF 5419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG			{	
5419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKILERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG			J	
SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDBESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG	5419	1195	750	
KDFASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDBESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG	7413	1333	455	·=
PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALKHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG			1	
ELEAIILRAKQQAVREDBESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG	1		1	_ · · · · · · · · · · · · · · · · · · ·
VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG			1	
YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG	1			
RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG			J	
RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG			1	RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEGERNVRTAMTN
			1.	
GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR	5420	117	1733	
	L	<u> </u>	<u></u>	GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR

SEQ	Predicted	Predicted end	Amino noid control
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			ECIISTLLFATLYILCHIFLTRFKKPAEFTT\GMMKMPPSTRL/
1	ì	ł	LLELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYYIQWLNGS
1		}	LIHGLWNLVFLFSNLSLIFLMPFAYFFTESEGFAGSRKGVLGRV
l			YETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYLP
1		[YLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEE
1	ļ	ļ	QLYCSAFEEAALTRRICNPTSCWLPLDMELLHRQVLALQTQRVL
i		i	LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID
]		1	EAAMPRGMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVVGF
ļ	}		YSSPLFRSLRPRWHDTAMTQIIGNCVCLLVLSSALPVFSRTLGL
i	1		TREDLLGDEGRENWLGNEYIVELYNAAFAGLTTLCLVKTETAAV
Į.	ļ		RABLIRAFGERE
5421	117	1733	NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG
		1	GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR
	1	1	ECIISTLIFATLYILCHIFLTRFKKPAEFTT\GMMKMPPSTRL/
	1		LLELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYYIQWLNGS
			LIHGLWNLVFLFSNLSLIFLMPFAYFFTESBGFAGSRKGVLGRV
1			YETVVMLMLITLLVLGMVWVASAIVDKNKANRESLYDFWEYYLP
1			YLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEE
1	Į.		QLYCSAFEEAALTRRICNPTSCWLPLDMELLHRQVLALQTQRVL
)	}		LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID
			EAAMPRGMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVVGF
			YSSPLFRSLRPRWHDTAMTQIIGNCVCLLVLSSALPVFSRTLGL
ĺ			TRFDLLGDFGRFNWLGNFYIVFLYNAAFAGLTTLCLVKTFTAAV
			RAELIRAFGERE
5422	3	1263	SCGESLPTWLAGASRPGIGRKGGAWGGRGGSSPAQVLLSPGPVF
	ĺ		KAGCNWWHLSRDQAGVQRCDLGSSQPPPLGFKRFSCLSLPSSWD
			YRSTVLCVSKMEADLSGFNIDAPRWDQRTFLGRVKHFLNITDPR
ì			TVFVSERELDWAKVMVEKSRMGVVPPGTQVEQLLYAKKLYDSAF
			HPDTGEKMNVIGRMSFQLPGGMIITGFMLQFYRTMPAVIFWQWV
[NQSFNALVNYTNRNAASPTSVRQMALSYFTATTTAVATAVGMNM
ľ			LTKKAPPLVGRWVPFAAVAAANCVNIPMMRQQELIKGICVKDRN
ł			ENEIGHSRRAAAIGITQVVISRITMSAPGMILLPVIMERLEKLH
			FMQKVKVL/SAPLQVMLSGCFLIFMVPVACGLFPQKCELPVSYL
			EPKLQDTIKAKYGELEPYVYFNKGL
5423	3186	905	GVSMALGEEKAEAEASEDTKAQSYGRGSCRERELDIPGPMSGEQ
			PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHOPQASD
			ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVEKTKLSSSE
]	İ	EFPQTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG
		!	LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQGHQERAEPRG
			GSLAKVSSSLEPVVPQEPSSVVGLGPRPQWSPQPVFSGGDASGL
]		GRRRLSFQAEYWACVLPDSLPPSPDRHSPLWNPNKEYEDLLDYT
			YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP
			TNVSPNCPPAEATALPFSGPREPSLKQWPSRVPQKQGGMGLASW
1			SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPOL
			RTRDRGWPSPRPEREKRTSQSARRPTCTESRWKSEEEVESDDEY
]			LALPARLTQVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG
			PASFPSSSSQSQLPPGAALQGSGDPEGQNPCFLRSFVRAHDSAG
			EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK
		i	GGEQGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR
		ļ	SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLQKGEILLQCLLE
			NTPVLEDVLGRIAKQSGELESHADRLYDSILASLDMLAGCTLIP
		İ	DKKPMAAMEHPCEGV
5424	3186	905	GVSMALGEEKAEARASEDTKAQSYGRGSCRERELDIPGPMSGEQ
		j	PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQPQASD
			ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVEKTKLSSSE
		ļ	EFPQTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG
			LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQGHQERAEPRG
	j	ſ	GSLAKVSSSLEPVVPQEPSSVVGLGPRPQWSPQPVFSGGDASGL
			GRRRLSFQAEYWACVLPDSLPPSPDRHSPLWNPNKEYEDLLDYT
			YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP
			TNVSPNCPPAEATALPFSGPREPSLKQWPSRVPQKQGGMGLASW

		, _ , , , , , , , , , , , , , , , , , ,	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
)	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
j	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
}	Coquence	 	SOLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPOL
		1	RTRDRGWPSPRPEREKRTSOSARRPTCTESRWKSEEEVESDDEY
t	1	1	1
ļ	1	ļ	LALPARLTQVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG
1		1	PASFPSSSSQSQLPPGAALQGSGDPEGQNPCFLRSFVRAHDSAG
ĺ	1	1	EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGOLPRK
1			GGEQGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR
1	1		SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLQKGEILLQCLLE
Í	ĺ		NTPVLEDVLGRIAKQSGELESHADRLYDSILASLDMLAGCTLIP
}	Į.		DKKPMAAMEHPCEGV
5425	1086	115	GFCPSPSLGHOPPRVLHPTMSMAVETFGFFMATVGLLMLGVTLP
			NSYWRVSTVHGNVITTNTIFENLWFSCATDSLGVYNCWEFPSML
1			ALSGYIOACRALMITAILLGFLGLLLGIAGLRCTNIGGLELSRK
1		 	AKLAATAGAPH\ILPGICGMVAI\SWYAFNITR\DFSDPLYPGT
			KYELGPALYLGWSASLISILGGLCLCSACCCGSDEDPAASARRP
1	ļ		
		}	YQAPVSVMPVATSDQEGDSSFGKYGRNALRVAALCRGPRCLPTA
1			PKKRGPGRGPFPYSNLRGRPRPVPVAPPRPRPRVLHSHGPSQAK
			NCSWEVAYLPSEAGSLIF
5426	42	3435	ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP
			PAAHAKPDPGSGGQPAGPGAAGRALAVLTSFGRRLLVLIPVYLA
1			GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL
			TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK
			LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR
			KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL
		ļ	EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD
			TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL
			LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN
			POWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV
		İ	LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG
			VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP
			·-
			MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQBLDVQV
		· ·	KDDSRALTIGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM
ł	1		KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR
	1		PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY
			VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF
	1	1	DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL
	1	1	ERLTPRPTAABLEEVLQVNSLIQTQKSAELAAALLSIYMERAED
			LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI
ì		1	RKPHTESLELOVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL
		}	SSGOGOVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEEPELS
	t		GGPPHITSSAPEV\RORLTHVDSPLEAPAGPLGQVKLTLWYYSE
1	1		ERKLVSIVHGCRSLRONGRDPPDPYVSLLLLPDKNRGTKRRTSO
}			KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL
			LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS
F127	 	3435	ATSOSLGRADPPRGGTMERSPGEGPSPSPMDOPSAPSDPTDOP
5427	42	3435	
			PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA
		,	GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL
1			TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK
			LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR
1			KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL
	1		EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD
	1		TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL
			LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN
	1	İ	POWGETYEVMVHEVPGOEIEVEVFDKDPDKDDFLGRMKLDVGKV
	}		LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG
			VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP
			MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV
			KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM
Į			KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR
			PCHTTPDSQFGTBHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY
1			VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVBVF
1	į		DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL

SEQ	Predicted	The state of	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cvsteine, D=Aspartic Acid R-
10.	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine
1		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
ì		amino acid	P=Proline, Q=Glutamine, R=Arginine
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop
Ì	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
			ERLTPRPTAAELEEVLQVNSLIQTQKSAELAAALLSIYMERAED
	1	1	LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI
ĺ		ļ	RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL
Í	1		SSCOCOULI PAOL CIL MONICONES MENTE DE LE VADOL CLDRWFTL
1	}	}	SSGQGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEEPELS
ļ			GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE
	ĺ		ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ
}]	KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL
5428			LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS
3420	3	1839	SSRSERLSACAIAPPWLVSSRPARPAQLQRPGKMVEDGAEELED
ł			LVHFSVSELPSRGYGVMEEIRROGKLCDVTLKIGDHKRSAHDTV
	•		LAASIPYPHAMFTNDMMECKODEIVMOGMDPSALEALINFAVNC
1	1		NLAIDQQNVQSLLMGASFLQLQSIKDACCTFLRERLHPKNCLGV
			RQFAETMMCAVLYDAANSFIHQHFVEVSMSEEFLALPLEDVLEL
1			VSRDELNVKSEEQVFEAALAWVRYDREQRGTFL\RNLQSNIRLL
1	1		FCRPQFLSDRVQQDDLVRCCHKCRDLVDEAKDYLLMPERRPHLP
]	•	AFRTRPRCCTS IAGLIYAVGGLNSAGDSLNVVEVFDPIANCWER
1			CRPMTTARSRVGVAVVNGLLYAIGGYDGQLRLSTVQAYNTETDT
1			WTRVGSMNSKRSAMGTVVLDGQIYVCGGYDGNSSLSSVETYSPE
Ţ			TDKWTVVTSMSSNRSAA\GVTVFEGRIYVSGGHDGLQIFSSVEH
1	1		VNUUTATUUDA ACMANICA SI COMMANDE SI COMMANDO SI COMMAN
1			YNHHTATWHPAAGMLNKRCRHGAASLGSKMFVCGGYDGSGFLSI
			AEMYSSV\ADQWCLIVPM\HTRR\SRVSLGGPAVGRLYAVWGVT
	}		TGQSNL\SSVGDVLTPETDCWTFM\APMACHEGGVGVGCIPLLT
5429	828	202	I
3.25	020	202	RREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPF
			AQRERFHRFQPTYPYLOHEIDLPPTISLSDGREPPPYOGPCTLO
			LRDPEQQLELNRESVRAPPNRTIFDSDLMDSARIGGPCDDSGNG
			GISATCYGSGGRMEGPPP\TYSEVIGHYPGSSFOHOOSGGDDGT
			LEGTRLHHTHIAPLESAAIWSKEKDKOKGHPI.
5430	441	1507	QKRRKRRKKIMKTIQPKMHNSISWAIFTGLAALCLFOGVDVDC
1			GDATFPKAMDNVTVRQGBSATLRCTIDNRVTRVAWLNRSTILYA
} }	' }		GNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDN
1	i		HPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEP
1	j	i	TVTWRHISPKAVGFVSEDEYLEIQGITREQSGDYECSASNDV\A
1 1	1	į	APV\VRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSA
			EFQWYKDDKRLI/EGKKGVKVENRPFLSKLIFFNVSEHDYGNYT
! !			CVASNKLGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVL
]	1		HLLLKF
5431	2	1312	
1 - 1	-	1314	AAAAPGSRRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\
1 1			LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELELDEQQ
1			KKRLEAFLTQKAKVGELKDDDFERISELGAGNGGVVTKVQHRPS
1 1		}	GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGAFY
; !			SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVI,DGI,A
] [1	ľ	YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGOLIDSMANS
1	1	ł	FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIDDD
;	1		DAKELEAIFGRPVVDGEEGEPHSISPRPRPPGRPVSGHGMDSRP
[1	AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA
		ţ	DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV
5432	2	1312	AAAAPGSRRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\
	1		LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELELDEQQ
1		·	KKRLEAFLTQKAKVGELKDDDFERISELGAGNGGVVTKVQHRPS
	ļ		GI.IMADVI.TUI ETVDA FONOTTO
			GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGAFY
	1		SDGEISICMEHMDGGSLDQVLKEAKRIPBEILGKVSIAVLRGLA
			YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS
		1	FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIDDD
	į	1	DAKELEAIFGRPVVDGEEGEPHSISPRPRPPGRPVSGHGMDSRP
			AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA
			DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNOPGTPTRTAV
E / 77	360	1885	SVQEDKVGFEDPLHLCSWRARACPCTWPHC/CTGLLECLGFAGV
5433	300	2005	D. SPRINGI EDETUTC SAKKKUT, DC. L.M. DHC. M. LASTITISCA V. EX. VI.
2433	1	1000	LFGWPSLVFVFKNEDYFKDLGDDAGPTGNATGOADCVACCAC
3433		1	LFGWPSLVFVFKNEDYFKDLCGPDAGPIGNATGQADCKAQDERF SLIFTLGSFMNNFMTFPTGYIFDRFKTTVARLIAIFFYTTATLI

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
-			IAFTSAGSAVLLFLAMPMLTIGGILFLITNLQIGNLFGQHRSTI
l			ITLYNGAFDSSSAVFLIIKLLYEKGISLR/VLLHLHLCLQYLAC
1	1		STHFPPDAPGAHPIPTAPQLQLWPVPWEWHHKGREG/QQLSMKT
			GSYSQRSSFQRRKRPQGQGRSRNSAPSGATL/CSRRFAWHLVWL
1	1	į.	SVIQLWHYLFIGTLNSLLTNMAGGDMARVSTYTNAFAFTOFGVL
1	1		CAPWNGLLMDRLKQKYQKEARKTGSSTLAVALCSTVPSLALTSL
1			LCLGFALCASVPILPLQYLTFILQVISRSPLYGSNAAFLTLAFP
1	1		SEHFGKLFGLVMALSAVVSLLQFPIFTLIKGSLONDPFYVNVMF
1	1		MLAILLTFFHPFLVYRECRTWKESPSAIA
5434	 		
5434	66	652	RYAALIISLIQHKLLWRNQHCSRCVIMSPAQSAGLNWLF/GSGK
		1	HGPFLGCSQYPACDYVRPLKSSADGHIVKVLEGQVCPACGANLV
1		1	LRQGRFGMFIGCINYPECEHTBLIDKPDETAITCPQCRTGHLVQ
			RRSRYGKTFHSCDRYPECQFAINFKPIAGECPECHYPLLIEKKT
	<u> </u>	<u></u>	AQGVKHFCASKQCGKPVSAE
5435	4704	1597	PGDSSQRLAEMSNAKERKHAKKMRNQPTNVTLSSGFVADRGVKH
			HSGGEKPFQAQKQEPHPGTSRQRQTRVNPHSLPDPEVNEQSSSK
-	1		GMFRKKGGWKAGPEGTSQEIPKYITASTFAQARAAEISAMLKAV
1	l .		TOKSSNSLVFQTLPRHMRRRAMSHNVKRLPRRLQEIAQKEAEKA
[VHQKKEHSKNKCHKARRCHMNRTLEFNRRQKKNIWLETHIWHAK
1			RFHMVKKWGYCLGERPTVKSHRACYRAMTNRCLLQDLSYYCCLE
Ì			LKGKEEEILKALSGMCNIDTGLTFAAVHCLSGKROGSLVLYRVN
ł		l	KYPREMLGPVTFIWKSQRTPGDPSESRQLWIWLHPTLKQDILEE
Ì		1	IKAACQCVEPIKSAVCIADPLPTPSOEKSOTELPDEKIGKKRKR
[
)	ļ		KDDGENAKPIKKIIGDGTRDPCLPYSWISPTTGIIISDLTMEMN
l	İ	i	RFRLIGPLSHSILTEAIKAASVHTVGEDTEETPHRWWIETCKKP
(-		DSVSLHCRQEAIFELLGGITSPAEIPAGTILGLTVGDPRINLPQ
ı			KKSKALPNPEKCQDNEKVRQLLLEGVPVECTHSFIWNQDICKSV
1		1	TENKISDQDLNRMRSELLVPGSQLILGPHESKIPILLIQQPGKV
ł		1	TGEDRLGWGSGWDVLLPKGWGMAFWIPFIYRGVRVGGLKESAVH
į			SQYKRSPNVPGDFPDCPAGMLFAEEQAKNLLEKYKRRPPAKRPN
		4	YVKLGTLAPFCCPWEQLTQDWESRVQAYEEPSVASSPNGKESDL
ļ	1		RRSEVPCAPMPKKTHQPSDEVGTSIEHPREAEEVMDAGCQESAG
1			PERITDQEASENHVAATGSHLCVLRSRKLLKQLSAWCGPSSEDS
ł	ł	}	RGGRRAPGRGQQGLTREACLSILGHFPRALVWVSLSLLSKGSPE
1	1		PHTMICVPAKEDFLQLHEDWHYCGPQESKHSDPFRSKILKOKEK
			KKREKRQKP\GRASSDGPAGEEPVAGQEALTLGLWSGPLPRVTL
]			HCSRTLLGFVTQGDFSMAVGCGEALGFVSLTGLLDMLSSQPAAO
		İ	RGLVLLRPPASLQYRFARIAIEV
5436	1781	635	ASDSIPWSEARTTRKLAQRGCQWSLPERMPLVVFCGLPYSGKSR
] 2250	1,01)	RABELRVALAAEGRAVYVVDDAAVLGAEDPAVYGDSAREKALRG
			ALRASVERRLSRHDVVILDSLNYIKGFRYELY\CLARAARTPLC
1	}	1	1
1			LVYCVRPGGPIAGPQVAGANENPGRNVSVSWRPRAEEDGRAQAA
1		ľ	GSSVLRELHTADSVVNGSAQADVPKELEREESGAAESPALVTPD
		}	SEKSAKHGSGAFYSPELLEALTLRFEAPDSRNRWDRPLFTLVGL
1 .			EEPLPLAGIRSALFENRAPPPHQSTQSQPLASGSFLHQLDQVTS
1		1	QVLAGLMEAQKSAVPGDLLTLPGTTEHLRFTRPLTMAELSRLRR
	<u></u>		QFISYTKMHPNNENLPQLANMFLQYLSQSLH
5437	739	1672	CQEAASEFGGPLHTPAMFLRRLGGWLPRPWGRRKPMRPDPPYPE
			PRRVDSSSENSGSDWDSAPETMEDVGHPKTKDSGALRVSRAASE
	1		PSKEEPQVEQLGSKRMDSLKWDQPISSTQESGRLEAGGASPKLR
			WDHVDSGGTRRPGVSPEGGL\GVPGPGAPLEXPGRREKLLGWLR
	1		GEPGAPSRYLGGPEECLQISTNLTLHLLELLASALLALCSRPLR
[AALDTIGLRGPLGLWLHGLLSFLAALHGLHAVLSLLTAHPLHFA
1	1	Ì	
}			CLFGLLQALVLAVSLREPNGDEAATDWESEGLEREGEEQRGDPG
- C ())	 		KGL
5438	2443	1152	TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS
l	[ĺ	LAPPSLRRPMMCQSEARQGPELRAAKWLHFPQLALRRRLGQLSC
1			MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS
			VPTRLLSRAWGRLNQVELPHWLRRPVYSLYIWTFGVNMKEAAVE
1		131	DLHHYRNLSEFFRRKLKPQARPVCGLHSVISPSDGRILNFGQVK
		[NCEVEQVKGVTYSLESFLGPRMCTEDLPFPPAASCDSFKNQLVT
			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į.	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
ļ			REGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFPGSLMSVNP
1		1	GMARWIKELFCHNERVVLTGDWKHGFFSLTAVGAT\NWGSIRIY
			FDRDLHTNSPRHSKGSYNDFSFVTHTNREGVPMALRGEHLG/QS
			FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGEALGSL
5439	2443	1152	TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS
			LAPPSLRRPMMCQSEARQGPELRAAKWLHFPQLALRRRLGQLSC
Ì	į.	1	MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS
1			VPTRLLSRAWGRLNQVELPHWLRRPVYSLYIWTFGVNMKEAAVE
}	1		DLHHYRNLSEFFRRKLKPQARPVCGLHSVISPSDGRILNFGQVK
	İ	Ì	NCEVEQVKGVTYSLESFLGPRMCTEDLPFPPAASCDSFKNQLVT
j		Ì	REGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFPGSLMSVNP
1			GMARWIKELFCHNERVVLTGDWKHGFFSLTAVGAT\NWGSIRIY
1		1	FDRDLHTNSPRHSKGSYNDFSFVTHTNREGVPMALRGEHLG/QS
	<u> </u>		FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGEALGSL
5440	693	253	EPIPVTPDHRLVTMTHIV\QTFSPVNS\GQPPNYEMLKEEQEVA
		İ	MLGAPHNPAPPMSTVIHIRSETSVPDHVVWSLFNTLFMNTCCLG
]	1	FIAFAYSVKSRDRKMVGDVTGAQAYASTAKCLNIWALILGIFMT
L		l	ILLIIIPVLVVQAQR
5441	2	2054	CRDGGKNGFMVSPMKPLEIKTQCSGPRMDPKICPADPAFFSFIN
			NSDLWVANIETGEERRLTFCHQGLSNVLDDPKSAGVATFVIQEE
			FDRFTGYWWCPTASWEGSEGLKTLRILYEEVDESEVEVIHVPSP ALEERKTDSYRYPRTGSKNPKIALKLAEFOTDSOGKIVSTOEKE
}		li di di di di di di di di di di di di di	LVOPPSSLFPKVEYIARAGWTRDGKYAWAMFLDRPQQWLQLVLL
			PPALFIPSTENEEQ\RLASARAVPRNVQPYVVYEEVTNVWINVH
			DIFYPFPQSEGEDELCFLRANECKTGFCHLYKVTAVLKSQGYDW
	1	Ì	SEPFSPGEGEQSLTNAIWVNEETKLVYFQGTKDTPLEHHLYVVS
l			YEAAGEIVRLTTPGFSHSCSMSQNFDMFVSHYSSVSTPPCVHVY
{	-		KLSGPDDDPLHKQPRFWASMMEAAKIFHFHTRSDVRLYGMIYKP
}	}	1	HALQPGKKHPTVLFVYGGPQVQLVNNSFKGIKYLRLNTLASLGY
ļ	}]	AVVVIDGRGSCQRGLRFEGALKNQMGQVEIEDQVEGLQFVAEKY
ſ			GFIDLSRVAIHGWSYGGFLSLMGLIHKPQVFKVAIAGAPVTVWM
	1		AYDTGYTERYMDVPENNOHGYEAGSVALHVEKLPNEPNRLLILH
l	1		GFLDENVHFFHTNFLVSQLIRAGKPYQLQVALPPVSPQIYPNER
Į.			HSIRCPESGEHYEVTLLHFLQEYL
5442	1	3474	CGQRSRRRSPDMPEAKPAAKKAPKGKDAPKGAPKEAPPKEAPAE
			APKEAPPEDQSPTAEEPTGVFLKKPDSVSVETGKDAVVVAKVNG
1	-		KELPDKPTIKWFKGKWLELGSKSGARFSFKESHNSASNVYTVEL
Ì	1	1	HIGKVVLGDRGYYRLEVKAKDTCDSCGFNIDVEAPRQDASGQSL
Į.			ESFKRTSEKKSDTAGELDFSGLLKKREVVEEEKKKKKKDDDDLG
ł		ļ	IPPEIWELLKGAKKSEYEKIAFQYGITDLRGMLKRLKKAKVEVK
	1		KSAAFTKKLDPAYQVDRGNKIKLMVEISDPDLTLKWFKNGQEIK
			PSSKYVFENVGKKRILTINKCTLADDAAYEVAVKDEKCFTELFV
1	1		KEPPVLIVTPLEDQQVFVGDRVEMAVEVSEGAQVMWMKDGVEL
	}	1	TREDSFKARYRFKKDGKRHILIFSDVVQEDRGRYQVITNGGQCE
			AELIVEEKQLEVLQDIADLTVKASEQAVFKCEVSDEKVTGKWYK
j			NGVEVRPSKRITISHVGRFHKLVIDDVRPEDEGDYTFVPDGYAL
}			GSLSAKLNFLEIKVEYVPKQ\EPPKIPLGFASGGKTSENAD/IV
	1		VVAGNKLRLDV\SITGEAPSPFAT\WLKG\DEVFTTTEGRTRIE KRVDCSSFVIESAOREDEGRYTIKVTNPIGEDVASIFLOVVDVP
			DPPEAVRITSVGEDWAILVWEPPMYDGGKPVTGYLVERKKKGSQ
	1		RWMKLNFEVFTETTYESTKMIEGILYEMRVFAVNAIGVSOPSMN
			TKPFMPIAPTSEPLHLIVEDVTDTTTTLKWRPPNRIGAGGIDGY
			LVEYCLEGSEEWVPANTEPVERCGFTVKNLPTGARILFRVVGVN
1	1		IAGRSEPATLAQPYTIREIAEPPKIRLPRHLRQTYIRKVGEQLN
			LVVPFOGKPRPQVVWTKGGAPLDTSRVHVRTSDFDTVFFVRQAA
	1		RSDSGEYELSVQIENMKDTATIRIRVVEKAGPPINVMVKEVWGT
1			NALVEWQAPKDDGNSEIMGYFVOKADKKTMEWFNVYERNRHTSC
i			TVSDLIVGNEYYFRVYTENICGLSDSPGVSKNTARILKTGITFK
			PFEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKV
			VWMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV
1			NELGEALAECKLEVRVPO
			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1,0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ			
ĺ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
5443	66	1003	SRGQLDAGQSSEQHGGNRQPEQSRSRSSSSSSSSSSSSRRSRSAAEPA
			MALSMPLNGLKEEDKEPLIELFVKAGSDGESIGNCPFSQRLFMI
1			LWLKGVVFSVTTVDLKRKPADLQNLAPGTHPPFITFNSEVKTDV
ĺ	{		NKIEEFLBEVLCPPKYLKLSPKHPESNTAGMDIFAKFSAYIKNS
l			RPEANEALERGLLKTLQKLDEYLNSPLPDEIDENSMEDIKFSTR
ļ			KFLDGNEMTLADCNLLPKLHIVKVVAKKYRNFDIPKEMTGIWRY
1			LTNAYSRDEFTNTCPSDKEVEI\AYSDVAKRLHQVKSRLLKEVS
1			FMSSP
5444	2	344	SGPIGVTGAQMAKWLRDYLSFGGRRPPPQPPTPDYTESDILRAY
		-	RAQKNLDFEDPY*DSESRLEPDPAGPGDSKNPGDAKYGSPKHRL
(IKVEAADMARAKALLGGPGEELEADTEYLDPFDAQPHPAPPDDG
1	1		YMEPYDAQWVMSELPGRGVQLYDTPYEEQDPETADGPPSGQKPR
}	j		QSRMPQEDERPADEYDQPWEWKKDHISRAFAVQFDSPEWERTPG
	[SAKELRRPPPRSPQPAERVDPALPLEKQPWFHGPLNRADAESLL
	1		SLCKEGSYLVRLSETNPQDCSLSLRSSQGFLHLKFARTRENQVV
j			LGQHSGPFPSVPELVLHYSSRPLPVQGAEHLALLYPVVTQTP*Q
1	l .		*PDWGDRRPNGOVATGLPELWGAEAPSAAAHPGLHRERHPEGLP
			RAEKPGLRGPLLGLREPLGAGPRGPWGLQEPRRCOVWFSOAPAH
}			QGGGCGYGQSQGPSGRPRGGAGSRH
5445	2264	406	
5445	2364	486	ILSRGFLGSVEICIQLPLPASEPVLLLTWARRRWRETRSRREPT
ì			TLRAQSVCPWWI*ETRMNRSIPVEVDESEPYPSQLLKPIPEYSP
1			EEESEPPAPNIRNMAPNSLSAPTMLHNSSGDFSQAHSTLKLANH
i			QRPVSRQVTCLRTQVLEDSEDSFCRRHPGLGKAFPSGCSAVSEP
ł	l		ASESVVGALPAEHQFSFMEKRNQWLVSQLSAASPDTGHDSDKSD
}			QSLPNASADSLGGSQEMVQRPQPHRNRAGLDLPTIDTGYDSQPQ
l	!		DVLGIRQLERPLPLTSVCYPQDLPRPLRSREFPQFEPQRYPACA
1			QMLPPNLSPHAPWNYHYHCPGSPDHQVPYGHDYPRAAYQQVIQP
1	ļ		ALPGQPLPGASVRGLHPVQKVILNYPSPWDQEERPAQRDCSFPG
1			LPRHQDQPHHQPPNRAGAPGESLECPAELRPQVPQPPSPAAVPR
i			PPSNPPARGTLKTSNLPEELRKVFITYSMDTAMEVVKFVNFLLV
1			NGFQTAIDIFEDRIRGIDIIKWMERYLRDKTVMIIVAISPKYKQ
].			DVEGAESQLDEDEHGLHTKYIHRMMQIEFIKQGSMNFRFIPVLF
			PNAKKEHVPTWLQNTHVYSWPKNKKNILLRLLREEEYVAPPRGP
	Í		LPTLQVVPL
5446	972	161	SSWSWCTGRMRKTRLWGLLWMLFVSELRAATKLTEEKYELKEGQ
	1		TLDVKCDYTLEKFASSQKAWQIIRDGEMPKTLACTERPSKNSHP
1			VQVGRIILEDYHDHGLLRVRMVNLQVEDSGLYQCVIYQPPKEPH
1	1		MLFDRIRLVVTKGFSGTPGSNENSTQNVYKIPPTTTKALCPLYT
1			TPRTVTQAPPKSTADVSTPDSEINLTNVTDIIRVPVFNIVILLA
1	!		GGFLSKSLVFSVLFAVTLRSFVP*AHEPTRMSSDFOPHPSGSCA
1			KGGGRR
5447	207	617	MTARTLSLMASLVAYDDSDSEAETEHAGSFNATGQQKDTSGVAR
	1 -3.		PPGQDFASGTLDVPKAGAQPTKHGSCEDPGGYRLPLAQLGRSDR
1	İ		GSCPSQRLQWPGKEPQVTFPIKEPSCSSLWTSHVPASHMPLAAA
1	1		RFKQVKLSRNFPKSSFHAQSESETVGKNGSSFQKKKCEDCVVPY
	j		TPRRLRQRQALSTETGKGKDVEPQGPPAGRAPAPLYVGPGVSEF
1	ļ		
1	İ		IQPYLNSHYKETTVPRKVLFHLRGHRGPVNTIQWCPVLSKSHML
1			LSTSMDKTFKVWNAVDSGHCLQTYSLHTEAVRAARWAPCGRRIL
]		SGGFDFALHLTDLETGTQLFSGRSDFRITTLKFHPKDHNIFLCG
1			GFSSEMKAWDIRTGKVMRSYKATIQQTLDILFLREGSEFLSSTD
			ASTRDSADRTIIAWDFRTSAKISNQIFHERFTCPSLALHPREPV
1	j		FLAQTNGNYLALFSTVWPYRMSRRRRYEGHKVEGYSVGCECSPG
1			GDLLVTGSADGRVLMYSFRTASRACTLQGHTQACVGTTYHPVLP
	ĺ	!	SVLATCSWGGDMKIWH*AFHWLSLGEAIGDLAPARGYSGPGRSL
			KSPSPSKSLLVLLCGRAMFQPATCPWQLPALSK
5448	194	1833	MASKVTDAIVWYQKKIGAYDQQIWEKSVEQREIKGLRNKPKKTA
			HVKPDLIDVDLVRGSAFAKAKPESPWTSLTTKGIVRVVFFPFFF
			RWWLQVTSKVIFFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVI
			GPIWLMLLLGTVHCQIVSTRTPKPPLSTGGKRRRKLRKAAHLEV
			HREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAAFFLS
1	1		GSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIQNHEPQCET
L		<u> </u>	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
1 -			Amitho acto segment containing signal peptide
ID	beginning	nucleotide	(A≈Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
j	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	J .	
1		amino acid	P-Proline, Q-Glutamine, R-Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1 2011011	\=possible nucleotide insertion)
	bequeinee		
1	1	İ	IRPEETAWNTGTLRNGPSKDTQRTITNVSDEVSSEEGPETGYSL
l .	i		RRHVDRTSEGVLRNRKSHHYKKHYPNEDAPKSGTSCSSRCSSSR
1	1	İ	QDSESARPESETEDVLWEDLLHCAECHSSCTSETDVENHQINPC
}	}	Į.	VKKEYRDDPFHQSHLPWLHSSHPGLEKISAIVWEGNDCKKADMS
		ł.	THE THE THE TOTAL PROPERTY OF THE THE THE THE THE THE THE THE THE THE
1	1	İ	VLBISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA
1	1		TDLEQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI
ĺ			FFFLLCVAERTYKQVGIM+TSEGVLRNRKSHHYKKHYPNEDAPK
	1		SGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCAECHSSCT
ì	1		SETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI
	Ì	l	
i			VWEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLI
İ	1	i	LGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMV
1			IISFVVRVSLVWIFFFLLCVAERTYKQVGIM
5449	194	1833	MASKVTDAIVWYQKKIGAYDQQIWEKSVEQREIKGLRNKPKKTA
1	1	1	
j	J	J	HVKPDLIDVDLVRGSAFAKAKPESPWTSLTTKGIVRVVFFPFFF
1	1	[RWWLQVTSKVIFFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVI
	}	l	GPIWLMLLLGTVHCQIVSTRTPKPPLSTGGKRRRKLRKAAHLEV
	Į.		HREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAAFFLS
į		i	GSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIQNHEPQCET
1)	i	IRPEETAWNTGTLRNGPSKDTQRTITNVSDEVSSEEGPETGYSL
i		ı	RRHVDRTSEGVLRNRKSHHYKKHYPNEDAPKSGTSCSSRCSSSR
			QDSESARPESETEDVLWEDLLHCAECHSSCTSETDVENHQINPC
İ	1		VKKEYRDDPFHQSHLPWLHSSHPGLEKISAIVWEGNDCKKADMS
	j	İ	VLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA
			TDLEQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI
1	ļ	ŀ	
			FFFLLCVAERTYKQVGIM*TSEGVLRNRKSHHYKKHYPNEDAPK
ł	1	(SGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCAECHSSCT
		j	SETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI
•			VWEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYOIFGNAVSLI
ł	1	\	LGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMV
1			
L		l	IISFVVRVSLVWIFFFLLCVAERTYKQVGIM
5450	8136	1242	GQQFASFFG*NHPEVTVAMALTDIDLQLQFSMSQPEALLLLAAG
-	1	ſ	PADHLLLQLYSGHLQVRLVLGQEELRLQTPAETLLSDSIPHTVV
1		Į	LTVVEGWATLSVDGFLNASSAVPGAPLEVPYGLFVGGTGTLGLP
	l		YLRGTSRPLRGCLHAATLNGRSLLRPLTPDVHEGCAEEFSASDD
Í	į į		
ì			VALGFSGPHSLAAFPAWGTQDEGTLEFTLTTQSRQAPLAFQAGG
	[·	RRGDFIYVDIFEGHLRAVVEKGQGTVLLHNSVPVADGQPHEVSV
ł			HINAHRLEISVDQYPTHTSNRGVLSYLEPRGSLLLGGLDAEASR
			HLQEHRLGLTPEATNASLLGCMEDLSVNGQRRGLREALLTRNMA
į			AGCRLEEEEYEDDAYGHYEAFSTLAPEAWPAMELPEPCVPEPGL
J	1		
1		1	PPVFANFTQLLTISPLVVAEGGTAWLEWRHVQPTLDLMEAELRK
i			SQVLFSVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIHD
1			GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLPIQVNPVNDPP
	[HIIFPHGSLMVILEHTQKPLGPEVFQAYDPDSACEGLTFQVLGT
1	į l		SSGLPVERRDQPGEPATEFSCRELEAGSLVYVHCGGPAQDLTFR
1			VSDGLQASPPATLKVVAIRPAIQIHRSTGLRLAQGSAMPILPAN
ĺ	1		
1			LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWATQ
			AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSNL
1	1	1	SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGPS
			PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDDIQAGRVTYGA
1		•	TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTNV
1			LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWRG
1	1		
1			TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQGE
			SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRLL
1	(TTDDVAFSDADSGPADAQLVLTRKDLLFGSIVAVDEPTRPIYRF
1 .			TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASEP
{			YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHVT
1			AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMAF
l			SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAEI
}]		RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPPS
1			LDPVQSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPLE
ł	Į į		
L	L	l	GVLVELEVLPAAIPLEAQNFSVPEGGSLTLAPPLLRVSGPYPPT

Do beginning nicetotide location corresponding to first smino acid saino acid residue of residue of amino acid sequence	CEO I	Predicted	Predicted end	Amino acid segment containing signal peptide
Notation corresponding to first mains acid residue of samino acid residue of samino acid residue of samino acid sequence helistidine, I=lacucine, N=Apparagine, P=roticue of samino acid sequence helistidine, I=lacucine, N=Apparagine, P=roticue of samino acid sequence helistidine, I=lacucine, N=Apparagine, P=roticue, O=lacucine, N=Apparagine, P=roticue, O=lacucine, N=Apparagine, P=roticue, O=lacucine, N=Apparagine, P=roticue, O=lacucine, N=Apparagine, P=roticue, O=lacucine, N=Apparagine, P=roticue, O=lacucine, N=Apparagine, P=roticue, O=lacucine, N=Apparagine, P=roticue, O=lacucine, N=Apparagine, P=roticue, O=lacucine, N=Apparagine, P=roticue, O=lacucine, N=Apparagine, P=roticue, O=lacucine, N=Apparagine, P=roticue, O=lacucine, N=Apparagine, P=roticue, O=lacucine, N=Apparagine, P=roticue, O=lacucine, N=Apparagine, P=roticue, N=Apparagine, N	SEQ			
corresponding to first mino acid mino acid residue of amino acid sequence L-Leucine, M-Methionine, N-Apparagine, P-Proline, Q-Glutamine, R-Arginine, amino acid sequence Sequence Sequence Sequence Sequence L-Leucine, M-Methionine, N-Vajine, well-yptophan, Y-Tyrosine, X-Unknown, *-stop Codon, y-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide insertion LIGILSQUAREPORDEDISERSPRIVATEPORDEDISTRY HDOSETITIOS FVILMANASEMBRIGHIVATEPORDEDISTRY HDOSETITIOS FVILMANASEMBRIGHIVATEPORDEDISTRY HDOSETITIOS FVILMANASEMBRIGHIVATEPORTUNDO PPILIT TITOTOQ WARRANTAPI PRABARSTODOS SEDILVITICEPOR SENDITATION VILAGAPOTEVAS PTOAQUOMICAL FRARCILOGOS PPILIDES ACCORDINATE PROPERTI				
corresponding to first amino acid residue of samino acid residue of samino acid sequence shano acid sequen	NO:			
to first amino acid residue of amino acid residue of amino acid amino acid sequence ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, _*possible nucleotide insertion) ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide insertion) ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop LoLals_UnlepPodiggtokeBopQants_EspSymwuseDilnry HDOSETITIDS*YULMANASEMBRGSHPWAFTYTU.pvnDopPILOT Thrid_Unkmantspread_EspSymwuseDilnry HDOSETITIDS*YULMANASEMBRGSHPWAFTYTU.pvnDopPILOT Thrid_Unkmantspread_EspSymwuseDilnry HDOSETITIDS*YULMANASEMBRGSHPWAFTYTU.pvnDopPILOT Thrid_Unkmantspread_EspSymwuseDilnry HDOSETITIDS*YULMANASEMBRGSHPWAFTYTU.pvnDopPILOT Thrid_Unkmantspread_EspSymwuseDilnry Unkmantspread_EspSymwuseDilnry Thrid_Unkmantspread_EspSymwuseDilnry ##Tryptophantspread_EspSymwuseDilnry Griffic	ĺ			
amino acid residue of amino acid sequence sequence Sequence				
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TINGLOMBERGATAPITRAEARSTDODGGSEDLYTTIEGPSNORY VLRGAGTEVRSFTOOQLDGGLUUSEKTILDGGPFELSCRET TSGHEFFEVTAGKULLISLKSSGTLTUCPGSVOPLSSGTLRASS SAGTPOLLLIFEVANGOLUSEKTLIGGESTGLAUSPTOAGEVA GNILVEHEMP PSFWEARDTLEIGLSS PPARDVAATLAVAVSTE AACPORPSHLMKINGLIMVSERPLAADTLEIGLSS PPARDVAATLAVAVSTE AACPORPSHLMKINGLIMVSERPLAADOHLAGASSEARATTUTADVA REHDVIFQUTQFPSRQGLAUSEEPIHAAQHTLASQLAAGGLV YRAGGGGTOODGFFFRAHLGGFRAGASVAGFQTSEAFRITUTADVA REPPOOASVERLITUGGASPLINAGGHISVSTOAGHGAGASLAVANGSSVAGIF GLOMSGGSEPUPNETGARVAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG				LLGLSLQVLEPPQHGPLQKEDGPQARTLSAFSWRMVBEQLIRYV
VLRGAPGTEVRSFTQAQLDOGLVLFSHRGTLDOGFPFRLSDOEF TSPGHFFRVTAKCVULSLKKGSTLAVCPGSVDFSTURARS SAGTDFQLLHYRVWGGOLGRLFHRQODSTGRALWNFTQAVVA GNILVEHEMPEPSFPKAHDTLELQLSSPPARDWATLAVAVSFF AACCPGRSHLWKNKILWVSEGGRARITVAALDASHLLASVSSFG RSEHDVLFOVTQFSFGOLLVSEPPARDATLAVAVSFF BACCPGRSSHLWKNKILWVSEGGRARITVAALDASHLLASVSSFG RSEHDVLFOVTQFSGOLLVSEPPARDATLAVAVSFF BERDVLFOVTQFSGOLLVSEPPARDATLAVAVSFF BERDVLFOVTQFSGOLLVSEPPARDATLAVALDASHLASVSSFG RSEHDVLFOVTQFSGOLSVPDTSAGLSVVDPSAGLSVLAVANGSSVAGF BERDVLFOVTQFSGOLSVPTFTCADVDSGCHLAVVANGSSVAGF BERDVGFSTAGTSLVGGGGFYTCTDLDVSGCRLAVVANGSSVAGFT GLOSDAVAVSSREEPPARYALLOGPOVGHLAVGREFSAFSQFDY LOGGVVFFAFTNFSSSHDHFRVLALARGVAASAVAVTAALLOV RAGGFFFCQATATLDOFTVLDAGGLARATGSVFFFALLGGFRIGR VVAVPRARTEFOGSGLVEQFTCQDLBCDGLGFVGARDASSL AGDSLTLELRAGOVFRAVSLDFTATPTVMAARTSVALLSVPRA ARTHAGKRESSTFTGFFGFMASSFBAVAKGGFLSFLEARMFS TITMCLVALLLALLHIELPLFTKRENTSTRVMAARTSVALLSVPRA ARTHAGKRESSTFTGFFGFMASSFBAVAKGGFLSFLEARMFS TITMCLVALLLALLHIELPLFTKRENTSTRVMAARTSVALLSVPRA ARTHAGKRESSTFTGFFGFMASSFBAVAKGGFLSFLEARMFS TITMCLVALLLALLHIELPLFTKMTSTGHDVQUTLAKVRNOLA GDTETFRKVBFGGATELTARVFGCSPPFGGGADSNOPGLLGFCTKRNOLA GDTETFRKVBFGGATELTARVFGCSPPFGGGADSNOPGLLGFCTKRNOLA GDTETFRKVBFGGATELTARVFGCSPPFGGGADSNOFGLGFKKRNOLA GVSKNNDLTSCCFSGATKTMFBYGGLAVSNORGCLGFKKRNOL FYRMLSYKOVSDRAEYLGSCLLHKGYKSSFDOFVOTFAGNRENG VSKKNNDLTSCCFSGATKTMFBYGGLAVSNORGCLGFKKRNO PYRMLSYKOVSDRAEYLGSCLLHKGYKSSFDOFVOTFAGNRENG TAPAULTGHVEKGFFTSLKV1 LLMDPFDDDLAKGGEKSGTEILSL VDARMLSKHEKFFTSLKVV1 LLMDPFDDDLAKGGEKSGTEILSL VDARMLSKHEKFFTSLKVVVS CGARVOFGCOTRAHAVPLYDTLISPEATVAVILOTPO KALVLIGNVEKGFTSSLKVFTSTTCDDFATTGARVAVICDFTS CGARVOFTGGOTRAFTKYFDSFDLSVTTTVAVILOTPO ARYFLKKELLKLAVSSKFRELQKGI ITRIDSFMDKLIFAKTQUV GGRVAVIVTGAAPMSTSVMTFFRAMGCOVTEAKGTTTGGGCT FTLPGGMTSGHVVVLLAGLSDAAMFSTVAVICRAMGCOVTEAKGTTGGGCT FTLPGGMTSGHVVVLLAGLSDAAMFSTVATFRAMGCOVTACTGGCT FTLPGGMTSGHVVALGAUSAMFSTVATFRAMGCOVTACHTVANGGGGGGGGANA AKFPLKELLKLAVSSKFRELQKGTTFTGAARGCOVTACHTURGTKKLUK NIFKLAGGESTAVALUTALDSLAKARFEDVAKCTCCTCGGCT FTLPGGMTSGHVVALGAUGANAFFEDVAKCTCCTCGCTCT FTLPGGMTSGHVVALGAUGANFFEDVAKCTCCTCPYKERBS VTIKVYTITYTIT	1	1		HDGSETLTDSFVLMANASEMDRQSHPVAFTVTVLPVNDQPPILT
TSPGHFFRYTAGKQVLLSLKGSGTLTVCPGSVQPLSSGTLANGE SAGTDPQLLLYRVKGPQGLSLHFRQQDSTGRALUNFTQAEVYA GNILYBHEMPPEFWEAHDTLELQLSSPPARDVANTLAVUSPER AACCQRPSHLKKKLWVPEGGRARTTVAALDASVEPER AACCQRPSHLKKKLWVPEGGRARTTVAALDASVEPER AACCQRPSHLKKKLWVPEGGRARTTVAALDASVLASVGSPER BSENDULFOVTQPSRGQLLVGEPBLHAGQDHFLASGLAAGGLV YAHGGGGTQDGFHFRAHLQGPAGASVAGPOTSEAFAITVTQDVN ERPPQPQASVPLRLTRGSRAITSRQLSVVDPDSAPGIFTSVQ RAHHGGFLSLVGGGGFYTFTCQADVDSGRLAFVANDSSSVAGS GLABSGASPPLPMSLAVDILFGSTLAVGLARPLEVPQALGRSSL SOQULRVUSRREEPBAYALIQGGYGGLLVGGRTSARSGSGT LOGGVVFAFTNISSSSHHHRVALARGANGASAVAGTVTRALLHV WAGGPHPQGATURLDFYLDAGGLAARTGSVFFFRLLEGFRAGG AGDSLTLELHAGGVPFAVASDLDFATSPYNDAARTYSALLLHV WAGGPHPQGATURLDFYLDAGGLAARTGSVFFFRLLEGFRAGG AGDSLTLELHAGGVPFAVASDLDFATSPYNDAARTYSVALLSVFF TUPCLVLLLLALLILLIPLIFYLRKNATGKHDVQVLTAKPRIGLA GDTETTRKVEBGGA PLFTAVAGGGLAFGFEARAGG AGDSLTTLENAGGVPFAVASDLDFATSPYNDAARTYSVALLSVFF ARTAGKPESSTPTTGREGGMASSFEAVAKGGFLSFEARMSV IIPMCLVLLLLALLIPLLFYLRKNATGKHDVQVLTAKPRIGLA GDTETTRKVEBGGA PLFTAVAGGGLAFGFEARMSV IIPMCLVLLLLALLIPLLFYLRKNATGKHDVQVLTAKPRIGLA GDTETTRKVEBGGA PLFTAVAGGGT PLFTAVAGGGTA AKTROKPAV PESSEGGRTGDTTGRFSACMDALKFFCLWRNHERKGKKDRDSGGR KNSEDGSHSLEALRDAAFSQGLNPLLLFTMMFFTFNELSSGGR GVSGKNNOLTSCCTSDAKTMYEVFGRGLAVSDNGFCLGYTRSTF ALKNOCYMV PYRKLSYKOVSDARFLJGSCLLHAKGKSSPDGVIFTGNGFREM IISELACTYTSMAVPLYDTGSPEATVHLVKKADLAMVICTPPO RALVLIGNVEKGFTSLKVILLNDFFDDLXGGSGGTRK GVSGKNNOLTSCCTSDAKTMYEVFGRGLAVSDNGFCLGYTRSTF IISELACTYTSMAVPLYDTGSPEATVHTWKADLAMVICTPPO RALVLIGNVEKGFTSLKVILLNDFFDDLXGGSGGTETAGRF IISELACTYTSMAVPLYDTGSPEATVHTWKADLAMVICTPPO RALVLIGNVEKGFTSLKVILLNDFFDDLXGGSGGTENAGA GVSGKNNOLTSCCTSDAKTMYEVFGRGLAVSDNGFCLGYTRSTF GARVFFTOGDITSCHGVFTSLKVILLNDFFDDLXGGSGGTGTAGGTAGFT GARVFTGTGTTSCHGVFTSLKVILLNDFTDFDDLXGGGGGGGAK ATTRCVTSGAMATAGGATAGTAGTAGGTAGFTAGATTTTAGGTTAGGT				TNTGLOMWEGATAPIPAEALRSTDGDSGSEDLVYTIEQPSNGRV
SAGTDPOLLLYRVERGOLGSLEHEADONSTORELUNTPOLGEVIC CNILVERMEMPERPEWRANTITELOLGSSPARADVANTLAVAVSFE AACCORPSHILMRIKGLEWPEGGRARITVAALDASHLLASSYSE AACCORPSHILMRIKGLEWPEGGRARITVAALDASHLLASSYSE REEDVYLPOVYOFPSROOLLVSEEPIHASGPHFLOGOLAAGGIQ YRAGGGGTOQDGFHRRAHLQGPAGASVAGPQTSEAFAITVRUW ERPPOPGASVPLRITRGSRAPISRQLSVVDPDSAPGELITYRUW RERPOPGASVPLRITRGSRAPISRQLSVVDPDSAPGELITYRUW RAGGMONDGSGLEWPTSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS		İ		VLRGAPGTEVRSFTQAQLDGGLVLFSHRGTLDGGFPFRLSDGEH
GNILYEIMPREPWEAHDTLELQLSSPPARDVANTLAVUSPER AACPGRSHLMINKKLMVEGGGARTITVAALDSAKLLASVSPER AACPGRSHLMINKKLMVEGGGARTITVAALDSAKLLASVSPER REBDULFOVTOPERGOLLVGEEPIHAGGCHAGGGLV YAHGGGGTOQDGFHFRAHLQGPAGASVASPOTSEAFAITVADVN ERPFORASVERLTRGSRAGISRAQLSVVDEPSAFGEITSVOL REPFORASVERLTRGSRAGISRAGLSVVDEPSAFGEITSVOL RAPHGGEISLVGGGIGFVTRFTOADDUSGKLAFVANGSSVAGH QLEMSGGASPEPJENSLAVGIGFGYGHLLVGGRTSARSGSVG SOQULRVVSRREEPFSAYRLIGGFGYGHLLVGGRTSARSGSVG DOGURVVSRREEPFSAYRLIGGFGYGHLLVGGRTSARSGSVG SOQULRVVSRREEPFSAYRLIGGFGYGHLLVGGRTSARSGSVG SOQULRVVSRREEPFSAYRLIGGFGYGHLLUGGRTSARSGSVG SOQULRVVSRREEPFSAYRLIGGFGYGHLUGGRTSARSGSVG SOQULRVVSRREEPFSAYRLIGGFGYGHLUGGRTSARSGSVG AGDSITLELHAGGVPFAVASLDFATEPVANGARFALLSVFRA ARTRAGKESSTPTTGEGFMASSEPAVAKGGLFEAMFSV LIDMCLVLLLLALLULLFLLFTGREFTSPVALLSVFRA ARTRAGKESSTPTTGEGFMASSEPAVAKGGLFEAMFSV LIDMCLVLLLLALLULLFLLFTGREFTSPVALLSVFRA ARTRAGKESSTPTTGEGFMASSEPAVAKGGLFEAMFSV LIDMCLVLLLLALLULLLFLLBYTGREHMFSV LIDMCLVLLLLLALLULLLFLLBYTGREHMFSV LIDMCLVTLLLLALLULLLFLLBYTGREHMFSV LIDMCLVTLLLLALLULLFTGAATFACHTERMFSVALLSVFRA ARTRAGKESSTPTGEGFMASSEPAVAKGGLFAKTROGGGG KNESPGSSCHSLEALROAAFSGGINFILLPTTMLFTFRFFSPLD ALKROGYWU THALICTLTGAATFILLLTRRQPVLPLLDLANGSVGIRGGRGG KNESPGSSCHSLEALROAAFSGGINFILLPTTMLFTFFFFSPLP TPALICTLTTGAATFILLTTRQPVLPLLDLANGVGIRGRGGGGGGAKEN GVSGKNNDLTSCFSGDAKTMTEWFGGGLAVSNORGCLGYRKENO PYRKISTKOVSDRATHAGTSTATATTGOAAVGTTFAATATTGOAAVGTTFAATATTGAATATTGAATATTGAATATTGAATATTGAATATTGAATATTGAATATTAT				TSPGHFFRVTAOKOVLLSLKGSOTLTVCPGSVOPLSSOTLRASS
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AACPORPSHLMANKGLMVPSGQRARITVAALDSALAASGGLDV PAHGGGTOQDGFHRAHLOGPAGASVAGPOFTSEAPAITVUND REPPOPASVUELELITIGSSAPAISAGLSVVDPSACPAITEVEN REPPOPASVUELELITIGSSAPAISAGLSVVDPSACPAITEVEN REPPOPASVUELITIGSSAPAISAGLSVVDPSACPAITEVEN RAPHNGFLSLVGGGLGPVTRFTQADVDSGRLAFVANGSSVAGIF CLAMSDGASPPLPMSLAVDILERSIAVGLARFLEVPQALGASSL SQQLKVUSRBEPFBATZBLIGGFOGGGLLVGARFLEVPQALGASSL CLAMSDGASPPLPMSLAVDILERSALESARGSVEFFELGGFRIGR VVXVPRAATEFGGSGLVEGFTQGDLEDGRIGLEVGAFEGGRAGP AGDSLTLELMAGGVPAVASLDFATEFYNNAARFSVALLSVPEA ARTEAGKPESSTPTGREGFMASSPERVAKGGFLSFLEARMRSV IITMCLVLLLLALILLIPLTFYLKRAKTGKHUPVQLTAKPRNGLA GDTETFRKVEPGGATPLTAVPGGSPPPGGDELLGFGRTNP ALKNGGVAV FORSEGGFTCDTLGRFSACHDALKPFCLMRNHERGKKORDSGCF RINEGPSHBLEALADASSGGLANDLLAPFTMLFTFFNLSPLP TPALICILIFGAATFIALITARPQVIPLLDIMNGGVGIGGRAK RINEGPSHBLEALADASSGGLANDLLAPFTMLFTFFNLSPLP TPALICILIFGAATFIALITARPQVIPLLDIMNGGVGIGGRAK GVSGGNODLISSCFSDAKTMTSVPGGGLAVSDBGCGYKKEND PYRKLSYKOVSDRABFLGSCLLHKGYKSSPDQFVGIFAONREW IISELACTTISMVANPLTYDTLGFBALVHIVAKADLANVICOTPQ KALVLICNTSKAPFTSIKVILLANDFDDDLAKCRGKSGTEILSL YDARNIJGSGHFRKPVPSSPEDLSVICFTSGTTGDBKSAGTHILSL YDARNIJGSHFRKPVPSSPEDLSVICFTSGTTGDBKSAGTHILSL GGRVAVIVTGAAPMSTSVMTFFRAAMGCQVYEAYQOTECTGGC GGRVAVIVTGAAPMSTSVMTFFRAAMGCQVYEAYQOTECTGGC GGRVAVIVTGAAPMSTSVMTFFRAAMGCQVYEAYQOTECTGGC FTLDGMTSGHKVANSSKPELUKDLAMMPTSVMTSREGUCLKG TNYPKGYLKKPLKKANSSKPELUKDLAMMPTSVMTSREGUCLKG TNYPKGYLKKPLKKANSSKPELUKDLAMMPTSVMTSREGUCLKG TNYPKGYLKKPLKKANSSKPELUKDLAMMPTSVMTSREGUCLKG TNYPKGYLKAPEKENITNARSGVULGFTNGSLASSLSUKSV VVPDTDVLPSFFAAKLGVKGSFFELCONGVYREAGLECKKERSSLSVFV VVPDTDVLPSFFAAKLGVKGSFFELCONGVYREAGLECKKERSSLSVFV VVPDTDVLPSFFAAKLGVKGSFFELCONGVYREAGLECKKERSSLSVFV VVPDTDVLPSFFAAKLGVKGSFFELCONGVYREAGLECKKERSSLSVFV VVPDTTVLPSFFAAKLGVKGSFFELCONGVYREAGLECKKERSSLSVFV VVPDTTVLPSFFAAKLGVKGSFFELCONGVYREAGLECKKERSSLSVFV VVPDTTVLPSFFAAKLGVKGSFFELCONGVYREAGLECKKERSSLSVFV VVPDTTVLTSTLANDSKECUCLARSKYREAGRAGCTAGPPAAATLMGGLLX LIGHLXKARGASAFAKSVIGTTSFFAARSGAGGGGGAKE PGERSGQODDIBLETKAKGKKCIVLVTELMTGGTLKTYLKRFKVMKLUV RSWGGODDLARTTSFTINGCLCLARTTYLKFFFAAKLGCLARVI RSWGGODDLARTTSFTINGCLCTARTSGVARAG				
RSHENULFOVTOPPERGOLIVSEEPLIHAGOPHIPALOGOLIAGOLÜ YANGGGTOODFHRFRAILGOPAGASVAGGENFAITTURDVA ER PPOPOASVELBLITEGERAPISRAQUSVOPPESAPCIETEVO RAPHGGFILSLVGGGLGPVTRFTOADVDSGRIAFVANSSVAGIF QLSMSDGASPELMSLAVDILESAIEVQLRAPIESVPQAIGRSSI SOQOLKVISDREBPEANTLIOSDYOHLLVGGRTAFSSPOTI DOGEVVFAFTIFSSSHOHREVLALAGVONASAVVNIVVARALIEV WAGGPHPQGATLELDPTVLDAGELANKTGSVERFERLLEGPRIGR VVXPPRANTEBEGSOLVEOTODLEDGALGAVROMVAVVVAVVARALIEV WAGGPHPQGATLELDPTVLDAGELANKTGSVERFERLLEGPRIGR VVXPPRANTEBEGSOLVEOTODLEDGALGAVENEGEGARGE AGDSLILSLHAQGVPPAVASLDFATEPYNAARPYSVALLSVEPA ARTHAGKPESSTTOTGEOPPASSEPPAVAGGFLEAMFSV LITMCLVILLILAILIDLIFTLKRRIKTGKHDVOLTAKRRIGA GDTETFRIKVEOGGAPPAVASLDFATEPYNAARPYSVALLSVEPA ARTHAGKPESSTTOTGEOPPASSEPPAVAGGFLEAMFSV LITMCLVILLILAILIDLIFTLKRRIKTGKHDVOLTAKRRIGA GDTETFRIKVEOGGAPPAVASLDFATEPYNAARPYSVALLSVEPA ARTHAGKPESSTTOTGEOPPASSEPPAVAGGFLEAMFSV LINGGYWW TARAINITERST TOTGEOPPASSEPPAVAGGFLEAMFSVALLSKOPPA RINGEGGTODTIGRESACHDALKPPCLAMPHSICKKERDSCGR KNSEPGSPHSLEALRDAAPSGVLPFLLIDIANGSVOISGGGRK GVSQKNNOLITSCFSDAKTHYSVYGGLAVSNOHGCLGYRKENO PYRKLSYKQVSDRASYLGSCLLHKGYYKSSPDOPVGIFAQNREW LISELACYTYSMAVAPLYDTLGPEAIVITLMOPPODDLKGRGKSGIELISL YDABNIGGEHFRPAVPEPSPBOLSVITSTSGTORAMYTCHYOL KALVLIGAVEKGFTPSLKVIILMDEPDDLKGRGKSGIELISL YDABNIGGEHFRAVDERVENTERVEPSPBOLAVTICHTYDKVONE GRAVFICKARAPSTSVANTEPPAMAGCOVYEKAHITYDKVONE AKTPLKKELLKLAVSSKKELGKGIIHRDSFRDKLIFTYNKVONYON GGRRVIVTGAARASSSANTLEMPEPSIEDSVITSTSGTPLANTITYDKVONE AKTPLKKELLKLAVSSKKELGKGIIHRDSFRDKLIKTITYDKVONE AKTPLKKELLKLAVSSKKELGKGIIHRDSFRDKLIKTITYDKVONE GRRVVIVTGAARASSSANTARSSPPLAGARPGGTAGFPAMATLWGGLK KINIFKLAGGEVIAPKENTILAPPEPSTAMAGCOVYERALLEDLAGVAVYS GGRRVIVTGAARASSSANTILAPPEPSTAMAGCOVYERALLEDLAGVAVYS GGRRVIVTGAARASSANTILAPPEPSTAMAGGVOYPERALDEDLAGKIKE SGLKSTEDVANTILAPPEPSTAMAGGVOYPERARGEGGANA KEVPERANDEVALS SAVESLCLSLSLSLSLSSFSREPVAGAFGGTAGFPAMATLWGGLLR LEMASSEVYSHANDOLARRESTANVLIKVENAGAGGGSAKKE VITIKYTIIITISLIGLILLAWVILLUPPILLARRIGELSKYPRTO AGPAPSTVPSSTKOPVSONGSTERTTGROVAGAPAGGGGANK AGPAPSTVPSSTKORKCVULTTELMTSGTALTTLKRFKYNKIKVL REMGGILKAGGG	,			•
### PARIGGGTQQDGFHFRAHLQGPAGSAVAPGTSEAFAITYDWN ERPPOPOASYUPLILTGGRAPJERAQLSVUPDFSAPGETEYEV RAPHNGFLSLVGGGLGPVTRFTQADVDSGRLAFVANGSSVAGIF QLSMSDGASPFLPMSLAVDILESAIEVQLRAPLEVPQLIGRSSL SQQQLKVVDSGEBPEAAYRLDGPTULDAGCENTAFSOFQTI DQGEVVFAFTNFSSSHDFRVLALLARGVNASAVVNTVTAALHIV WAGGPHQGATLALDPTVLDAGCLANTGSTSVFFRLLEGPRING VVRVPRARTSPGGSQLVEQFTQQDLEDGRIGLEVGREGGRAGE AGDSLTLELHAQVPDAVASLDFATEVYNAARGFSFFLAMFSV LIDMCLVLLLALLALLDLLFTLARGKEDGVQLVALARGPSGAPGA ARTEAGKPESSTFTGEPGPMASSFBFAVAGGFLSFLEAMFSV LIDMCLVLLLALLALLILLELFTLARGKEDGVQLVALAKPROLA GDTETPRKVEBGQAIPLTAVPGQGPPPGGQFDPELLQFCRTPNP ALKOQYWV 5451 1 2274 RDSSEQGTGDTLGRPSACHDALKPPCLWRNHERGKKDRDSCGR KNSERGSHSLEALRDAAPSQGLNFELLDFTKHLFTNFTLFSFLP TPALICILTFRAAIFLHLITRQFVPLLELLDHNGSVGIBGGARK GVSQKNNDLTSCCFSDAKTMYEVFGRGLAVSDNGPCLGYKRNO PYRKLSYKOVSDARSYLSGSCLHKGYKSSPDFVGIFAONRPEW LISELACYTSWNAPPLYDTLGPEAIPHINNGSVGIBGGARK GVSQKNNDLTSCCFSDAKTMYEVFGRGLAVSDNGPCLGYKRNO PYRKLSYKOVSDARSYLSGSCLHKGYKSSPDFVGIFAONRPEW LISELACYTSWNAPPLYDTLGPEAIPHINNGSVGIBGGARK GVSQKNNDLTSCCFSDAKTMYEVFGRGLAVSDNGPCLGYKRNO PYRKLSYKOVSDARSYLSGSCLHKGYKSSPDFVGIFAONRPEW LISELACYTSWNAPPLYDTLGPEAIPHINNGSVGIBGGARK GROWNIVTGAAAFLKCVEHAYEPPPDDVAISYLPLAIMFERIVQAVVYS CGARVFFCGDIRLLADDMTLKKPTLFFAVFRLUNKIYNKVONE AKTPLKKRLLKLAVSSKYKELGKGIIHRDSFHDRLIFATLVGKVONE AKTPLKKRLLKLAVSSKYKELGKGIIHRDSFHDRLIFATLVGKVONE GGRVRIVTGAARMSTSWNTFFRAAMGCOVFLACHCECKYEERSS GGRVRIVTGAARAGNATSWNTFFRAAMGCOVFLACHCKCKGPGFTGACFTGGCT FTLEGDWTSGHVOVPLACNTVLLEDVADMYFTVNNSGEVCIGC GGRVRIVTGAARACHASTSWNTFRAAMGCOVFLACHCKCKYEERSS VTIKYTIINLAGGEVLAPEKTENTYNSGOPULQIFVHGESLRSSLUGV VVPDTOVLDSFAARLGVKASFEELCONGOVVRALEDOKALLIPOKTLKIIDRK KNIFKLAGGEVARPARDVLAARSFRANVINKVELLEDLGKICKE SGLKTFEGVKAIFLLAGLLLAVALLAQLSDAARNEEDVRCKCICPPYKRNG HIVNKISGNOCCCLHVVERPWRGPDVARCLCRCCKYEERSS VTIKYTIINLSILGALLLAVGLAGANSNOGGFLAFCFOIKTRGHCKYKNGG HIVNKHISGNOCCCLHVVERPWRGPVDVARCLCRCCKYEERSS VTIKYTIINLSILGALLLAWSLIKKSEGRYKEERBEMIKGIGHHNI KRIPTANDGAARPEPHRESTVTATATSGVAQQPPAAAAPGGGAV KGUDDTGTDFPAAPADFORAPEPHRESTVTATATSGVAQQPPAAAPGGGAV KGUDDTGTDFAAPANDVLAARSFRANVINVUERSERDMCKAGTKVIV GGCLGONNDE				1 -
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AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE		 		
	5454	111	1520	
POEERSOOODDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY	1]		1
	1			PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY
KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI	L	<u> </u>	<u> </u>	KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	Bequence	\=possible nucleotide insertion)
<u> </u>	bequence	 	VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL
ļ	}		RSWCROILKGLOFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD
1			LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM
1	1		LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII
			EGCIRONKDERYSIKDLLNHAFFQEETGVRVELAEEDDGEKIAI
[KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAOEMVESG
}			YVCEGDHKTMAKAIKDRVSLIKRKREOROL*
5455	1359	377	LTMVSPATRKSLPKVKAMDFITSTAILPLLFGCLGVFGLFRLLO
5455	1359	3 //	
1			WVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNG
ł	}	1	GALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEIL
i			QCFGYVDILVNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALT
i		(KALLPSMIKRRQGHIVAISSIQGKMSIPFRSAYAASKHATQAFF
			DCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTT
			TAQGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLRTLAPG
	ļ	ļ	LFFSLMASRARKERKSKNS
5456	2	2332	CGAGLVAAGAVLVLYPASRAGERTRVPGSPAPSSLPLHSPGACG
1	1		TEVDMDPQRSPLLEVKGNIELKRPLIKAPSQLPLSGSRLKRRPD QMEDGLEPEKKRTRGLGATTKITTSHPRVPSLTTVPQTQGQTTA
			OKVSKKTGPRCSTALATGLKNOKPVPAVPVQKSGTSGVPPMAGG
1.			KKPSKRPAWDLKGQLCDLNAELKRCRERTQTLDQENQQLQDQLR
ì			DAQQQVKALGTERTTLEGHLAKVQAQAEQGQQELKNLRACVLEL
i			EERLSTOEGLVOELOKKQVELOEERRGLMSQLEEKERRLOTSEA
})		ALSSQAEVASLRQETVAQAALLTEREERLHGLEMERRRLHNQL
			QELKGNIRVFCRVRPVLPGEPTPPPGLLLFPSGPGGPSDPPTRL
1			SLSRSDERRGTLSGAPAPPTRHDFSFDRVFPPGSGODEVFEEIA
Į			MLVQSALDGYPVCIFAYGQTGSGKTFTMEGGPGGDPQLEGLIPR
ĺ	İ		ALRHLFSVAQELSGQGWTYSFVASYVEIYNETVRDLLATGTRKG
}			QGGECEIRRAGPGSEELTVTNARYVPVSCEKEVDALLHLARONR
			AVARTAQNERSSRSHSVFQLQISGEHSSRGLQCGAPLSLVDLAG
1		}	SERLDPGLALGPGERERLRETQAINSSLSTLGLVIMALSNKESH
ì			VPYRNSKLTYLLQNSLGGSAKMLMFVNISPLEENVSESLNSLRF
ì	ĺ		ASKVEPSVLFGTAQSNRKWKTDPDLCVCVCVCVCVCVCVCVCVP
}			MSMYRVRGGRVAGGCFIGWRAPCPRAIK
5457	1-2	1540	DDFVERRRWTRTTCLVRSPPHVPVCGHACSWNGGSLDPLKGTPA
3437		1340	LLRSAERLMRKVKKLRLDKENTGSWRSFSLNSEGAERMATTGTP
			TADRGDAAATDDPAARFQVQKHSWDGLRSIIHGSRKYSGLIVNK
1		1	APHDFOFVOKTDESGPHSHRLYYLGMPYGSRENSLLYSEIPKKV
i	1	1	RKEALLLLSWKQMLDHFQATPHHGVYSREEELLRERKRLGVFGI
	{	1	TSYDFHSESGLFLFQASNSLFHCRDGGKNGFMVSPGPGCVSPMK
J	J	}	PLEIKTQCSGPRMDPKICPADPAFFSFINNSDLWVANIETGEER
1			RLTFCHOGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTASW
Į			EGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRT
1			GSKNPKIALKLAEFOTDSOGKIVSTOEKELVOPFSSLFPKVEYI
	1	1	ARAGWTRDGKYAWAMFLDRPQQWLQLVLLPPALFIPSTENEEQA
1			ASLCQSCPQECPAVCGVRGGHQRLDQCS
5458	6642	4022	FVPGLREPOWEPAOPSATMSAPSEEEEYARLVMEAOPEWLRAEV
3430	0042	7022	KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQFEELEVDYEA
-		1	IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY
	1		VRKVLELQTELKQLRNVLTNTQSENERLASVAQBLKEINQNVEI
		1	QRGRLRDDIKEYKFREARLLQDYSELEEENISLQKQVSVLRQNQ
	1	1	VEFEGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET
			LKTEREOKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA
		1	EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS
	1]	DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG
1	1		SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG
			DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ
	1		HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS
		1	DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML
1	[DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA
1			DGGTGDSSPSPGSSLPSPLSDPRREPMNIYNLIAIIRDQIKHLQ AAVDRTTELSRQRIASQELGPAVDKDKEALMEEILKLKSLLSTK
			I AMYURIJEHORURIASURIASURIAYAVIKURDAHREEJHAHASIHSIK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	_	
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
<u> </u>	bequence		REQITTLRTVLKANKQTAEVALANLKSKYENEKAMVTETMMKLR
			NELKALKEDAATFSSLRAMFATRCDEYITQLDEMORQLAAAEDE
		l .	
1			KKTLNSLLRMAIQQKLALTQRLELLELDHEQTRRGRAKAAPKTK
l	<u> </u>	1	PATPSVSHTCACASDRAEGTGLANQVFCSEKHSIYCD
5459	316	1262	RGGHRLSGMASNFNDIVKQGYVRIRSRRLGIYQRCWLVFKKASS
1		1	KGPKRLEKFSDERAAYFRCYHKVTELNNVKNVARLPKSTKKHAI
		1	GIYFNDDTSKTFACESDLEADEWCKVLQMECVGTRINDISLGEP
l		1	DLLATGVEREQSERFNVYLMPSPNLGCYMGECALQITYEYICLW
l .			DVQNPRVKLISWPLSALRRYGRDTTWFTFEAGRMCETGEGLFIF
l		(QTRDGEAIYQKVHSAALAIAEQHERLLQSVKNSMLQMKMSERAA
l			SLSTMVPLPRSAYWQHITRQHSTGQLYRLQDVSSPLKLHRTETF
İ		{	
L		<u></u>	PAYRSEH
5460	45	2097	RPGCRAGELSTGSRARERVRNRVSAPCGQDSRRCDPBVLRGRSP
l		į.	GLGLAEMPSCGACTCGAAAVRLITSSLASAQRGISGGRIHMSVL
		(GRLGTFETQILQRAPLRSFTETPAYFASKDGISKDGSGDGNKKS
			ASEGSSKKSGSGNSGKGGNQLRCPKCGDLCTHVETFVSSTRFVK
1		1	CEKCHHFFVVLSEADSKKSIIKEPESAAEAVKLAFQQKPPPPPK
]]	KIYNYLDKYVVGQSFAKKVLSVAVYNHYKRIYNNIPANLRQQAE
1	ſ		VEKOTSLTPRELEIRRREDEYRFTKLLQIAGISPHGNALGASMQ
		1	QQVNQQIPQEKRGGEVLDSSHDDIKLEKSNILLLGPTGSGKTLL
ſ			AQTLAKCLDVPFAICDCTTLTQAGYVGEDIESVIAKLLQDANYN
		Ì	VEKAQQGIVFLDEVDKIGSVPGIHQLRDVGGEGVQQGLLKLLEG
ĺ			
}		}	TIVNVPEKNSRKLRGETVQVDTTNILFVASGAFNGLDRIISRRK
		1	NEKYLGFGTPSNLGKGRRAAAAADLANRSGESNTHQDIEEKDRL
}			LRHVEARDLIEFGMIPEFVGRLPVVVPLHSLDEKTLVQILTEPR
			NAVIPQYQALFSMDKCELNVTEDALKAIARLALERKTGARGLRS
1		1	IMEKLLLEPMFEVPNSDIVCVEVDKEVVEGKKEPGYIRAPTKES
			SEEEYDSGVEEEGWPRQADAANS
5461	1481	160	INPPPPPKSPCGRARKWRRRRRPGAPEAAVMELPSGPGPERLFD
1			SHRLPGDCFLLLVLLLYAPVGFCLLVLRLFLGIHVFLVSCALPD
	}		SVLRRFVVRTMCAVLGLVARQEDSGLRDHSVRVLISNHVTPFDH
l			NIVNLLTTCSTPLLNSPPSFVCWSRGFMEMNGRGELVESLKRFC
1	1	ł	ASTRLPPTPLLLFPEEEATNGREGLLRFSSWPFSIQDVVQPLTL
ì		i	QVQRPLVSVTVSDASWVSELLWSLFVPFTVYQVRWLRPVHRQLG
	1 .	1	
	[EANEEFALRVQQLVAKELGQTGTRLTPADKABHMKRQRHPRLRP
1			QSAQSSFPPSPGPSPDVQLATLAQRVKEVLPHVPLGVIQRDLAK
1	Į.		TGCVDLTITNLLEGAVAFMPEDITKGTQSLPTASASKFPSSGPV
	<u> </u>		TPQPTALTFAKSSWARQESLQERKQALYEYARRRFTERRAQEAD
5462	663	3353	KIKEROMSANNSPPSAOKSVLPTAIPAVLPAASPCSSPKTGLSA
		1	RLSNGSFSAPSLTNSRGSVHTVSFLLQIGLTRESVTIEAQELSL
1			SAVKDLVCSIVYQKFPECGFFGMYDKILLFRHDMNSENILQLIT
1			SADEIHEGDLVEVVLSALATVEDFQIRPHTLYVHSYKAPTFCDY
}	1	}	CGEMLWGLVRQGLKCEGCGLNYHKRCAFKIPNNCSGVRKRRLSN
1			VSLPGPGLSVPRPLQPEYVALPSEESHVHQEPSKRIPSWSGRPI
j	}		WMEKMVMCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGMQC
1			KDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDTDIPMDIDN
1	1		
1			NDINSDSSRGLDDTEEPSPPEDKMFFLDPSDLDVERDEEAVKTI
1		Į.	SPSTSNNIPLMRVVQSIKHTKRKSSTMVKEGWMVHYTSRDNLRK
I		1	RHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNIS
	1		QGSNPHCFEIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQS
		Į.	wekairqalmpvtpqasvctspgqgkdhkdlstsisvsncqiqe
}			NVDISTVYQIFADEVLGSGQFGIVYGGKHRKTGRDVAIKVIDKM
1	1		RFPTKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFVVMEK
1	l		LHGDMLEMILSSEKSRLPERITKFMVTQILVALRNLHFKNIVHC
	1		DLKPENVLLASAEPFPOVKLCDFGFARIIGEKSFRRSVVGTPAY
1	1		LAPEVLRSKGYNRSLDMWSVGVIIYVSLSGTFPFNEDEDINDQI
1			
1	1	1	QNAAFMYPPNPWREISGEAIDLINNLLQVKMRKRYSVDKSLSHP
1			WLQDYQTWLDLREFETRIGERYITHESDDARWEIHAYTHNLVYP
	L	<u> </u>	KHFIMAPNPDDMEEDP
5463	237	1012	LLSVTMTTSRCSHLPEVLPDCTSSAAPVVKTVEDCGSLVNGQPQ
L	1	L	YVMQVSAKDGQLLSTVVRTLATQSPFNDRPMCRICHEGSSQEDL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1		amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	to first	I .	
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
1			LSPCECTGTLGTIHRSCLEHWLSSSNTSYCELCHFRFAVERKPR
1	}	}	PLVEWLRNPGPQHEKRTLFGDMVCFLFITPLATISGWLCLRGAV
			DHLHFSSRLEAVGLIALTVALFTIYLFWTLVSFRYHCRLYNBWR
l .	ľ		RTNQRVILLIPKSVNVPSNQPSLLGLHSVKRNSKETVV
5464	195	677	SPSMNPRKKVDLKLIIVGAIGVGKTSLLHQYVHKTFYEEYQTTL
ļ			GASILSKIIILGDTTLKLQIWDTGGQERVRSMVSTFYKGSDGCI
[[LAFDVTDLESFEALDIWRGDVLAKIVPMEQSYPMVLLGNKIDLA
			DRKYQSILENHLTESIKLSPDQSRSRCC
5465	5278	3348	KGDPREFIRVHREALECDYVSAHLHEWIDLIFGYKQQGPAAVEA
3.43	32.0		VNVFHHLFYEGOVDIYNINDPLKETATIGFINNFGQIPKQLFKK
		!	PHPPKRVRSRLNGDNAGISVLPGSTSDKIFFHHLDNLRPSLTPV
1		1	KELKEPVGQIVCTDKGILAVEQNKVLIPPTWNKTFAWGYADLSC
1		1	RLGTYESDKAMTVYECLSEWGQILCAICPNPKLVITGGTSTVVC
Į		1	VWEMGTSKEKAKTVTLKOALLGHTDTVTCATASLAYHIIVSGSR
1		1	DRTCIIWDLNKLSFLTQLRGHRAPVSALCINELTGDIVSCAGTY
1	1	1	IHVWSINGNPIVSVNTFTGRSQQIICCCMSEMNEWDTQNVIVTG
1	1	1	HSDGVVRFWRMEFLQVPETPAPEPAEVLEMQEDCPEAQIGQEAQ
		1	DEDSSDSEADEQSISQDPKDTPSQPSSTSHRPRAASCRATAAWC
1	1	f .	TDSGSDDSRRWSDQLSLDEKDGFIFVNYSEGQTRAHLQGPLSHP
1		}	HPNPIEVRNYSRLKPGYRWERQLVFRSKLTMHTAFDRKDNAHPA
		\	**
			EVTALGISKDHSRILVGDSRGRVFSWSVSDQPGRSAADHWVKDE
		ļ	GGDSCSGCSVRFSLTERRHHCRNCGQLFCQKCSRFQSEIKRLKI
			SSPVRVCQNCYYNLQHERGSEDGPRNC
5466	3	992	HACAHASAHASGRLVRWWRKRRSVMGIQTSPVLLASLGVGLVTL
			LGLAVGSYLVRRSRRPQVTLLDPNEKYLLRLLDKTTVSHNTKRF
1			RPALPTAHHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSDEDQG
1		1	YVDLVIKVYLKGVHPKFPEGGKMSQYLDSLKVGDVVEFRGPSGL
j			LTYTGKGHFNIQPNKKSPPEPRVAKKLGMIAGGTGITPMLQLIR
1		ļ	AILKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFKLW
ŀ		1	FTLDHPPKDWAYSKGFVTADMIREHLPAPGDDVLVLLCGPPPMV
		1	QLACHPNLDKLGYSQKMRFTY
5467	2103	4	GEALRVGTRGCRRDLPDPQARIFIQKKDLEEDESVTAAHLKSRG
1	ł		RSPRKIDQFCNSSNMVHGSVTFRDVAIDFSQEEWECLQPDQRTL
			YRDVMLENYSHLISLAGSSISKPDVITLLEQEKEPWMVVRKETS
			RRYPDLELKYGPEKVSPENDTSEVNLPKQVIKQISTTLGIEAFY
1			FRNDSEYRQFEGLQGYQEGNINQKMISYEKLPTHTPHASLICHT
1		}	HKPYECKECGKYFSCGSNLIQHQSIHTGEKPYKCKECGKAFQLH
1			IQLTRHQKFHTGEKTFECKECGKAFNLPTQLNRHKNIHTVKKLF
1			ECKECGKSFNRSSNLTQHQSIHAGVKPYQCKECGKAFNRGSNLI
1	j		QHQKIHSNEKPFVCKECGMAFRYHYQLIEHCQIHTGEKPFECKE
1			CGKAFTLLTKLVRHQKIHTGEKPFECRECGKAFSLLNQLNRHKN
			IHTGEKPFECKECGKSFNRSSNLVQHQSIHAGIKPYECKECGKG
	}	· ·	FNRGAHLIOHOKIHSNEKPFVCRECEMAFRYHCOLIEHSRIHTG
[1	DKPFECQDCGKAFNRGSSLVQHQSIHTGEKPYECKECGKAFRLY
1		1	LOLSOHOKTHTGEKPFECKECGKFFRRGSNLNOHRSIHTGKKPF
			ECKECGKAFRLHMHLIRHQKLHTGEKPFECKECGKAFRLHMQLI
			RHQKLHTGEKPFECKECGKVFSLPTQLNRHKNIHTGEKAS
5468	225	2976	SFLTDLFOSLAQLENLCKQLYETTDTTTRLQAEKALVEFTNSPD
3400	243	2370	CLSKCOLLLERGSSSYSOLLAATCLTKLVSRTNNPLPLEQRIDI
ļ			RNYVLNYLATRPKLATFVTQALIQLYARITKLGWFDCQKDDYVF
1	1		RNAITDVTRFLQDSVEYCIIGVTILSQLTNEINQVSATAFLIRA
Ì			DTTHPLTKHRKIASSFRDSSLFDIFTLSCNLLKQASGKNLNLND
1	1		ESQHGLLMQLLKLTHNCLNFDFIGTSTDESSDDLCTVQIPTSWR
1			SAFLDSSTLQLSTIGRCEYEKTCALLVQLFDQSAQSYQELLQSA
			SASPMDIAVQEGRLTWLVYIIGAVIGGRVSFASTDEQDAMDGEL
1			VCRVLQLMNLTDSRLAQAGNEKLELAMLSFFEQFRKIYIGDQVQ
			KSSKLYRRLSEVLGLNDETMVLSVFIGKIITNLKYWGRCEPITS
	1		KTLQLLNDLSIGYSSVRKLVKLSAVQFMLNNHTSEHFSFLGINN
	}		QSNLTDMRCRTTFYTALGRLLMVDLGEDEDQYEQFMLPLTAAFE
			AVAQMFSTNSFNBQEAKRTLVGLVRDLRGIAFAFNAKTSFMMLF
			EWIYPSYMPILQRAIELWYHDPACTTPVLKLMAELVHNRSQRLQ
			

Predicted Predicted Predicted No: Designing Incleotide Cacation Cocytesponding Corresponding				
Incation location corresponding to first amino acid residue of residue of residue of amino acid residue of amino acid sequence P-P-P-OINE, Q-Glutamine, R-Arginine, S-Serine, T-Threonine, N-Asparagine, P-P-P-OINE, Q-Glutamine, R-Arginine, S-Serine, T-Threonine, N-Valine, maino acid sequence S-Serine, T-Threonine, V-Valine, M-Tryptophan, V-Typosine, X-Unknown, **Stop Coden, /-possible nucleotide deletion, v-Possible nucleotide deletion, v-Possible	, -	l .		
cortisponding to first amino acid residue of amino acid amino acid sequence sequence	1	J		
to first amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence seque	NO:			
to first amino acid residue of amino acid sequence ### Pryptophan, Y=Tyrosine, Y=Muknown, *=Stop Codon, /=possible nucleotide deletion, V=possible nucleotide insertion) ### Pryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide insertion) ### Pryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide insertion) ### Pryptophan, Y=Tyrosine, X=Unknown, *=Stop PywSsmotLiphertSkintyHTMOSRITIGESPYHTMILLSIS ### PRSDLIPHETSKINTYHTMOSRITIGESPYHTMILLSIS ### PRSDLIPHETSKINTYHTMOSRITIGESPYHTMILLSIS ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLSIS ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLSIS ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLSIS ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLSIS ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLSIS ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLSIS ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLSIS ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLONGULLAMKOSFKES ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLONGULAMKOSFKES ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLONGULAMKOSFKES ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLONGULAMKOSFKES ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLONGULAMKOSFKES ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOS	ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
to first amino acid residue of amino acid sequence ### Pryptophan, Y=Tyrosine, Y=Muknown, *=Stop Codon, /=possible nucleotide deletion, V=possible nucleotide insertion) ### Pryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide insertion) ### Pryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide insertion) ### Pryptophan, Y=Tyrosine, X=Unknown, *=Stop PywSsmotLiphertSkintyHTMOSRITIGESPYHTMILLSIS ### PRSDLIPHETSKINTYHTMOSRITIGESPYHTMILLSIS ### PRSDLIPHETSKINTYHTMOSRITIGESPYHTMILLSIS ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLSIS ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLSIS ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLSIS ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLSIS ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLSIS ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLSIS ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLSIS ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLONGULLAMKOSFKES ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLONGULAMKOSFKES ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLONGULAMKOSFKES ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLONGULAMKOSFKES ### PRSDLIPHETSKINTYHTMOSRITIGESPHYHTMILLONGULAMKOSFKES ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOSFCHILMESS ### PRSDLIPHETSKINTYHTMOSRITIGHTANGULAMKOS		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
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VPENNGSAGCUCHLIMDUVSADNTILDHAGOGLIMKGS FEES EHWYRAPADNITUMTNYSDILLTUMNSYPPONLYMINTYANITUMTNYSDILLTUMNSYPPONLYMINTHILTYANITUMTNICHTULTUMNSYPPONLYMINTHILTYANITUM I WESINDRADFRIYNTYILEPSLEIAASTLKSGISYRARVANAO CYNTTYSENES PSTKMINSYREP PEOHLLIGYSVCTUVILAVCIL CYVSITKIKKEWNDQIPNIPARSRLVAITIODAQGSQMEKBSRQ EPAKCPHWRNCLIKLIPCFLEHMMKRDEDPHKAAKEMPPOGSGK SAMCPUEIS KTVLWEBSIS VYMCVELFERAVEKOPLHLEPS FORSPESSRDDFQBGREGIVARLTESIFLDLLGEEMGGFCQD MGESCLLPPSGSTSAHMPNDEPPSAGPKERPEKQDILKRUP PPASPTOSPONILTCTETLVIAGNPAYKSPSNSLSQSPCPRELG PDPLIARHLESVPEMPCVPCLSETTTVOPPETWOLIKRUN LOHGAAAAPVSAPTSGYQEFVHAVEQGGTQASAVVGLGPPEAG YKAPSSLLASSAVSPKKCGPASSASGEGEVYPERGOLIRDUN LOHGAAAAPVSAPTSGYQEFVHAVEQGGTQASAVVGLGPPEAG YKAPSSLLASSAVSPKKCGPASSASGEGEVYPERGOLIRDUCCHOPPA PVPVPLPTTGLDREPPRSPOSSILPSSSPEHIGLEPOEKVEMP KPPLPGGATDPUVOSLCSGIVASSACGTGAVKGPPEAG YKAPSSLLASSAVSPKKCGPASSASGEGVEYPERGOLIRDUCCHOPPA RVPSGISEKSKSSSSPHPAPGNAGSSGTPKIVNFVSVGPTYM RVS 17 1418 TACRIRTSINRGIAAVKEDAVEMILASYGLAYSLIMKPTGFMSDF KNWGLVFINSKERRTKAVLCMVAGATAAVFETLIAYSDLGYTI INKLHHVDESVGSKTRRAFLYLAAPPFMDAMATHAGILLKKKY SFLUGASISTVAQVVVVAILLHSHELGEFJD ILLSILYMGA LUNGTTLLIGYYNNIHDIIPDRSGPELGGGATIRMLSFMPHA LUNGTTLLIGYYNNIHDIIPDRSGPELGGGATIRMLSFMPHA YGMLTEIRAVYAPAFDKNPSNKLUSTSNTVTAAHIKKFFTVCMA LSLTLCFFMPHTFNNSKELIDIIGNSSAATEAVALITATYPVGMM YGMLTEIRAVYAPAFDKNPSNKLUSTSNTVTAAHIKKFFTVCMA LSLTLCFFMPHTFNNSKELIDII IGVOPAPABAGAYMWSSAYDHVX KTWAIKKISPFHQTYCQRTUREIOILLURPHRENNESAT GGGDSAMTOMPPTEEVUTIIVEMRENB SGGDSAMTOMPPTEE	İ	f .		
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### Sequence	(sequence	Codon, /=possible nucleotide deletion,
KIMPOGESEKI KREIRUPFSDKOPHHLECKELQLIEBLEVG RDDPROTEGT-OFUTIKELRAALDSTYRKIMEDEPDKWEDTER EFSSWISTNETQLKGI KGEALDTANHGEVKRAVEETRINGTEN EFSSWISTNETQLKGI KGEALDTANHGEVKRAVEETRINGTEN EFSSWISTNETQLKGI KGEALDTANHGEVKRAVEETRINGTEN EFSSWISTNETQLKGI KGEALDTANHGEVKRAVEETRINGTY ETISMIKSELKVITEVSSRERAGKOGGDELAANLSSEYRALVTL EVERMISNPEDCVQYKE TVENSLEELISGSKEVORGABKILD NIJEAQQLLIHQOKTKRI SAKKRPVQQOLAQGGGLDP HBELIKLESTILDGLERGRERGERI QVTLRKWERFETNKETY YLPGYGSSHERFISSSSLESSSELSKEDTKETS KARTESI AND LVKRASETPEGPONKQLLQQACKSI KROVKKLUEDTLEEETYI S 5474 2 780 TFDVRQLQASRRGIAVASNCSPRWFAGEEMAFVKSGWLLRGS LKRKKRNFDLMSDCHLIYYDDCTRQHI EDKVHMPMDCITT. QCCRDTOPPOKKSCHOMI EDKVHMPMDCITT. LQQASYGFYGGAYPDGTQVVYANGQAVBYYQYPYAGLYO PANOVI IREKYRDNSDLALGHLAYAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA			1 20 4 20 11 20 1	\=nossible nucleotide insertion)
RDPVRDTGGTCHVTLKELRAAIDSTYRKIMEDPDKWEDTTSR EFSSHISTINETUNGKISKERAIDTANHGEVKRAEITROYKK ETISHLKSEILKVIJTEVSSENEAQKGGDELAALSSSFRALIE EVERMLSNEGDCOVYKEITVINGLERISGSKEVSTOPAGNEKILD NIJERAQCILLHHQQKTKRISAKKRUVQQQIAQAQQGGGLDH HEBLIKKLESTLOGLERSRERGERIQVTURKWERFETINETV YLEVGTSSHERFILSSSLESSESSELEKTRESTSRTSSIAVQA LVKEASEIPLGPONGQLLQQAKSIKROVKKLEDTLEEESYIT YLEVGTSSHERFILSSSLESSESSELEKTRESTSRTSSIAVQA LVKEASEIPLGPONGQLLQQAKSIKROVKKLEDTLEEESYIT YLEVGTSSHERFILSSSSLESSESSELEKTRESTSRTSSIAVQA LVKEASEIPLGPONGQLLQQAKSIKROVKKLEDTLEEESYIT YLEVGTSSHERFILSSSLESSESSELEKTRESTSRTSSIAVQA LVKEASEIPLGPONGQLLQQAKSIKROVKKLEDTLEEESYIT YLEVGTSSHERFILSSSLESSESSELEKTRESTSRTSSIAVQA LVKEASEIPLGPONGQLLQQAKSIKROVKKLEDTLEEESYIT YLEVGTSSHERFILSSSLESSESSELEKTRESTSRTSSIAVQA LUVERSEIPLGSTRONGSLESSELEKTRESTSRTSSISSELEKTRESTSRTSSIAVQA LUVERSEIPLGSSEMILGVCHOCKTISLCAESTDOLLAGA LUVERSEIPLGSAMMIGIVCHOCKTISLCAESTDOLLAGA LUVERSEIPLGSAMMIGIVCHOCKTISLCAESTDOLLAGA LQOPSTORMANIA LUCORDATISLCAESTDOLLAGAAATORAGASISLEVKY PANQVIIRRENGSAMMIGIVCHOCKTISLCAESTDOLLAGAAATORAGASISLEVKY PANQVIIRRENGSAMMIGIVCHOCKTISLCAESTDOLLAGAAATORAGASISLEVKY STERNITVOPPOVEVEEBLERASOORAKUSISLEROHMITTYTYTY STERNITVOPPOVEVEEBLERASOORACHISLESTAMITTYTYPET STERNITVOPPOVEVEEBLERASOORACHISLESTAMITTYTYTYT VIKITINLENGURERIKALQKAUTISHIF FEHRITTYTYTYT VIKITINLENGURERIKALQKAUTISHIF FEHRITTYTYTYT VIKITINLENGURERIKALQKAUTISHIF FEHRITTYTYTYT SHLWYISPPANYGSASQLLATTYSEGSICULVISLEGISHITYTYTYTYT SHLWYISPPANYGSASQLLATTYSEGSICULVISLEGISHITYTYTYTYTY VIKITISPPANYGSASQLLATTYSEGSICULVISLOORAGATISHITYTYTYTYTY SHLWYSPYNYGSASGLLATTYSEGSICULVISLOORAGATISHITYTYTYTYTY SHLWYSPYNYGSASGLLATTYSEGSICULVISLOORAGATISHITYTYTYTYTYTY SHLWYSPYNYGSASGLLATTYSEGSICULVISLOORAGATISHITYTYTYTYTYTYTYTYTYTYTYTYTYTYTYTYTYTYTY		sequence	ļ	VI.MPOEGSEKTIKEHRVEFSDKGPHHLCBKRLOLIEELCVKLPV
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MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVMXS DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLK LENQQLIMQRATP 5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDL VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKT LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVX DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKII MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKS DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLK LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKI QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEG			[DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL
DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLE LENQQLIMQRATP 5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDLU VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKT LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVX DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKII MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKK DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLE LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKI QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEG	1		1	MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDBQVMVWKSNF
LENQQLIMQRATP 5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDE VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKT LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVR DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITAASDSTLKIIL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKS DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLE LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKI QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQ	1		1	DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC
5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDI VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKT LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVR DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKII MEGRLLYTLHGQPATTVAFSRTGEYFASGGSDEQVMVWKS DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLI LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKI QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQ	1	ł	(
VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKT LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVR DVRTHRLLQHYQLHSAAVWGLSFHPSGNYLITASSDSTLKII MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKS DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLI LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKI QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQ				VITTE THUDNINGE STUFFAHTATUR SVH FOSDGOS FVTASDDKT
LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVE DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKII MEGRILYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKS DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLE LENQQLIMQRATP LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKI QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQ	5479	2	835	
DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKII MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKS DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLH LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEBISQKRLKIEEDKI QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQ	1			VKVWATHRUKT DI SUSUMINWVKCARE SEDGRUI VSASDUKI VK
MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKS DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLE LENQQLIMQRATP LSLTSRMEEAELVKGRLQAITDKRKIQEBISQKRLKIEEDKI QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQ		}		
DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLE LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEBISQKRLKIEEDKI QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQ				
LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEBISQKRLKIEEDKI QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQ	1	ł	Ì	MEGRILYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF
LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEBISQKRLKIEEDKI QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQ	1	1		DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC
5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEBISQKRLKIEEDKI QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQ	1			
QHLKKKALREKWILLDGISSGKEQEEMKKQNQQDQHQIQVLEC	E400	444	1952	
	3400	777		
	1			LRLEKEIQDLEKAELQISTKERAILKKLKSIERTTEDIIRSVKV
	1	1	†	
	1	J	1	EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR
			1	KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ
	1		1	KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH
EPVYANPPYRPTTPQRETVTPGPNFOERIKIKTNGLGIGVNI			}	EPVYANPPYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI
HNMGNGLSEERGNNFNHISPIPPVPHPRSVIQQAEEKLHTP(1			HNMGNGLSEERGNNFNHISPIPPVPHPRSVIQQAEEKLHTPQKR
	L			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	D Decline, M=Methionine, NaAsparagine,
	amino acid	residue of	P-Proline, Q-Glutamine, R-Arginine,
1			S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	l .	\=possible nucleotide insertion)
			LMTPWEESNVMQDKDAPSPKPRLSPRETIFGKSEHQNSSPTCQE
1	ł	ł	DEEDVRYNIVHSLPPDINDTEPVTMIFMGYQQAEDSEEDKKFLT
	ł .	1	GYDGIIHAELVVIDDEEEEDEGEAEKPSYHPIAPHSQVYQPAKP
1	ĺ	(TPLPRKRSEASPHEKHKS
5481	3	1422	
3401	1 3	1422	NSPGSVCLCQCVCPSLLHCLPPLLLLLLLLLLLHESPQPPALRV
1	1	ł	VATSSDRNFMNKHQKPVLTGQRFKTRKRDEKEKFEPTVFRDTLV
	i		QGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDILVAGSMLA
i	ľ	İ	PGGTRIDDGDKTKMTNHCVFSANEDHETIRNYAQVFNKLIRRYK
J			YLEKAFEDEMKKLLLFLKAFSETEQTKLAMLSGILLGNGTLPAT
1			ILTSLFTDSLVKEGIAASFAVKLFKAWMAEKDANSVTSSLRKAN
1		}	LDKRLLELFPVNRQSVDHFAKYFTDAGLKELSDFLRVQQSLGTR
	1		KELQKELQERLSQECPIKEVVLYVKEEMKRNDLPETAVIGLLWT
1	ł	ł	CIMNAVEWNKKEELVAEQALKHLKQYAPLLAVFSSQGQSELILL
1		1	
1	{		QKVQEYCYDNIHFMKAFQKIVVLFYKADVLSEEAILKWYKEAHV
5482	1400		AKGKSVFLDQMKKFVEWLQNABEESESEGEEN
3482	1492	528	THVVMTGMCYAPHQVLSYINGVTTSKPGVSLVYSMPSRNLSLRL
T .	ĺ		EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPS
			CRLQGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFFAPA
{	i		LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGP
1	1		GAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDA
			IAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGALTP
1	j ,		TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMGAVP
	· '		VMVPAQSQAGSLV
5483	1	788	FFFFKGCRAGRGNESDYRKLEEMHQRFLVSERSKDDLQLRLTRA
	_	, 750	FNDIVOLPHDOCEFICA COMINGRA DE PROPERTOR
			ENRIKQLETDSSEEISRYQEMIQKLQNVLBSERENCGLVSEQRL
j			KLQQENKQLRKETESLRKIALEAQKKAKVKISTMEHEFSIKERG
			FEVQLREMEDSNRNSIVELRHLLATQQKAANRWKEETKKLTESA
			EIRINNLKSELSRQKLHTQELLSQLEMANEKVAENEKLILEHQE
			KANRLQRRLSQAEERAASASQQLSVITVQRRKAASLMNLENI
5484	3	1997	IMADMEDLFGSDADSEAERKDSDSGSDSDSDQENAASGSNASGS
]			ESDQDERGDSGQPSNKELFGDDSEDEGASHHSGSDNHSERSDNR
			SEASERSDHEDNDPSDVDQHSGSEAPNDDEDEGHRSDGGSHHSB
}			AEGSEKAHSDDEKWGREDKSDQSDDEKIQNSDDEERAQGSDEDK
1			LQNSDDDEKMQNTDDEERPQLSDDERQQLSEEEKANSDDERPVA
1		·	SDNDDEKQNSDDEEQPQLSDEEKMQNSDDERPQASDEEHRHSDD
[EEEQDHKSESARGSDSEDEVLRMKRKNAIASDSEADSDTEVPKD
]		NSGTMDLFGGADDISSGSDGEDKPPTPGQPVDENGLPQDQQEEE
1	ļ		PIPETRIEVEIPKVNTDLGNDLYFVKLPNFLSVEPRPFDPQYYE
			DEFEDEEMLDEEGRTRLKLKVENTIRWRIRRDEEGNEIKESNAR
[, , , , , , , , , , , , , , , , , , ,		IVKWSDGSMSLHLGNEVFDVYKAPLQGDHNHLFIRQGTGLQGQA
	l		VFKTKLTFRPHSTDSATHRKMTLSLADRCSKTQKIRILPMAGRD
			PECQRTEMIKKEEERLRASIRRESQQRRMREKQHQRGLSASYLE
	i		PDRYDEEEEGEESISLAAIKNRYKGGIREERARIYSSDSDEGSE
}			EDKAQRLLKAKKLTSDEVRPNLFNSRGLSCTQEPTALNEELTDQ
[AGTN
5485	161	1074	
		20/3	KRKILSSMMDSEAHEKRPPILTSSKQDISPHITNVGEMKHYLCG
[CCAAFNNVAITFPIQKVLFRQQLYGIKTRDAILQLRRDGFRNLY
, 1	j		RGILPPLMQKTTTLALMPGLYEDLSCLLHKHVSAPEFATSGVAA
			VLAGTTEAIFTPLERVQTLLQDHKHHDKFTNTYQAFKALKCHGI
			GEYYRGLVPILFRNGLSNVLFFGLRGPIKEHLPTATTHSAHLVN
			DFICGGLLGAMLGFLFFPINVVKTRIQSQIGGEFQSFPKVFQKI
[WLERDRKLINLFRGAHLNYHRSLISWGIINATYBFLLKVI
5486	1404	142	IPGSTISWSPAAARGLSVCRCCRLHPASAMDLFGDLPEPERSPR
			PAAGKEAQKGPLLFDDLPPASSTDSGSGGPLLFDDLPPASSGDS
)	j	
		*	GSLATSISQMVKTEGKGAKRKTSEEEKNGSEELVEKKVCKASSV
			IFGLKGYVAERKGEREEMQDAHVILNDITEECRPPSSLITRVSY
			FAVFDGHGGIRASKFAAQNLHQNLIRKFPKGDVISVEKTVKRCL
			LDTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLG
			DSRAILCRYNEESQKHAALSLSKEHNPTQYEERMRIQKAGGNVR
i			DGRVLGVLEVSRSIGDGQYKRCGVTSVPDIRRCQLTPNDRFILL
		— ——— ——	

SEG Predicted Incleotide	ID NO:	beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	nucleotide location corresponding to first amino acid residue of amino acid sequence	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) ACDGLFKVFTPEEAVNFILSCLEDEKIQTREGKSAADARYEAAC NRLANKAVQRGSADNVTVMVVRIGH
No: nucleotide corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence ac	5487 5488	nucleotide location corresponding to first amino acid residue of amino acid sequence	location corresponding to first amino acid residue of amino acid sequence	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \ -possible nucleotide insertion ACDGLFKVFTPEEAVNFILSCLEDEKIQTREGKSAADARYEAAC NRLANKAVQRGSADNVTVMVVRIGH
Location Corresponding Lofirst amino acid amino acid residue of amino acid residue of amino acid amino acid amino acid amino acid sequence Serian, T-MIPTHOPINE, V-Valine, P-PFOline, Q-Glutamine, R-Arginine, Serian, T-MIPTHOPINE, V-Valine, W-Tryptophan, Y-Tyrosine, X-Unknown, *-Stop Codon, *-possible nucleotide deletion Codon, *-possible nucleotide deletion ACDGLEVFFFEEAVEN/ISCLEDER/IGTEE/SEADARYEAC NELANKAV/GRSADMY/WAVE/IGH ACDGLEVFFFEEAVE/IGTEE/SEADARYEAC NELANKAV/GRSADMY/WAVE/IGH ACDGLEVFFFEEAVE/IGTEE/SEADARYEAC NELANKAV/GRSADMY/WAVE/IGH ACDGLEVFFFEEAVE/IGTEE/SEADARYEAC NELANKAV/GRSADMY/WAVE/IGH ACDGLEVFFFEEAVE/IGTEE/SEADARYEAC NELANKAV/GRSADMY/WAVE/IGH ACDGLEVFFFEAVE/IGTEE/SEADARYEAC NELANKAV/GRSADMY/WAVE/IGH ACDGLEVFFEAVE/IGTEE/SEADARYEAC NELANKAV/GRSADMY/WAVE/IGH ACDGLEVFFEAVE/IGTEE/SEADARYEAC NELANKAV/GRSADMY/WAVE/IGH ACDGLEVFFEAVE/IGTEE/SEADARYEAC NELANKAV/GRSADMY/WAVE/IGH ACDGLEVFFEAVE/IGTEE/SEADARYEAC NELANKAV/GRSADMY/IGSV/GRSADMY/GRSADM	5487 5488 5489	location corresponding to first amino acid residue of amino acid sequence	corresponding to first amino acid residue of amino acid sequence	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) ACDGLFKVFTPEEAVNFILSCLEDEKIQTREGKSAADARYEAAC NRLANKAVQRGSADNVTVMVVRIGH
to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence Sescrine, T-Threonine, V-Valine, W-Typtophan, Y-Typtophan, Y-Suby, Codon, /=possible nucleotide deletion, \	5487 5488	corresponding to first amino acid residue of amino acid sequence	to first amino acid residue of amino acid sequence	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) ACDGLFKVFTPEEAVNFILSCLEDEKIQTREGKSAADARYEAAC NRLANKAVQRGSADNVTVMVVRIGH
to first amino acid residue of secries, T-freenine, V-Valine, Secries, T-freenine, V-Valine, Manino acid amino acid sequence codon, /-possible nucleotide deleties, Valonown, *-stop codon, /-possible nucleotide deleties, Valonown, *-stop codon, /-possible nucleotide dissertion) ACEGLEKATPERENVETICE.CEDERTGTERGKSAADARYEAAC NELANIAVQROSADNYTUWUVRIGH ACEGLEKATPERENVETICE.CEDERTGTERGKSAADARYEAAC NELANIAVQROSADNYTUWUVRIGH ACEGLEKATPERENVETICE.CEDERTGTERGKSAADARYEAAC NELANIAVQROSADNYTUWUVRIGH CKCKSSOKQHSPUPBERAIPLITOSATTO. 5488 1072 259 AMASGGERGKWGESVAAVWVUGSGMTDLUSITSELPKTGETIH GKKFFIGRGKGAN,CVQAARIGAMTSMVCVCKOSFOKDYIEN LKONDISTERTYGTADATTATSITUMEOGNITUKGANLLI KTEDLERAAANVISRAKMVCQLEITEATSLEALTMARKSSVTLANIAVGKFFIGRGKGAN,CVQAARIGAMTSMVCVCKOSFOKDYIEN LKONDISTERTYGTADATTATSITUMEOGNITUKGANLIL KYTEDLERAAANVISRAKMVCQLEITEATSLEALTMARKSSVTLANIAVGKFFIGRGKGAN,CVQAARIGAMTSMVCVCKOSFOKDYIEN LKONDISTERTYGTADATTATSITUMEOGNITUKGANLIL KYTEDLERAAANVISRAKMVCQLEITEATSLEALTMARKSSVTLANIAVGKFFIGRGKGAN,CVQAARIGAMTSMVCVCKOSFOKDYIEN LKONDISTERTYGTADATTATSITUMEOGNITUKGANLIL KYTEDLERAAANVISRAKMVCQLEUTEATSLEALTMARKSSVTLANIAVGKFTANAANVISRAKMVCQLEUTEATSLEALTMARKSSVTLANIAVGKFTANAA	5487 5488	to first amino acid residue of amino acid sequence	amino acid residue of amino acid sequence	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) ACDGLFKVFTPEEAVNFILSCLEDEKIQTREGKSAADARYEAAC NRLANKAVQRGSADNVTVMVVRIGH
amino acid residue of amino acid sequence solvente, T-Threonine, V-Valline, M-Typtophan, Y-Tyrosine, X-Unknown, *-Stop Codon, /-possible nucleotide deletion, \	5487	amino acid residue of amino acid sequence	residue of amino acid sequence	S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) ACDGLFKVFTPEEAVNFILSCLEDEKIQTREGKSAADARYEAAC NRLANKAVQRGSADNVTVMVVRIGH
residue of amino acid sequence Codon, /=possible nucleotide deletion,	5487	residue of amino acid sequence	amino acid sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) ACDGLFKVFTPEEAVNFILSCLEDEKIQTREGKSAADARYEAAC NRLANKAVQRGSADNVTVMVVRIGH
amino acid sequence Codon	5487 5488 5489	amino acid sequence 535	sequence	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) ACDGLFKVFTPEEAVNFILSCLEDEKIQTREGKSAADARYEAAC NRLANKAVQRGSADNVTVMVVRIGH
Sequence Apossible nucleotide insertion ACCIGIANT PERSONALIZED PRIGERS AND APPEAR ACCIGIANT PERSONALIZED PRIGERS AND APPEAR S187	5487	sequence 535		\=possible nucleotide insertion) ACDGLFKVFTPEEAVNFILSCLEDEKIQTREGKSAADARYEAAC NRLANKAVQRGSADNVTVMVVRIGH
ACDGLEVETEREAVBTLISCLEDERIGTREGKSAADARYEAAC NELANIKAVQUSGANDYTAWYRIGH 5487 535 182 AVSLEQIRGLOTPAFVPLPLQPCPSNCDMERVTLALLLAGITA LEANDPFANKADPFYYDMKNLQLSGI.ICGGLIAIAGIAAVLSGK CKCHSSQKQHSPYPEKAT PLITGSSATTC 5488 1072 259 AMAASGEPOROWGEEVAVVVVGSCMTDLVSLTSELPRTGETIH GHKFFIGFGRGANQCQDARALGANTSWCVCKVGKDSFONDYIEN LKQNDISTEFTYOTKDATGTASIIVNDEQRIIIVLVGASHLL NTEDLRAAANVISRAKVWCQDLEITPATSLELPKTGETIH PRAPAIADLDPOPTYLSDVPCCNESEAEILTGLTVGSAADAGE AALVLLKGROCVVITLGAEGCVVLSQTEPEPKHIPTEKVAVD TYVSPKI 5489 81 893 GKGFVAAFIQANIFITDPKIFIGQWREEPKHPLLLLGETEPLK LERDCRSPUBWAAASPDLAIACLCHCQDLSSGAFPNRGVLGGV LPPTVEWNIKVFVATSSGSIAIRKXQQSVVGFLEANKIPKELD IAGGENNRHWRENVPGEKKPORGIPLPOINFEKUD ALGEDNRSWREENVGSKRONGIPLFOINFEKUD ALGEDNRSWREENVGSKRONGIPLFOINFEKUD ALGEDNRSWREENVGSKRONGIPLFOINFEQVCODFDSF FSAKEENIIYSFIGLAPPDSKOSEKABEGGTEAQKESSEDVG NLPPAGERIBEEGGTTATESTEIAMGAGGGGEEETAGGEGE GEDEDS 5490 81 893 GKGFVAAFIDQSNIFFLTDPKIFIGGWREEPKMPLLLLGFTEPLK LERDCRSPUBWAAASPDLALACLCHCQDLSSGAPPNRGVLGGV LEPTVEWNIKVFVATSSGSIAIRKXQQVVGFLEANKIDPKELD IAGGEDNRBWREENVEGKKONGIPLPFOINFEQVCODFDSF FSAKEENIIYSFIGLAPPDSKOSEKABEGGTEAQKESSEDVG NLPRAQEKREEGGTTATESTIAKGAGGGAVGFLEANKIDPKELD IAGGEDNRBWREENVEGKKONGIPLPFOINFEQVCODFDSF FSAKEENIIYSFIGLAPPDBKOSEKABEGGTEAGESEPUG NLPRAQEKREEGGTTATESTEIAHGAGGGAAGKESEBUG NLPRAQEKREEGGTTATESTEIAHGAGAGGAKKVCONCTKFK GODMASSFILPRAGAITOSGGELSSGDDSGEVEPPRSPEIEETSC LAELFEKAAAHLGOLIQVASREQLIYIYAAYEVKKLDPGKNROI PEKKGRANTGFGGVISSIYHEETIREEDHYCKNENTOKA SFPEPFSKGKKMBAKKALGDSSPQAMGYIAVVKKLDPGKNROI PEKKGRANTGFGGVISSIYHEETIREEDHYCKSENTOH ITKAIKSKNVUNVNVOBEGRALLHHACCNGHKELVTVLLQHRAD INCOMMEGGTAHLYSACCEFILOVELINGAGAPTVOKKNENTOK SFPEPFSKGKKMBAKKALGDSSPQAMGYIAVVKKLDPGKNROI PEKKGRANTGFGGVISSIYHEETIREEDHYCKNENTOKA RNIMGREPSGRALRVUNAASENKEELKSLGFARFIITGPSGFGDP GGTLLSVTGEVGGVVSFFLLVYDRETGREGORGERSPROTTFTCKSO SVSVSGPGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	5487 5488 5489	535	182	ACDGLFKVFTPBEAVNFILSCLEDEKIQTREGKSAADARYEAAC NRLANKAVQRGSADNVTVMVVRIGH
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LEANDDPANKBOPRYJDKKALOJASGLICGGLIATAGIAAVLSGK CKCKSSQKGHSPVPEKAIPLITPGSATTC 5488 1072 259 AWAASGEROROWGEVAAVVVVSSCMTDLVSITSRLPKTGETIH GHKFFIGFGGKGANGCVQAARLGAMTSWCKVGKDSFGNYIEN LKQNDISTEFTYGTKDAATGTGSITVNNCGQNITUTVAGANLLL NTEDLRAAANVISRAKVWCQLEITPATSLEALTWARRSGVKTL PNPAPAIADLOPGYTLSDVPCCNESEREITLAVGASADAGE AALVLLKGRCCGVVITTLGAEGCVVLSQTEFEPKHPILLIGETEPLK TYPSFKI 5489 51 893 GKGPVAAFIDQSNIFLTDPKIFIGGWREEPKMPLLLIGETEPLK LERDCKSEVBWAAAS PDLALACLCHCQDLS SGAPFNKNIDFKELD LAGDEDNRRWMERNVDGEKKPONG IPLPFQI FNEEQVCGDFDFS FSAKEENITYSFJCLAPPPDSKGSKEKAEGGETAQKEGSEDVG NLPFAQGENREEGETTAETETETAMGAGGGAEEEEETAEGEEP GEDEDS 5490 81 893 GKGPVAAFIDGSNIFLTDPKIFIGGWREEPKWPLLLIGFTEPLK LERDCKSPVBWAAAS PDLALACLCHCQDLS SGAPFNKOUFSCH NLPFAQGENREEGETTAETETETAMGAGGGAEEEEETAEGEEP GEDEDS 5490 81 893 GKGPVAAFIDGSNIFLTDPKIFIGGWREEPKWPLLLIGFTEPLK LERDCKSPVBWAAAS PDLALACLCHCQDLS SGAPFNRGVLGGV NLPFAQGENREEGETTAETETETAMGAGGGAEEEEETAEGEEP GEDEDS 5490 5491 204 1194 GSAPRISIGPTGAAAADEDWARPESKPYONG IPLPFQIFNEOVCGOFDFSF FSAKEENITYSFIGLAPP PDG KSEKKAEEGGEFTAQKEGSEDVG NLPFAQGENREEGEGTATETTETETAMGAGGGAEEEEETAEGGEP GEDEDS 5491 204 1194 GSAPRISIGPTGAAAADEDWARPESKPYTOSKEERPPDTFGRSE GORDASSFILAGAATTGSGGGLSGCDDGGEVEPPBTPBTERSE GORDASSFILAGAATTGSGGGLSGCDDGGEVEPPBTPBTERSE GORDASSFILAGAATTGSGGGLSGCDDGGEVEPPBTPBTERSE LAELFEKAAAHLOGLUVASREQLLYLYARYKOVKVONCTTKPK SFTPFECKKKEAMTGGGVISSJYHEETIREDRNIFTYCRENNIDH ITKAIKSKNYUVNVKUEEGERALLHHACDRGHEEDVTLLIGHAD INCOMMENGALHYASACEETLUVELLIGGSADPTLEDDGGCLP PEKKKEANTGFGGVISSJYHEETIREDDRIFTPCCRENNIDH ITKAIKSKNYUVNVKUEEGERALLHHACDRGHEEDVTLLIGHAD TOPBDARBEITTRAVASLEPDCHPEILMKOMLICVONSIGBRRMML LQNPCLAYAALLQAQVWRIMDPEILAKLHRKKHVTPLIPPKKSQ SVSNGPGPGGGGLCHPRVLLINGGRPAPGGSLTEGGAMPGGICHGPG VGVPLEKGOVONSPRAPT PROPVTGGGLPPGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	5488		182	I AVSIJEOTECT TO THE PROPERTY OF THE PROPERTY AND THE PROPERTY OF THE PROPERTY AND THE PROP
CKCKSSOKOHSPVERKAIPLITPGSATTC 5488 1072 259 AMASGEPOROKOEVAVVVOSCMTDIVSITSELPKTGETIH GHKFIGPGKOROKOEVAVVVOSCMTDIVSITSELPKTGETIH LKQRDISTEPTYQTKDARTGTASI IVANEGORIIVUKGANLLI NTEDLRARANVISRAKVMYOQLETPATSILEALTIMARRSGVKIL FNPAPAIADLDPOPTYTISDVFCCHESEAEILTGITVGSANDAGE AALVLLKRGCQVVITIGAGCVVLSQTEPEPKHIPTEKYKAVO TVSFKI 5489 81 893 GKGPVAAFIDQSNTFLIDPKIFLGOWREEPKHPITEKYKAVO TVSFKI LERDCRSPVEWBAAASPLALACLCHCQOLSSGAFPNRGVLGGV LPPTVEWVIKVFVATSGSIAIRKKQQEVVGFLERNHIPKEKD IAGGENNRHWRENVPGEKKPONGIPLP PQI NNEGQVCOFFESH FSAKERNIIYSFLGIAPPPDSKGSEKAEBGGFTEAQKEGSEDVG NIPEAQEKNRHMERNVPGEKKPONGIPLP PQI NNEGQVCOFFESH GEBES 5490 81 893 GKGPVAAFIDQSNTFLIDPKIFLGQWREEPKHPLLLGBTEPLK LERDCRSPVEWBAAASPDLALACLCHCQOLSSGAFPNRGVLGGV LPPTVEWVIKVFVATSSGSIAIRKKQQEVVGFLERNHIPKELD IAGGENNRHWRENVPGEKKPONGIPLP PQI NNEGQVCOFFESH GEBES 5490 81 893 GKGPVAAFIDQSNTFLIDPKIFLGQWREEPKHPLLLGBTEPLK LERDCRSPVEWBAAASPDLALACLCHCQOLSSGAFPNRGVLGGV LFPTVEWVIKVFVATSSGSIAIRKKQQEVVGFLERNHIPKELD IAGGENNRHWRENVDGRKEPKONGIPLP PREQQVCOFFDSF FSAKEENIIYSFLGIAPPPDGKGSEKAEBGGFTEAQKEGSEDVG NLPRAQEKKRENVONGVEREEGEFETEIAMEGAEGEAEGEEFEETAGGEEP GEBES 5491 204 1194 GSAPRILGAPTAQAREDPOWARPPSKPYTQSKEDRPDTEGRSE GEBES 5492 GSAPALLGAPTAQAREDPOWARPPSKPYTQSKEDRPDTEGRSE JABLFEKAAAHLQGLIQVASKEQLIVIYARKKQUKNCNTYKKP SFFTPFEKGKREAMKLAGESPSQAMGETIAVKKLDPGKNPQI PEKKGKEANTGFGGPVISSLYHEETIREDKNIFDVIRCNCNTHKF SFFTPFEKGKREAMKLAGSSPSQAMGETIAVKKLDPGKNPQI PEKKGKEANTGFGGPVISSLYHEETIREDKNIFDVIRCNCTHKP ITKAIKSKYNDVNVKDEBGRALLHMACHGVIRCNTGKNPQI PEKKGKEANTGFGGPVISSLYHEETIREDKNIFDVIRCNCTHKP ITKAIKSKYNDVNVKDEBGRALLHMACHGVORTHATPVAGA INCQDREGGTALHVASACEFLDIVELLLQSGADFTLRDQDGCLP EEVTGCKTYSTULJQRHTTGKA 5492 3 1896 ASKNPLSAVCTTGIMSSLAVRDPAMDRSLRSVFVGNIPYEATEE QLKDIFSEVGGVYSFRLVYDRETTGKKGGGGCGCQDCTALSAM RNLAGGEFSGGRALEVNDAASKENKEELKSLGGAAPTIDSPYOD IDPEDAPESITRAVASLPPEOMFFLKKOMGCORGDSRAMPTARAMET VLSTRYMERROMETCAMETROMERROMAGRAGGTOTO GTGNGGAGIOGGGNOTPOLORGDBAPATHTPTCAMPOPTALLERCHMYDFLTAKERYTTTCAMPOPTALLERCHMYDFLTAKERYTSCHAMPTSSSGOSQ PSSSFSGOSOVTPODORGRANGANGGTDSANGGSGOSQ PSSSFSGOSOVTPODORGANGGTDSANGGRANGGTOIC	5489	1072		
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GHKFFIGFGKGANCCQAARLGAMTSMVCKVGKDSFONDYIEN LKQRDISTEFTYTYTKDAATGTASIIVNNEGONIIVIAGANLLLI NTEDLRAAANVISRAKVMVCQLEITPATSLEALTMARRSGVKTL PNPAPAIADLDPOPYTLSDVPCCHESEAEILTGITVGAADAGE AALVLLKRGCQVVITIGAGGCVVLSQTEEPKHIPTEKVKAVD TTVSFKI S489 81 893 GKGFVAAPIDGSNTFLTDPKIFIGGWEEPKHPLILGFTELK LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVLGGV LPFTVEWNIKVFVATSSGSIAIRKQQEVVGFLEANHIPTEKKKAVD TTVSFKI LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVLGGV LPFTVEWNIKVFVATSSGSIAIRKQQEVVGFLEANHIPTEKKAVD NLPEAQEKREKPONITJP.PQINEEQVCODFDSF FSAKEENIIYSFLGLAPPDDGKGSEKAEBGGFTEAQKEGSEDVG NLPEAQEKREKPONITJP.PQINEEQVCODFDSF FSAKEENIIYSFLGLAPPDDGKGSEKAEBGGFTEAQKEGSEDVG GEDEDS 61 893 GKGFVAAPTDGSNTFLTDPKIFLGQWEEPKKPLLLIGRFTELK LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVLGGV LFFTVEWNIKVFVATSSGSIAIRKQQEVVGFLEANHIPKELD IAGGEDNRAWMEREWNOERKEKPONITJP.PINEEQVCCDFDSF FSAKEENIIYSFLGLAPPDDGKGSEKAEBGGFTEAQKEGSEDVG NLPEAQEKRWEENVOERKEVPONITJP.PINEEQVCCDFDSF FSAKEENIIYSFLGLAPPDDGKGSEKAEBGGFTEAQKEGSEDVG NLPEAQEKRWEENVOERKEVPONITJP.NEEQVCCDFDSF FSAKEENIIYSFLGLAPPDDGKGSEKAEBGGFTEAQKEGSEDVG NLPEAQEKRWEENVOERTGKEVPONITJPERGYCC NLPEAQEKREKERVONITJP.NEEQVCCDFDSF FSAKEENIIYSFLGLAPPDDGKGSEKAEBGGFTEAQKEGSEDVG NLPEAQEKREKERVONITJP.NEEQVCCDFDSF FSAKEENIIYSFLGLAPPDGKGSEKAEBGGFTEAQKGSEDVG NLPEAQEKREKVPONITJP.NEEQVCCDFDSF FSAKEENIIYSFLGLAPPDGKGSEKAEBGGFTEAQKGSEDVG NLPEAQEKREVPONITJSFLIVERTEKERGGEFTEAGGEGE GEDEDS 5491 204 1194 GSAPRIJGAPTAQARDPDWWARPPSERPYTGSKEDRPDTREGSE GEDEDS 5492 STAFFGGGKKAEMNAALGSSPSQAMGETIAAVKKLDPGAWNPQI PEKKGKEANTGFGGPVISSLYHEETIREDKNITDVCNCNTPKF SFPFFESKKKEAMNALGSSPSQAMGETIAAVKKLDPGAWNPQI PEKKGKEANTGFGGPVISSLYHEETIREDKNITDVCNCNTPKF SFPFFESKKKAAMNALGSSPSQAMGERHELTAAVKLDPGAMPGLLLTAARKGVTTATVKKLDPGAMPGLLTAARKGVTTAAVKLDPGAMPGLLTAARKGVTTAAVKAUCNTTTAATAAACEPTLATVAAACEPTLATVAAACEPTLATVAAACEPTLATVAAACEPTLATVAAACEPTLATVAAACEPTLATVAAAACEPTLATVAAAACEPTLATVAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	5489	1072		<u> </u>
LKQNDISTRETTQTKDAATGTASIIVNNEGQNIIVIVAGANLILL NTEDLRAANVISRAKWACQLEITEABLATMARSGWKTL PNPAPAIADLDPQFYTLSDVFCCNESEAEILTGLTVGSAADAGE AALVLLKRGCQVVIITLGABGCVLISQTEPEPKHIPTEKVKAVD TTVSPKI 5489 81 893 GKGPVARFIDQSNIFLTDPKIFLGQMREEPKMPLLLIGETEPLK LERDCRSPVEPMAANSPDLALACLCHCQDLSSGAFPNRGVLGGV LEPPTVEMVIKVPVARSGSIAIRKKQQEVVGFLEANKIDFKELD IAGDEDNRRWMENVPGEKKPQNGIPLPPQIFBEGYCGDFDSF FSAKEENIIYSFLGLABPPDSKGSEKAEEGGGTTAQKEGSEVG NLPPAGEKNEEEGGTTATETTEEIAMEGAEGGEAEEGETTAGGEP GEDEDS 5490 61 893 GKGPVARFIDQSNIFLTDPKIPLGQWREEPKMPLLLIGETEPLK LERDCRSPVSPWAMASPDLALACLCHCQDLSSGAFPNRGVLGGV LEPTVEMVIKVPVATSSGSIAIRKKQQEVVGFLEANKIDFKELD IAGDEDNRRWMENVPGEKKPQNGIPLPGOFVAFLEANKIDFKELD IAGDEDNRRWMENVPGEKKPQNGIPLPGOFVAFLEANKIDFKELD IAGDEDNRRWMENVPGEKKPQNGIPLPGOFVAFLEANKIDFKELD IAGDEDNRRWMENVPGEKKPQNGIPLPPGTFERGYCCDFDSF FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETTAQKEGSEVG NLPRAGEKNEESGGTATEETEEIAMEGAEGGEAEEGEETAGGEEP GEDEDS 5491 204 1194 GSAPRLSLGPTGAQARDPDWARPPSRPYTQSKEDRPDTEGRSE OGDRASSFLPAGAATTGDSGELSSGDDSGEVEPHSPETEBETSC LAELFEKAAHLQGLIQVASREGLLYVARKVQVKVGNCTNFKP SFPDFEGKQKKBANTGGGGVLGASREGLLYVARKVQVKVGNCTNFKP SFPDFEGKQKKBANTGGGGVLGASREGLLYVARKVQVKVGNCTNFKP SFPDFEGKQKKBANTGGGGVLSSLYHEETIEDNITPDYCGRNIDH ITKAIKSKNVDVNVKDEEGRALLHWACDRGHKELVTVLLQHRAD INCQNNEGGTALHVASACEPLDIVSELLQGGADPTLRODGCCLP BEVTGCKTVSLVLQRHTTGKA 5492 3 1896 ASKNPLSAVCTTGIMSSLAVRDDAMDRSLRSVFVONIPYRATE GLKDIFFSGVSVVSFRLVVDRTGTGKSVGYGFCNOPOCTALSAM RNLMGREFSGRALRVDMAASEKKELKSLGPAAPTIDSPYODP GGTLLSVTGGGTPAGFTGAGGSSLTPGGANOPOLIAMRPVKDI 1DPEDAPESITRAVASLPPEQMFELMKGMKLCVQNSHQEANML LQNNQLAYALLQAQVVWRIMDEFIAKKGHLGCHTROPSSHDRG GGTLLSVTGGGTPAGFTFAGGGSSLTPGGANOPOLIAMRPVKDI PPLMYTTIGGGTPAGFTFAGGFSLTPGGANOPOLIAMRPVKDI PPLMYTTIGGGTPAGFTFAGGFSLTPGGANOPOLIAMRPVKDI TOGGTLAGFTVGGAPPAGPGGFGTPAGFTBGGGSTTPGGANOPOLIAMRP VGPVPLERGQVVARGFTGAGPPGGSTCPGGANOPOLIAMRGTGTIG GTGMGAGTGGGGMGGAGTGGGSCNAGGGGGGGASKAGGGG PSSFSPGGOVTPOLOGRAALTHGHAGHTAGHTGGGTDAGSTLFGG PSSFSGOGOVTPOLOGRAALTHGHAGGHTGGGGASKGGGG PSSFSFGGOVTPOLOGRAALTHGHAGHTGAGGTGASKGGGGG PSSFSFGGOVTPOLOGRAALTHGHAGHTGAGGGGGGGGGGASKGGGGG PSSFSFGGOVTPOLOGRAAL			259	
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SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
		<u> </u>	GHLTRTKLLASKAHGSEPPSVPGLPDQSSPVPRVPSPIAQATGS
İ			PVQEEAIVIIQSALRAHLARARHSATGKRTTTAASTRRRSASAT
ſ	{		HGDASSPPFLAALPDPSPSGPQAVAPLPGDDVNSDDSDDIVIAP
L _	ł	1	SLPTKNFPV
5494	71	536	RSKAKIGTPTREVPSTDMKVRRESSSSLTHRPAPSPATPRLLGT
	İ		RRVLLGVSEGTGCADAMELVLVFLCSLLAPMVLASAAEKEKEMD
ì		Ì	PFHYDYQTLRIGGLVFAVVLFSVGILLILSRRCKCSFNQKPRAP
L			GDEEAQVENLITANATEPQKAEN
5495	273	2168	DSLLLIQVDTMPFTLHLRSRLPSAIRSLILQKKPNIRNTSSMAG
			ELRPASLVVLPRSLAPAFERFCQVNTGPLPLLGQSEPEKWMLPP
1	}		QGAISETRMGHPQFWKYEFGACTGSLASLEQYSEQLKDMVAFFL
1		ł	GCSFSLEEALEKAGLPRRDPAGHSQAGAYKTTVPCVTHAGFCCP
	ĺ		LVVTMRPIPKDKLEGLVRACCSLGGEQGQPVHMGDPELLGIKEL
			SKPAYGDAMVCPPGEVPVFWPSPLTSLGAVSSCETPLAFASIPG
1			CTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSIASVSASO
1	{		KIRELESMIGIDPGNRGIGHLLCKDELLKASLSLSHARSVLITT
1	į		GFPTHFNHEPPEETDGPPGAVALVAFLQALEKEVAIIVDORAWN
1			LHQKIVEDAVEQGVLKTQIPILTYQGGSVEAAQAFLCKNGDPOT
1			PRFDHLVAIERAGRAADGNYYNARKMNIKHLVDPIDDLFLAAKK
1			IPGISSTGVGDGGNELGMGKVKEAVRRHIRHGDVIACDVEADFA
1			VIAGVSNWGGYALACALYILYSCAVHSQYLRKAVGPSRAPGDQA
[WTQALPSVIKEEKMLGILVQHKVRSGVSGIVGMEVDGLPFHNTH
5405			AEMIQKLVDVTTAQV
5496	3	2408	QDTKMHEIYKGNITPQLNKNTLKTSAATDVWAVYFSQFWIDYEG
			MKSGKGRPISFVDSFPLSIWICQPTRYAESQKEPQTCNQVSLNT
{			SQSESSDLAGRLKRKKLLKEYYSTESEPLTNGGQKPSSSDTFFR
1			FSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLHESLILLSE
			NLRKDVEAVTGSPASQTSICIGILLRSAELALLLHPVDQANTLK
			SPVSESVSPVVPDYLPTENGDFLSSKRKQISRDINRIRSVTVNH
	Į į		MSDNRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYLSDKH
			LGKISEDESSGLVYKSGSGEIGSETSDKKDSFYTDSSSVLNYRE
			DSNILSFDSDGNQNILSSTLTSKGNETIESIFKAEDLLPEAASL
			SENLDISKEETPPVRTLKSQSSLSGKPKERCPPNLAPLCVSYKN
			MKRSSQMSLDTISLDSMILEEQLLESDGSDSHMFLEKGNKKNS
			TTNYRGTAESVNAGANLQNYGETSPDAISTNSEGAQENHDDLMS
1 1			VVVFKITGVNGEIDIRGEDTEICLQVNQVTPDQLGNISLRHYLC NRPVGSDQKAVIHSKSSPEISLRFESGPGAVIHSLLAEKNGFLQ
1			CHIKNFSTEFLTSSLMNIQHFLEDETVATVMPMKIQVSNTKINL
		[KDDSPRSSTVSLEPAPVTVHIDHLVVERSDDGSFHIRDSHMLNT
] [l	GNDLKENVKSDSVLLTSGKYDLKKQRSVTQATQTSPGVPWPSQS
		ļ	ANFPEFSFDFTREQLMEENESLKQELAKAKMALAEAHLEKDALL
			HHIKKMTVE
5497	1821	3308	SISKLLKRRSNIDAYLLSNSCAFFAPRLFSLASQIIREQQSPNV
1			CFIYKYSGFPSLECQCHFVSPHSSCYINFFSFPPFFFVCFQLSN
			GFSHYSLSSESHVGPTGAGLFPHCLPASRLLPRVTSVHLPDYAH
[YYTIGPGMFPSSQIPSWKDWAKPGPYDQPLVNTLQRRKEKREPD
1 1			PNGGGPTTASGPPAAAEEAQRPRSMTVSAATRPGEEMEACEELA
] 1			LALSRGLQLDTQRSSRDSLQCSSGYSTQTTTPCCSEDTIPSQVS
			DYDYFSVSGDQEADQQEFDKSSTIPRNSDISQSYRRMFQAKRPA
1	ł	1	STAGLPTTLGPAMVTPGVATIRRTPSTKPSVRRGTIGAGPIPIK
] 1	İ		TPVIPVKTPTVPDLPGVLPAPPDGPEERGEHSPESPSVGEGPQG
] [[[VTSMPSSMWSGQASVNPPLPGPKPSIPEEHRQAIPESEAEDQER
1 1	[}	EPPSATVSPGQIPESDPADLSPRDTPQGEDMLNAIRRGVKLKKT
			TINDRSAPRES
5498	2434	1492	ILTHQEIFTGEKPCECGKASIQMSHLSQQKIYSGENPFACKVCG
1			KVFSHKSNLTEHEHFHTREKPFECNECGKAFSQKQYVIKHQNTH
]			TGEKLFECNECGKSFSQKENLLTHQKIHTGEKPFECKDCGKAFI
[ĺ	QKSNLIRHQRTHTGEKPFVCKECGKTFSGKSNLTEHEKIHIGEK
		}	PFKCSECGTAFGQKKYLIKHQNIHTGEKPYECNECGKAFSQRTS
]]			LIVHVRIHSGDKPYECNVCGKAFSQSSSLTVHVRSHTGEKPYGC
L1		1	NECGKAFSQFSTLALHLRIHTGKKPYQCSECGKAFSQKSHHIRH
			The state of the s

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
]	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
		L	QKIHTH
5499	324	926	GFGQIGRGHKITTYPFSPRKSGRKGMAQSQGWVKRYIKAFCKGF
		}	FVAVPVAVTFLDRVACVARVEGASMQPSLNPGGSQSSDVVLLNH
1	İ		wkvrnfevhrgdivslvspknpeqkiikrvialegdivrtighk
	ł		NRYVKVPRGHIWVEGDHHGHSFDSNSFGPVSLGLLHAHATHILW
1			PPERWQKLESVLPPERLPVQREEE
5500	1978	1286	KPDWRLQNLPPRLYLWRSSRFGFGHLKKRLQMDFKIEHTWDGFP
			VKHEPVFIRLNPGDRGVMMDISAPFFRDPPAPLGEPGKPFNELW
i			DYEVVEAFFLNDITEQYLEVELCPHGQHLVLLLSGRRNVWKQEL
l	l	}	PLSFRVSRGETKWEGKAYLPWSYFPPNVTKFNSFAIHGSKDKRS
	1		
			YEALYPVPQHBLQQGQKPDFHCLEYFKSFNFNTLLGEEWKQPES
	L		DLWLIEKCDI
5501	2927	2226	CRPPVSARVAPGHQGAVGGSGRRPARVEVVDAAARPSSRPFSLP
1		1	AAIMLALISRLLDWFRSLFWKEEMELTLVGLQYSGKTTFVNVIA
Į.			SGQFSEDMIPTVGFNMRKVTKGNVTIKIWDIGGQPRFRSMWERY
1	[CRGVNAIVYMIDAADREKIEASRNELHNLLDKPQLQGIPVLVLG
1	}		NKRDLPNALDEKQLIEKMNLSAIQDREICCYSISCKEKDNIDIT
L	L		LQWLIQHSKSRRS
5502	3	824	NSAFPVWVPERTALLTCPLGAAPGSSREAPGIAGPPNSTAMSKL
			GKFFKGGGSSKSRAAPSPQEALVRLRETEEMLGKKQEYLENRIQ
1	(REIALAKKHGTONKRAALQALKRKKRFEKOLTOIDGTLSTIEFO
Į.	}		REALENSHINTEVLRNMGFAAKAMKSVHENMDLNKIDDLMQEIT
	†	Ì	EQQDIAQEISEAFSQRVGFGDDFDEDELMAELEELEQEELNKKM
1	1		TNIRLPNVPSSSLPAQPNRKPGMSSTARRSRAASSQRAEEEDDD
ì			IKOLAAWAT
5503	216	654	KGVRRRGRVRSDSEDSHLGYFKMSFLLPKLTSKKEVDOAIKSTA
1 3303	220.	034	EKVLVLRFGRDEDPVCLQLDDILSKTSSDLSKMAAIYLVDVDQT
1			AVYTQYFDISYIPSTVFFFNGQHMKVDYGGEDPALRSIKAVRRT
ł			
			SPAGTLGEKPVNS
5504	58	3563	QLSFSFQAPVTFDDITVYLLQEEWVLLSQQQKELCGSNKLVAPL
1			GPTVANPELFRKFGRGPEPWLGSVQGQRSLLEHHPGKKQMGYMG
l	i		EMEVQGPTRESGQSLPPQKKAYLSHLSTGSGHIEGDWAGRNRKL
1	1		LKPRSIQKSWFVQFPWLIMNEEQTALFCSACREYPSIRDKRSRL
1]		IEGYTGPFKVETLKYHAKSKAHMFCVNALAARDPIWAARFRSIR
			DPPGDVLASPEPLFTADCPIFYPPGPLGGFDSMAELLPSSRAEL
}	1	}	EDPGGDGAIPAMYLDCISDLRQKEITDGIHSSSDINILYNDAVE
l	1	1	SCIQDPSAEGLSEEVPVVFEELPVVFEDVAVYFTREEWGMLDKR
1	1		QKELYRDVMRMNYELLASLGPAAAKPDLISKLERRAAPWIKDPN
ļ	1		GPKWGKGRPPGNKKMVAVREADTQASAADSALLPGSPVEARASC
1			CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQFPWLVIDPKETKL
ł			FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHEVSKAHRLCV
1	1		NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN
1	1	1	DFEKILQLLQSTGTVILGKYRNRTACTQFIKYISETLKREILED
ł		į	VRNSPCVSVLLDSSTDASEQACVGIYIRYFKQMEVKESYITLAP
1			LYSETADGYFETIVSALDELDIPFRKPGWVVGLGTDGSAMLSCR
1	1	{	GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDRH
		1	IRTVFKFYQSSNKRLNELQEGAAPLEQEIIRLKDLNAVRWVASR
1			RRTLHALLVSWPALARHLORVAEAGGOIGHRAKGMLKLMRGFHF
1	1		VKFCHFLLDFLSIYRPLSEVCOKEIVLITEVNATLGRAYVALES
ı			-
1			LRHQAGPKEEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV
1.	J		LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI
j.			LNLARYFECSLPTGYSEEALLBEWLGLKTIAQHLPFSMLCKNAL
1	1	ł.	AQHCRFPLLSKLMAVVVCVPISTSCCERGFKAMNRIRTDERTKL
		1	SNEVLNMLMMTAVNGVAVTEYDPQPAIQHWYLTSSGRRFSHVYT
1	1	1	CAQVPARSPASARLRKEEMGALYVEEPRTQKPPILPSREAAEVL
L	1		KDCIMEPPERLLYPHTSQEAPGMS
5505	3312	1219	NCSPRSLSAAKMENRNNNKLPSNLPQLQNLIKRDPPAYIEEFLQ
1			QYNHYKSNVEIFKLQPNKPSKELAELVMFMAQISHCYPEYLSNF
1			PQEVKDLLSCNHTVLDPDLRMTFCKALILLRNKNLINPSSLLEL
1		ł	FFELFRCHDKLLRKTLYTHIVTDIKNINAKHKNNKVNVVLQNFM
L		L	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	1	to first	L=Leucine, M=Methionine, N=Asparagine,
ì	corresponding		P=Proline, Q=Glutamine, R=Arginine,
1	to first	amino acid	S=Serine, T=Threonine, V=Valine,
}	amino acid	residue of	
ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			YTMLRDSNATAAKMSLDVMIELYRRNIWNDAKTVNVITTACPSK
	1	}	VTKILVAALTFFLGKDEDEKQDSDSESEDDGPTARDLLVQYATG
1			KKSSKNKKKLEKAMKVLKKHRKKKKPEVFNFSAIHLIHDPQDFA
1	ļ		EKLLKOLECCKERFEVKMMLMNLISRLVGIHELFLFNFYPFLQR
]			FLOPHOREVTKILLFAAQASHHLVPPEIIQSLLMTVANNFVTDK
i			NSGEVMTVGINAIKEITARCPLAMTEELLQDLAQYKTHKDKNVM
1]	MSARTLIHLFRTLNPOMLOKKFRGKPTEASIEARVQEYGELDAK
Í			DYIPGAEVLEVEKEENAENDEDGWESTSLSEEEDADGEWIDVOH
})	1	SSDEEQQEISKKLNSMPMEERKAKAAAISTSRVLTQEDFQKIRM
i		Ì	
ł			AQMRKELDAAPGKSQKRKYIEIDSDEEPRGELLSLRDIERLHKK
1			PKSDKETRLATAMAGKTDRKEFVRKKTKTNPFSSSTNKEKKKQK
1			NFMMMRYSQNVRSKNKRSFREKQLALRDALLKKKKRMK
5506	1	1531	FRGDLCGQRGGSAPGEGGSSAWPAPAHPLPEREREALCPGRS
			CSGGGGEETPGTTPVWSPLEGGGDEELRPNPYVRFPYRWWAVVV
1	1		LAAFPSLGAGGETPEAPPESWTQLWFFRPVVNAAGYASFMVPGY
1			LLVQYFRRKNYLETGRGLCFPLVKACVFGNEPKASDEVPLAPRT
1			EAAETTPMWQALKLLFCATGLQVSYLTWGVLQERVMTRSYGATA
			TSPGERFTDSQFLVLMNRVLALIVAGLSCVLCKQPRHGAPMYRY
1	'		SFASLSNVLSSWCOYEALKFVSFPTQVLAKASKVIPVMLMGKLV
į	1		SRRSYEHWEYLTATLISIGVSMFLLSSGPEPRSSPATTLSGLIL
			LAGYIAFDSFTSNWQDALFAYKMSSVQMMFGVNFFSCLFTVGSL
1	i		LEOGALLEGTRFMGRHSEFAAHALLLSICSACGQLFIFYTIGQF
1	1	1	GAAVFTIIMTLRQAFAILLSCLLYGHTVTVVGGLGVAVVFAALL
ĺ			
			LRVYARGRLKQRGKKAVPVESPVQKV
5507	3704	1271	PRGTRRCRPAGRASRRARRRPPCPGPAAPGSLEIGGFGTAAGKK
1	· .		VAVADVQFGPMRFHQDQLQVLLVFTKEDNQCNGFCRACEKAGFK
			CTVTKEAQAVLACFLDKHHDIIIIDHRNPRQLDAEALCRSIRSS
	1	1	KLSENTVIVGVVRRVDREELSVMPFISAGFTRRYVENPNIMACY
		j	NELLQLEFGEVRSQLKLRACNSVFTALENSEDAIEITSEDRFIQ
1	l .		YANPAFETTMGYQSGELIGKELGBVPINEKKADLLDTINSCIRI
	1	1	GKEWQGIYYAKKKNGDNIQQNVKIIPVIGQGGKIRHYVSIIRVC
			NGNNKAEKISECVQSDTHTDNQTGKHKDRRKGSLDVKAVASRAT
ì		1	EVSSORRHSSMARIHSMTIEAPITKVINIINAAQESSPMPVTEA
1			LDRVLEILRTTELYSPQFGAKDDDPHANDLVGGLMSDGLRRLSG
ı		1	NEYVLSTKNTQMVSSNIITPISLDDVPPRIARAMENEEYWDFDI
i		1	FELEAATHNRPLIYLGLKMFARFGICEFLHCSESTLRSWLQIIE
1			ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDEVAAL
		1	IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF
1 .		1	QLTTGDDKCNIFKNMERNDYRTLRQGIIDMVLATEMTKHFEHVN
1		'	1 7
}		1	KFVNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMLI KCADVSNPCRPLOYCIEWAARISEEYFSOTDEEKOOGLPVVMPV
i			
1		1	FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF
· L	<u> </u>	<u> </u>	KYWKGLDEMKLRNLRPPPE
5508	1151	691	LSSVFSRRSASMFAVGCSMGPFLHYWYLSLDRLFPASGLRGFPN
1]	1	VLKKVLVDQLVASPLLGVWYFLGLGCLEGQTVGESCQELREKFW
1			EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL
	1	1	KYRSPVPLTPPGCVALDTRAD
5509	1238	619	RKSRGCQNALSASGPAAAAAAIMVRKLKFHEQKLLKQVDFLNWE
1		1	VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP
1			ERDOFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR
1	1		LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM
1	1		EDFYTWVDSSKIKRHVLEYNEERDDFDLEA
ļ		 	
5510	96	1195	PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM
			AEGEROPPPDSSBEAPPATONFIIPKKEIHTVPDMGKWKRSQAY
1			ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID
1			ETPPVDQPSRFGNKAYRTWYAKLDERAENLVATVVPTHLAAAVP
	1		EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ
1			IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI
			WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT
Į	-		GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF
	1	ì	KFGSLLPIHPVTSG
	•		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
)	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1 1 1 1 1 1 1	\=possible nucleotide insertion)
5511	276	1980	KLSRVLNLPPENLITSISAVPISQKEEVADFQLSVDSLLEKDND
1		1	HSRPDIQVQAKRLAEKLRCDTVVSEISTGQRTVNFKINRELLTK
		ļ	TVLQQVIEDGSKYGLKSELFSGLPQKKIVVEFSSPNVAKKPHVG
		Ì	HLRSTIIGNFIANLKEALGHQVIRINYLGDWGMQFGLLGTGFQL
1			FGYEEKLQSNPLQHLFEVYVQVNKEAADDKSVAKAAQEFFQRLE
i			LGDVQALSLWQKFRDLSIEEYIRVYKRLGVYFDEYSGESFYREK
1	1		SQEVLKLLESKGLLLKTIKGTAVVDLSGNGDPSSICTVMRSDGT
{		•	SLYATROLAAAIDRMDKYNFDTMIYVTDKGQKKHPQQVFQMLKI
1			MGYDWAERCQHVPFGVVQGMKTRRGDVTFLEDVLNEIQLRMLQN
1			MASIKTTKELKNPQETAERVGLAALIIQDFKGLLLSDYKFSWDR
İ	ì	1	VFQSRGDTGVFLQYTHARLHSLEETFGCGYLNDFNTACLQEPQS
			VSILQHLLRFDEVLYKSSQDFQPRHIVSYLLTLSHLAAVAHKTL
1			QIKDSPPEVAGARLHLFKAVRSVLANGMKLLGITPVCRM
5512	120	1015	DPSLLLTITVTGVTVLVLVLKSMNSRRREPITLQDPEAKYPLPL
1]	-3.5	IEKEKISHNTRRFRFGLPSPDHVLGLPVGNYVQLLAKIDNELVV
1	}		RAYTPVSSDDDRGFVDLIIKIYFKNVHPQYPEGGKMTQYLENMK
			IGETIFFRGPRGRLFYHGPGNLGIRPDQTSEPKKTLADHLGMIA
I			GGTGITPMLQLIRHITKDPSDRTRMSLIFANQTEEDILVRKELE
			BIARTHPDQFDLWYTLDRPPIGWKYSSGFVTADMIKEHLPPPAK
	1		STLILVCGPPPLIQTAAHPNLEKLGYTQDMIFTY
5513	2	837	ARWRLPSDSPRIPPAGAETPGRGSCRNYLPSSSPPFPEPSSFPS
			PPTSRGGPGSRDTMSDSEEESQDRQLKIVVLGDGASGKTSLTTC
1			PAQETFGKQYKQTIGLDFFLRRITLPGNLNVTLQIWDIGGQTIG
			GKMLDKYIYGAQGVLLVYDITNYQSFENLEDWYTVVKKVSEESE
i			TQPLVALVGNKIDLEHMRTIKPEKHLRFCQENGFSSHFVSAKTG
}			DSVFLCFQKVAAEILGIKLNKAEIEQSQRVVKADIVNYNQEPMS
1			RTVNPPRSSMCAVQ
5514	1295	449	VNRPSWIMGNFRGHALPGTFFFIIGLWWCTKSILKYICKKQKRT
İ			CYLGSKTLFYRLEILBGITIVGMALTGMAGEQFIPGGPHLMLYD
1	1		YKQGHWNQLLGWHHFTMYFFFGLLGVADILCFTISSLPVSLTKL
Ì			MLSNALFVEAFIFYNHTHGREMLDIFVHQLLVLVVFLTGLVAFL
ĺ			EFLVRNNVLLELLRSSLILLQGSWFFQIGFVLYPPSGGPAWDLM
)	,	,	DHENILFLTICFCWHYAVTIVIVGMNYAFITWLVKSRLKRLCSS
			EVGLLKNAEREQESEERM
5515	1572	260	FVRLVGRGDCDPLLSVCLTTMPLYEGLGSGGEKTAVVIDLGEAF
ĺ			TKCGFAGETGPRCIIPSVIKRAGMPKPVRVVQYNINTEELYSYL
			KEFIHILYFRHLLVNPRDRRVVIIBSVLCPSHFRETLTRVLFKY
			FEVPSVLLAPSHLMALLTLGINSAMVLDCGYRESLVLPIYEGIP
			VLNCWGALPLGGKALHKBLETQLLEQCTVDTSVAKEQSLPSVMG
			SVPEGVLEDIKARTCFVSDLKRGLKIQAAKFNIDGNNERPSPPP
			NVDYPLDGEKILHILGSIRDSVVEILFEQDNEEQSVATLILDSL
			IQCPIDTRKQLAENLVVIGGTSMLPGFLHRLLAEIRYLVEKPKY
			KKALGTKTFRIHTPPAKANCVAWLGGAIFGALQDILGSRSVSKE
			YYNQTGRIPDWCSLNNPPLEMMFDVGKTQPPLMKRAFSTEK
5516	3	735	NSREPPOAGPGPSPRKSPTASSFLFPWRPLASSFWMGAQGAQES
			IKAMWRVPGTTRRPVTGESPGMHRPEAMLLLLTLALLGGPTWAG
			KMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW
			DVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDR
			YFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWNY
			PLEEPTTEPPVNLTYSANSPVGR
5517	246	499	SEIYVAMRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA
			TDGTSDLPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK
5518	3	1375	DAWADAWYRAWDLNMDFPCLWLGLLLPLVAALDFNYHRQEGMEA
		= · -	FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP
			EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR
			IHIMPSMNPDGFEAVKKPDCYYSIGRENYNQYDLNRNPPDAFEY
]		NNVSRQPETVAVMKWLKTETPVLSANLHGGALVASYPFDNGVQA
			TGALYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN
			GVTNGYSWYPLQGGMQDYNYIWAQCFEITLELSCCKYPREEKLP
			SFWNNNKASLIEYIKQVHLGVKGQVFDQNGNPLPNVIVEVQDRK
			THE TAX TAX TAX TAX TAX TAX TAX TAX TAX TAX

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	(A=Aranine, C=Cysteine, D=Aspartic Acid, K=
NO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S≃Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			HICPYRTNKYGEYYLLLLPGSYIINVTVPGHDPHITKVIIPEKS
1	i		QNFSALKKDILLPFQGQLDSIPVSNPSCPMIPLYRNLPDHSAAT
	1		KPSLFLFLVSLLHIFFK
5519	87	477	IKSKLNQQVEVQESEWRLTEAKGPTMGKESGWDSGRAAVAAVVG
1	1	1	GVVAVGTVLVALSAMGFTSVGIAASSIAAKMMSTAAIANGGGVA
			AGSLVAILQSVGAAGLSVTSKVIGGFAGTALGAWLGSPPSS
5520	117		
5520	111/	943	PTEGRQKVLKTFTVPRSALAMTKTSTCIYHFLVLSWYTFLNYYI
1	1		SQEGKDEVKPKILANGARWKYMTLLNLLLQTIFYGVTCLDDVLK
1			RTKGGKDIKFLTAFRDLLFTTLAFPVSTFVFLAFWILFLYNRDL
1	ł	ł	IYPKVLDTVIPVWLNHAMHTFIFPITLAEVVLRPHSYPSKKTGL
Ì		1	TLLAAASIAYISRILWLYFETGTWVYPVFAKLSLLGLAAFFSLS
i			YVFIASIYLLGEKLNHWKWVSVQILQRWRLESVGICFQWPDWKS
1			PAKHQLVKNIR
5521	546	911	KILNMQKSCEENEGKPQNMPKAEEDRPLEDVPQEAEGNPQPSEE
j	}		GVSQEAEGNPRGGPNQPGQGFKEDTPVRHLDPEEMIRGVDELER
1	([LREEIRRVRNKFVMMHWKQRHSRSRPYPVCFRP
5522	1224	637	GSRPLGQRSREKMWVFGYGSLIWKVDFPYQDKLVGYITNYSRRF
			WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVGKEEEVK
		j	AYLDFREKGGYRTTTVIFYPKDPTTKPFSVLLYIGTCDNPDYLG
1		{	
	1]	PAPLEDIAEQIFNAAGPSGRNTEYLFELANSIRNLVPEEADEHL
5523	<u> </u>	1000	FALEKLVKERLEGKQNLNCI
5523	3	1280	SKGKKRMGSSMSAATARRPVFDDKEDVNFDHFQILRAIGKGSFG
		-	KVCIVQKRDTEKMYAMKYMNKQQCIERDEVRNVFRELEILQEIE
1	1		HVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQFSEDTV
i		İ	RLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI
1	1	ł	ATIIKDGERATALSGTKPYMAPEIFHSFVNGGTGYSFEVDWWSV
1			GVMAYELLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEM
1	ł	1	VALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVEPG
]		FVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRD
1	Ì	İ	SSQSENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPES
		ì	RDAAEPVEDEAERSALPMCGPICPSAGSG
5524	85	2318	RERERDHRPGESSOGOSGAGGCFPSPTMELRCGGLLFSSRFDSG
		1	NLAHVEKVESLSSDGEGVGGGASALTSGIASSPDYEFNVWTRPD
1		i	CAETEFENGNRSWFYFSVRGGMPGKLIKINIMNMNKQSKLYSQG
1	1	1	MAPFVRTLPTRPRWERIRDRPTFEMTETQFVLSFVHRFVEGRGA
1		ĺ	TTFFAFCYPFSYSDCOELLNOLDORFPENHPTHSSPLDTIYYHR
		}	ELLCYSLDGLRVDLLTITSCHGLREDREPRLEQLFPDTSTPRPF
1	-		
ļ	}	}	RFAGKRIFFLSSRVHPGETPSSFVFNGFLDFILRPDDPRAQTLR
1			RLFVFKLIPMLNPDGVVRGHYRTDSRGVNLNRQYLKPDAVLHPA
1)	IYGAKAVLLYHHVHSRLNSQSSSEHQPSSCLPPDAPVSDLEKAN
1	[Į	NLQNEAQCGHSADRHNABAWKQTEPAEQKLNSVWIMPQQSAGLE
}			ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE
			NMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV
	1	1	AIYKASGIIHSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPPA
	<u> </u>		FPSRYTVELFEQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL
l	1	1	RAWMLKHVRNSRGLSSTLNVGVNKKRGLRTPPKSHNGLPVSCSE
İ]	l	NTLSRARSFSTGTSAGGSSSSQQNSPQMKNSPSFPFHGSRPAGL
1			PGLGSSTQKVTHRVLGPVRGKPVWEPLQHVFGCLGHCWGK
5525	105	834	SNTLDFERHLFIMGQQISDQTQLVINKLPEKVAKHVTLVRESGS
1	1	1	LTYEEFLGRVAELNDVTAKVASGQEKHLLFEVQPGSDSSAFWKV
	İ		VVRVVCTKINKSSGIVEASRIMNLYQFIQLYKDITSQAAGVLAO
		(SSTSBEPDENSSSVTSCOASLWMGRVKQLTDEERCCICMDGRAD
			LILPCAHSFCQKCIDKWSDRHRNCPICRLQMTGANESWVVSDAP
	1		
E536	 	ļ	TEDDMANYILNMADEAGQPHRP
5526	3	853	RRPCNPVRAAKRTGAAARAPRGLEVTMLRVAWRTLSLIRTRAVT
			QVLVPGLPGGGSAKFPFNQWGLQPRSLLLQAARGYVVRKPAQSR
1			LDDDPPPSTLLKDYQNVPGIEKVDDVVKRLLSLEMANKKEMLKI
]	KQEQFMKKIVANPEDTRSLEARIIALSVKIRSYEEHLEKHRKDK
1			AHKRYLLMSIDQRKKMLKNLRNTNYDVFEKICWGLGIEYTFPPL
			YYRRAHRRFVTKKALCIRVFQETQKLKKRRRALKAAAAAQKQAK
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No. nucleotide location corresponding to first anno acid amino acid residue of anino acid acquence Serine, Tethreonine, V-Valine, P-P-P-Dine, Q-Golutanine, R-Argynine, S-Serine, Tethreonine, V-Valine, P-P-P-Dine, Q-Golutanine, R-Argynine, S-Serine, Tethreonine, V-Valine, P-P-P-Dine, Q-Golutanine, R-Argynine, S-Serine, Tethreonine, V-Valine, P-P-P-Dine, Q-Golutanine, R-Argynine, S-Serine, Tethreonine, V-Valine, P-P-P-Dine, Q-Golutanine, R-Argynine, S-Serine, Tethreonine, V-Valine, P-P-P-Dine, Q-Golutanine, R-Responsible, V-P-P-Dine, Q-Golutanine, R-Responsible, V-P-P-Dine, Q-Golutanine, R-Responsible, V-P-P-Dine, Q-Golutanine, R-Responsible, V-P-P-Dine, Q-Golutanine, R-Responsible, V-P-P-Dine, Q-Golutanine, R-Responsible, V-P-P-Dine, V-P-	(-			Amino acid segment containing signal peptide
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Corresponding to first amino acid semino acid residue of anino acid sequence anino acid sequence seque	1 110:		t e	Glucamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of anino acid an	ł			H=Histidine, I=Isoleucine, K=Lysine,
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amino acid residue of anino acid acid acid acid acid acid acid acid		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
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PANJESSIPSKEAPPRKAGAVSEEEEEEKKSSPYKKIKIKKKS KNVATEGTSTUKEFSVEVOPELAGGODUMCODPEKTISELUV OTAPKKKINKOKKIGLEPSGOTAANVPKKAKTNIPEVHOOKANI AMKOLEVPRVLEABSIGIGSAPTOOLOMKUTSTAPEKULUIGA AETSGKATLAFAIPMIRAULGMOKRINAAPPSKTEAPPGETTETE AGAAFTSGKATLAFAIPMIRAULGMOKRINAAPPSKTEAPPGETTETE AGAAFTSGKATLAFAIPMIRAULGMOKRINAAPPSKTEAPPGETTETE AGAAFTSGKATLAFAIPMIRAULGMOKRINAAPPSKTEAPPGETTETE AGAAFTSGKATLAFAIPMIRAULGMOKRINAAPPSKTEAPPGETTETE AGAAFTSGKATAAPAIPMIRAULGMOKRINAAPPSKTEAPPGETTETE AGAAFTSGKATAAPAIPMIRAULGMOKRINAAPPSKTEAPPGETTETE AGAAFTSGKATAAPAIPMIRAULGMOKRINAAPPSKTEAPPGETTETETE AGAAFTSGKATAAPAIPMIRAULGMOKRINAAPPSKTEAPPGETTETETE AGAAFTSGKATAAPAIRGAGAFTATLEKERVPEKONEENLOKEOON LKQELDOKSATCAAPPSKLICHUTTTETELAVOKIDAVA FTGIKTALLVOGBADARUKHAPPEKULUHANDOKTAKLOLLUMCKIT HURAPAARILUKAPAARULUPHANDOKTAKLOLLUMCKITAA ROKKYULLTRABATUTLITETKIHCETDERDEYPTEMOYPEK BOTUVESSTATULUHQAPAATLIKKERTHISOGUMINAO BOKKYULLTRABATUTLITETKIHCETDERDEYPTEMOKYOK BOKKYULLTRABATUTLITETKIHCETDERDEYPTEMOKYOK BOKKYULLTRABATUTLITACHANDOKTAKLOLLUMCKILLOKE BOKKYULLTRABAGULIPKIHCHACHANDOKTAKLOLLUMCKILLOKE BOKKYULLTRABATUTLITACHANDOKTAKULOKEAPILIAO BOKKYULLTRABATUTLITACHANDOKTAKULOKEAPILIAO BOKKYULLTRABATUTLITACHANDOKTAKULOKEAPILIAO BOKKYULLTRABATUTLITACHANDOKTAKULTATIKATAANA COPTSAN 895 6PEISACRIMGACKUKVHDISLATISITLITERYLEKATMAKKEKE LAPUKAGAAAALEITAAANAO COPTSAN 6PEISACRIMGACKUKVHDISLATISITLITERYLEKATMAKKEKE LAPUKAGAAAALEITAANAO COLTIKAAATTIMEEN OVALVAKUKULATAATAA COLTIKAAATTIMEEN OVALVAANAO COLTIKAAATTIMEEN OVALVAKUKULTAAANAO LAPUKAGAAAALINAANAO CATATA		1	l	KFQTKGIKVVGKWKEVKIDPNMFADGOMDDLVCFEELTDYOLVS
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AGABTRSPOKABAESDALPODTVIESBALBSIAABARAKTGGT VSDQALIPGODDAGEOPSSILERKPVPKQNEMEENLDKSOTGON LKQELODKSATCKAYPKRPLIGIVITPTRELAVQVKQHIDAVAR PTGIKTAILVGGASTOKQORMARRPETVYTPTRELAVQVKQHIDAVAR PTGIKTAILVGGASTOKQORMARRPETVYTPTRELAVQVKQHIDAVAR PTGIKTAILVGGASTOKQORMARRPETVYTPTRELWELIKKIKK ROFKVIDITNARATVETILETKIKETETBERDWELIKKIKKIKK ROFKVIDITNARATVETILETKIKETETBERDWELIKKITYTFIMOYPE RSIVFANSISCIKRISGILKVLDIRPLITHACHHOKQRIRNLEQ PARLECVLLIARQIRSESTRIKKIGTIKKUETBIKYTPTMOYPE RSIVFANSISCIKRISGILKVLDIRPLITHACHHOKQRIRNLEQ PARLECVLLIARQIKSESTRIKOKQOKLINNEVSIYTPTMOYPE RTARANNEGISLMI.10PDVJNRKKIYXTIKKOEDIPLFPVOTK YNDVVERIRIKAQIKSESTRIVOKQOKLINNEVSIYTPTMOYPE PARLECVLLIARQIKSESTRIVOKQOKLINNEVSIYTPTMOYPE PARLECVLLIARQIKSESTRIVOKQOKLINNEVSIYTPTMOYPE RTARANNEGISLMI.10PDVJNRKKIYXTIKKOEDIPLFPVOTK YNDVVERIRIKAQIKSESTRIVOKQOKLINNEVSIYTPTVOTK YNDVVERIRIKAQIKSESTRIVOKQOKLINNEVSIYTPTVOTK PYTOSKEPPLIVASPSKESSALGUSKOKKKKIKKKKKKKKKKKKKKK YPTOSKEPPLIVASPSKESSALGUSKOKKKKIKKKKKKKKKKKKKK YPTOSKEPPLIVASPSKESSALGUSKOKKKKIKKKKKKKKKKKKKKK YPTOSKEPPLIVASPSKESSALGUSKOKKKKKIKKKKKKKKKKKK PYTOSKEPPLIVASPSKESTRIVOKOKOKUKKKKKIKKE PYTOSKEPPLIVASPSKESTRIVOKOKOKUKKKKKIKKE PYTOSKEPPLIVASPSKESSALGUSKAKKKKIKKENDESPKIT LKDYLISMIGADOHININTYTVEMALIOOSGILPPVQAGGIQOTL AANKELLESENTININNENPYKRGTVILIMOKADEVITKEIKK PYTEMBSKKMAVTRITIKYCKPSHEBRARLEVYDLIFTIRDPE KENTILSELEVSESCLEVSIKERIVILITISPOKOKUKOKVSGL LSHTISRVILMISGLSEPAAROPRIMEKRIKLEVYDHOKKEVK PYTEMBSKKMAVTRITIKYCKPSHEBRIVATURYDHOKADEVITKEIKK SETTISVILMISGLSEPAAROPRIMEKRIKLEVYDHOKADEVI AAAMENPHILERIVEQUULED SS30 4541 2606 401WAISYCHKLEVGHROBERDARANDERSININGVANGVUSGL LSHTISRVILMISGLSENAVANDESTLOVILLARIICK CORETOTRSASPSNIKAQFROSHPKUDVOPOLEDDLITARLISH FORKKLITISCUSLAYSAPSILLIGDEVDAPAVUTMISKESCHILIFTILSH ANTOPOSPARANDAVUNGHRIKALURANDAVININGLIPULGENING PASHLYBKRASCORGSSCSSSETSDDDSSRRRIDKINGG CORPETOTRSASPSNIKAQFROSHPKYDLIPHIAGRALSTVILLARIICK CORPETOTRSASPSNIKAQFROSHPKYDUPOLEDDLITALISH ANTOPOSPARANDAVUNGHRIKALURANDVANINGLIPULCK CORPETOTRSASPSNIKAQFROSHPKYDUPOLEDDLITALISH ANTOPOSPARANDAVINGHRIKALURANDAVINIOLIPUL EKTISV	l		i	AWADDFVPRPVDRALSFLGFSAPTPIQALTLAPAIRDKLDILGA
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FTGIKTAILVGGMSTOKOGRMLARREITVATFGRLWELIKEKH YHIRNINGIGURECUVUERDARWEGHFARLGOLLERKHOSGYPRE ROTLVESATLILUVIGAPARILHKKHTKKMDKTAKLDLLMOKIGM RIGKFKVIDLTSHREATVETLITETKIHCETDEKDFYLYTHGYPG RSLVFANSISCIKRLSGLLKVLDINPLITLAGMHGKGRENLEG PARLEDCVLLATOVAARGLDIRVCVHHVQVERTSITVHSG RTARATNRGISLELHLIGDEDVINFKKIYKTIKKDEDIPLFVOTK YMDVVEERIRLARQIIEKSEVRINGACLHNSWIEGAAAALEIELE EDWYKGGKADQGERRRGKGWKVLKKELRILGPETTSGKTK YPTGSGKPPLLVSAPSKSESALSCLSKQKKKKTKKPKEPQPEQD QPSTSAN 5528 3 895 GPFLSACRWGGCKVKVEDSLAFISITLRRYLELGATMAKSKFE YVRDFEADDTCLAHCWVVVRLDGRMFHRFAEKHFRFKPMDSRAL CLHTKCAGTTWEELEDIVILAYGSSDEYSFVERKINNFKRRASK FMHVASGPASSVEYWEDVFEOQPLLYPPGDGGKVVYYPSOGT LKVYLSWRGADCHINNINTVYWALIQOGGLTPVQAGGRLGGTL AADKNE LIFSEFNINNINEPPWTRGTVLIMGKDEWMKREKLK PTEMESKMAWATTRITRCCPSHLPPACLGRL 5529 48 640 TFFLVSABLKTEKLINPBAAERRWEDDGEGGWLSVKMGRVSGL LSWILSRVHLNSLGLSBPGAARDERIMERALEVVDLIRTIRDPE KPNTLEELEVVSESCVEVQEINEEETIVIIRTTPTVPHCSLATI GIGLGRVKLGCLFFRKILEIVISEGTHSTEEDINKQINDKERV AAAMENPRILESCLSEVGAROPRIMERALEVYDLIRTIRDPE KPNTLEELEVVSESCVEVQEINEEETIVILARTTPTVUHGSLATIL GIGLGRVKLGCLFFRKILEIVISEGTHSTEEDINKQINDKERV AAAMENPRILESCLSPADARDERIMENSUKGCVDLITHMLOR DPKRRALEEIERHBULGGVDSPATXVIHJVSKGVLIGUTIFMLOR DPKRRALEEIERHBULGGVDSPATXVIHJVSKGVLIGUTIFMLOR DPKRRALEEIERHBULGGVOGSPATXVATURSKGVLITHMLOR VCGOPPFGEANDSETLIMINDCKTYVSHVSKCKCULITHMLOR DFKRRALEEIERHBULGGVOGSPATXVATURSKGVLITHMLOR VCGOPPFGEANDSETLIMINDCKTYVSHVSKCKCULITHMLOR DFKRRALEEIERHBULGGVOGSCSFATNASGTLEVSKGVLITHMLOR TATVPGSPARAADSVLNGHREKSCLCDSAKKODLESGUTIFMLOR DFKRRALEEIERHBULGGVOGSSFATXVAGTRESTRWCISST GNAGOYPAVGGIKFFSDHAADTTTELERIKKSKLKNNVLOLDFLC GRYSKGRGGGNSTXYIJORGGSFSTDDDSEBRRRLDKNSGF TYSHRRNSEGGGSKYPINSGTCWARKSPENMOLASRSAGLUVSLK LMSLCLGGGLINGSTXYIJORGGSFSPLEHTRIKMCISST GNAGOYPAVGGIKFFSDHAADTTTELERIKKSKALKNNVLOLDFLC EKTISVAIQNNFKBGELLCASSFASCCHVI SSS32 3395 1402 SDRWVVGKRSTLTEDFTFFCGGELLHSVLOCKSVFDVLOGEEMR FULDMTDRKGVHFUNDLAGGGSVGCNACHLKKMHAKGFGKTILK GPNDPKLEDFTSASSELPEPTVGGGGIGGGSCTLAKGHTIKA GFNDPKLEDFTSASSELPEPTVGGGGIGGGTLKKGHTLK GPNDPKLEDFTSASSELPEPTVGGGGIGGTGGTTUAKKMHAKGFGKTILK GPNDPKLEDFTSASSELP	1			LKQELDDKSATCKAYPKRPLLGLVLTPTRELAVOVKOHTDAVAD
HIRBURGURCUVOBADRIMURKHITKADURSGULEMLINBGYNTEK ROTUVESALTLURIOADARILLIKHITKADURSIGNINLEG RGKEVITDLITRIBATUETLITEKHITKADURSKILLIKUPTUR RGKEVITDLITRIBATUETLITEKHITGETDEKDFYLYYFIMQYPG RSLVFARISCIKRISGILKVLDIMPLITLACMIGKORIRNILEG PARLECCVILATIVOARGIDIPKVQHVIHYGVPRTSEIYVHRSG RTARATINBGISLMLIGEBUVINFKKIYKTLKKDEDIPLFVQTK YMDVVKERIRLARGIESEYSINFOACHHSWIEGAAAALEITLE EDMYKKGKADQQEERRROKQMKVLKKELEHLLISGPLFTESQKTK YPTGSKRPPLIVSAPSKISESALSCLSKQKKKKTKKPKEPPEPPEP OPSTSAN 5528 3 695 GPFLSACRMWGACKVKHDSLATISITLRRYLRIGATMAKSKFF YVRDFSADDTCLAHCWVVRLDGRNPHRAEKHDFAKPNDESRAL GLHTKCACTVWEELEDIVIAYGGSDEYSFVFKRTNWFKRRASK FMTHUASOFASSYYFWRDYFEODPLIVPGOFORVVVYPENOT LKDYLSWRQADCHINNLYNTVFHALIQGSGLTPVQAGELQOTIL AADKNEILFSFNINNNUS PEPMYRKGTVLHQKVDEWMTKEIKL PTEMEGKMAAVTRITRKPCKSHIHPRAPCLRNI LKDYLSWRQADCHINNLYNTVFHALIQGSGLTPVGAGELQOTIL AADKNEILFSFNINNNUS PEPMYRKGTVLHQKVDEWMTKEIKL PTEMEGKMAAVTRITRKPCKSHIHPRAPCLRNI GLCLRVKLORCLPFKHLEHLSTYSEGTHSEDIWGINKERV KPRTLEELEVVSSEGGARQORINEERALVYDLIRTIRDPE KPRTLEELEVVSSEGGARQORINEERALVYDLIRTIRDPE KPRTLEELEVVSSEGGARQORINEERALVYDLIRTIRDPE KPRTLEELEVVSSEGGARQORINEERALVYDLIRTIRDPE KPRTLEELEVVSSEGGARQORINEERALVYDLIRTIRDPE KPRTLEELEVVSSEGGARQORINEERALVYDLIRTIRDPE KPRTLEELEVVSSEGGARQORINEERALVYDLIRTIRDPE KPRTLEELEVVSSEGGARQORINEERALVYDLIRTIRDPE KPRTLEELEVVSSEGGARQORINEERALVYDLIRTIRDPE KPRTLEELEVVSSEGGARQORINEERALVYDLIRTIRDPE KPRTLEELEVSKORLDFFORMUSHETYDLIRTIRDPE KPRTLEELEVSKORLDFFORMUSHESUNKNINDKERV AAMENPHLRSIVEGCVLEPP AAMENPHLRSIVEGCVLEPP PARABLEITYJEBURGNUSHERVSKORLDFTORMUSHESIST GLCLRVKLORCLPFFKHLEHTYTSTETTRKPCKSMILTATLGR DFRRASLEEIERHPWLGGUPSPATKYNILTUSYKNISEBEHN SIQRMVLGGIABARDIVTHLUSYKNISEBEHN SIQRMVLGGIABARDIVTHUSHYKNISTATLLSK ATVPGSPARAADSVLNGIRSKGLCDSAKODLDELAGAALTVUP PABLIPTASGGKCLFFVEDEBEDEDERLENKINDKOSTOVLIRRKPS VTRALTSRKSAPVLNQIFFERGGGGGSKFNSISTOVVLRKMEN ASPATVHRRITHRKSGGRGSSCSSSTSDDDSESRRINGKOST TSWHRENDSEGGPGSGEORGGGSKFNSSISTOVLIRRKSMILSST GNAGGVPAVGGIKFFDIMADTTTELERIKSKALKONVLQLPLC EKTISVNIGUNFREGLICASSPPSCCHUNIULDAL TNUELLSSLESEVYLAGGRIKRRAGVGVSSPSTUGESLIYMLEKC LGGAFTPATRAANSQLVGAVVQAMSROMDGE	1	1		PTGIKTAILVGGMSTOKOORMLNRRPETVVATDGDI.WET.TVEVU
ROTLVESATLITUNGAPARILHKUHTKMÖNTKALLIMAKITAN RIGKEN KUIDLIKRNEATVEILTETK HICETDEKOFYLYYFIMOYPG RSLYPANSISCIKRISGLIKVLDIMPLITHACMHOKORILROU RSLYPANSISCIKRISGLIKVLDIMPLITHACMHOKORILROU PARLEDCVILATDVAARGLDI PKOVAVIHYOYPTSEIVHESG RTARATNBOLSLMLIGEPUNTPKKIYKHYLKOEDIPLPPVOTK YMDVVERIRLARQIEKSEYNNFQACLHNSWIEQAAAALEIELE EDMYKGKAKOQOERRROKOMVLKKELHSIGPLFTESOKTK YPTOSGKPPLLVSAPSKSESALSCLSKQKKKKKKKKPKEPQPEOP OPETSAN 5528 3 895 GPFLSACRMWGACKVKVHDSLATISITLRRYLRIGATMAKSKFE YVRDFEADDTCLAALCWVVVRLDGRNHRRAEKNNFAKPDGSRAL CLMYKCAGVTVEELEDIVLAYGOGDESYRKTNNFAKRPDSRAL CHMYKAGOPASSYYFWRDYFEDDPLLYPPGFDGRVVYFENGAL LADKNELLESEFNINVNNEPHNYFENDDGLIVPGAQGELQOTL AANKNELLESEFNINVNNEPHNYFENDGGLIPVGAQGELQOTL AANKNELLESEFNINVNNEPHNYRKGTVLIWQKVDEVMTKEIKL PTEMEGKMAVVTRITRIKPCKPSHLBPAPCLEWI. 5529 48 640 TFRLVSAHLKTRKLINPEARERRROWDSGROWLSVKMGRVSGL LSWILSRVLMUSGLSEPGAAROPRINEERKALEVYDLIFTINDPE KPHTLESEFNINVNSCUSENBERGRUNISVKMGRVSGL LSWILSRVLMUSGLSEPGAAROPRINEERKALEVYDLIFTINDPE KPHTLESEVYSSECVEVOELENEERLVITPTVPHGSLATL IGLLRVKLORCLPKHKLEIYISEGTHSTEEDINKQINDKRV AAAMENPHLRIVEQVELIEPENVYFFEKQGLVKLTDFGFSNK FOPGKKLITISGSLAYSAPEILLIGDEYDAFAVINISLGVILFMU VCQOPFFGAAMDSHITIMIDKCYYTPFSHVSKKCKULTTRRLOR DEKRALEVYBLGUTIFML VCQOPFFGAAMDSHITIMIDKCYYTPFSHVSKKCKULTRRLOR DEKRALEVILGANGA VCQOPFFGAAMDSHITIMIDKCYYTPFSHVSKKCKULTRRLOR DEKRALEVILGANGA VTRAITSKKSAPVLNQIFEGGSDGGGGAKPRISTOTVVLRRKES QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH ATVPGSPARAADSVLNGIRSKGI.CDSAKKDDLPELLAGRALSTVE PASLIKPTASGRKCLERVEDEEDEDEDKEMKRISTOTVVLRRKES QEKEIQTRSASPSNIKAGFROSSESSESTEDSERRILDKNSGG TYSWIRRDSSEGPPGSGGGGGGGKKPSNASGGVDKASPSENNAG GGSPSSGSGGGNTWTSGTTRRCAGPSNSMLLASRSAGLIVESIK LMSCLUSQLHGSTKYI IDPONISSPSVKVQRKSTWMCI SET GNAGOVPAVGGIKFFSDIMADTTTELERI KSKNIKNNVLQLPLU EKTISVIORNYKEGLILGASPASCCHV TALEFTAANSQLVALVORMSGRADGE TYSWIRRDSSEGPPGSEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1			YHLRNUROLRCI VVDEADRMURKGUDAET OOT LEMT ADGOODS
RGKFKVIDLTRNEATVETLITETKIHCETDEKDFYLYYFIMOYPG RSLYFANSISCIRRISGILKVLDIMPICHLARMGKORGIRENLEQ FABLEDCVLLATDVARGLDIFKVOHVIHYQVPRTSEIYVHRSG BTAPATNELSLAMLIGPEDVINFKKIYKTIKKOMPICHPVQTKY YMDVVKERIRLARQIFKSEYRNFQACHRISWIEQAAAALEIELE EDMYKGGKADQGEERRGKQMKVLKKELRHLISGPLFTESQRTK YPTYGSKAPLLVSAFØKSESALSCLSKGKKTKKPKPEPQPEOP OPSTSAN 5528 3 895 GFFLSACRNWGACKVKHDSLATISITLERYLRIGATMAKSKFE YVRDPEADDTCLARCWVVVHDLGRNFHRPAEKHNFAKPNDSRAL QLMTKCAQTVMEELEDIVIAYGGSBEYSVFVKRTINFKRRASK FMTHVASOFASSVYFVKRTYPPEOPDLIVPPOFDGRVVVYPENQT LKDYLSWRQADCHINNLYNTVFWALIQGSGLTPVQAGGLQOTTL AADKNEILFSFNINNNNEPPDYNKGTVLHQKVDEVMYKEIKL PTEMESKMAYTRITKYPCKPSHLPPAPCLBWL LSWYLSBYLDWHLSKEIKLIPFEABPLCLBWL TFRLVSAHLKFRKLINPEABERFRRDDDSGGWLSVKMQRVSGL LSWYLSRVLWLSGLSEPGAARQPRIMEEKALEVYDLIRTIRDFF KRYTLEELEVVSBSCVEVQEINEEERIVIIRFTPTVPHCSLATL IGLCRVKLORCLPFKHLEITYISECHTSDINKQINDKERV AAMENPHLREIVEQCVLEPD 4541 2606 AQ TYMAISYCHKLINGHEDEKPVVYFEKGGLVKLTDFGFSNK FOPGKKLTTSCGSLAVSAPEILLIGDBYDAPAVDIMSLGVILFML VCQQPFFQEAMDSSTLTMIMDCKYTVYSHVSKEKKDLITTRHLER DPKRRASLEEIENHBWLGGVDPSPATKVNIFLVSKNISEEBHN SIIQRMVLIGDIADRDAIVEALETINRYNHITATTFILARILRER OPKRRASLEEIENHBWLGGVDPSPATKVNIFLVSKNISEEBHN SIIQRMVLIGDIADRDAIVEALETINRYNHITATTFILARILRER OPKRRASLEEIENHBWLGGVDPSPATKVNIFLVSKNISEEBHN SIIQRMVLIGDIADRDAIVEALETINRYNHITATTFILARILRER OPKRRASLEEIENHBWLGGVDSSKDSKORGSKVDLUFLAGRALSTVY PASLIKPTASRSAPUNOJFEGGESDDFFDMDENLPPKLSRLKMNI ASPGTVHKRYHRRKSGGGGSSSSTSDDDSSRRRRAGGARSLEVESLK LMSGCLGSGLIGSTKYIIDPROGLSFSSVVQBKSTWMCISSK GGSPSSGGGGNPTNTSGTTRRCAGPSNBMQLASRSAGLVESLK LMSGLGSGLIGSTKYIIDPNOLSFSSVVQBKSTWMCISSK GNAGQVPAVGGIKFFSDIMADTTTELERIKSKNLKNNVLQLPLC EKTIGSVIGONFREGLICASPSPSCCHUNIVLDAV TNVELDSSLEGVASPSSCHUNITENSFTFSTGESLLYMLEKC LGFAFTPATRAANSQLVGAVVQAMSRSPSTGESLLYMLEKC LGFAFTPATRAANSQLVGAVVQAMSRSPSTGESLLYMLEKC LGFAFTPATRAANSQLVGAVVQAMSRSPTURFNTPNDSYG KPLVVRREABLLYRDVKUSFFTVGGGGILGGGGGGLICFFNTLFENITSPHTSAFKN FULNTDRKGVIFTAMAGGSSVEGGBRIQGERVLIKFRITPPNTSAFKI GPNPKLEDFYSASSELFBYTGGGGILDTFPNTISAFKN FULNTDRKGVIFTAMAGGGSVEGGBNLQEILSKGLCGFMULKGGNPTLK GPNPKLEDFYSASSELFBYTGCGGILDTFPNTISAFKN FULNTDRKGVIF	I	1	}	POTIVECATITIVOADADII UUUMMAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
RSLYFANSISCI KRISGILKVLDIMPLITHACHHOKQELRILEQ PARLEDCULATIOVARGEDI PKOYUNGVRTSEI TVYRRGG PARLEDCULATIOVARGEDI PKOYUNGVRTSEI TVYRRGG PTARATMEGISIMLIG PEDVINKKI YKTIKKDEDI PLFPYOTK YMDVVKERI ILAGRI PKESPYRNFQACLINNSH IGAAAALBI ELE EDMYKGGKAQQQEERRGKQKMVLKKELRILLEQPLPTESQKTK YPTYOSOKPPLLVSAFSKSESALSCLSKQKKKKTKKPKEFQPEQD QPSTSAN 5528 3 695 GPFLSACRNWGACKVKVHDSLAFISITLERYLELGATMAKSKFF YVRDPEADDTCLAHCWVVVRLDGRNFHRPAEKINFAKENDSRAL CLAMKCAQTVMEBLEDI VIAYQGSDEVSFYFKKKTINWFKRASK FMTHVASQFASSYVFVWRDYFBOQFLLYPPEGGRVVYPSENGT LKDYLSWRQADCHINNLYNTVFWALIQSGILTPVQAQGRIGGTL AADKNBILLESEFNINYNNEPPHYRRGTVLIWQKUDEVMTKEIKL PTEMEGKNAVTRITHFYCKPHLIPBACLEWL 5529 48 640 TFRLVSAHLKTKLINPEAAERRWRDWDSRQGKUGSUKWQRVSGL LSWTLSRVLWIJSGLSBBGAARQFRIMEEKALEVYLLIFTITIADPE KPATILEELEVVSSSCVEVOGNIEEERYLVIIRFTPTYPHICSIATL IGICLEVKLQRCLEPFKKLEIVYISEGTHSTEEDINKQINDKERV AAMMENHILEIVSCVUGNIEEERYLVIIRFTPTYPHICSIATL IGICLEVKLQRCLEPFKKLEIVYISEGTHSTEEDINKQINDKERV AAMMENHILRIIVSCVUGNIEERYLVIIRFTPTYPHICSIATL IGICLEVKLQRCLEPFKKLEIVYISEGTHSTEEDINKQINDKERV AAMMENHILRIIVSCVUGNIEERYLVIIRFTPTYPHICSIATL IGICLEVKLQRCLEPFKKLEIVYISEGTHSTEEDINKQINDKERV AAMMENHILRIIVSCVUGNIEERYLVIIRFTPTYPHICSIATL IGICLEVKLQRCLEPFKKLEIVYISEGTHSTEEDINKQINDKERV AAMMENHILRIIVSCVUGNIEERYLVIIRFTPTYPHICSIATL IGICLEVKLQRCLEPFKKLEIVYISEGTHSTEEDINKQINDKERV AAMMENHILRIIVSCVUGNIEERYLVIIRFTPTYPHICSIATL IGICLEVKLQRCLEPFKCURDENDESIATLITHLQR DPKRRASLEETENIPMLQGVDJSPATKYNIPLVSKKNLSEERIN SIIQMVLGDIADRADIVELETTINKTATTYTPLLARSTLIREK QEKEIQTRSASPSNIKAQFRQSWFTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVO PASLEYTASGRKCLFRVEDEBEEDEERKMENSISTQVVLRRKEB VTNRITSRKSAPVLNQIFFEGEBELIFFKLMSINLINGNICLIST GRAGQVPAVGGIKFFSDIMADTTTELERIKSINLINGNICLIST GRAGQVPAVGGIKFFSDIMADTTTELERIKSINLINGNIVLOLPLC EKTISVNIQNPKEGLICASSPASCULS EKTISVNIQNPKEGLICASSPASCULS GSPSSGGGNPTNTSGTTRCAGPSNINGLASSFASCELVESIK MYGELISSSLEEPYLARGKRAVGKVLSSFSTVGESLIYMLEKC LGPATPATRAANSQLYGAVVQANSGRODGE SAMMVGKRINITEDTETGGEELLHSVLQCKSVPDVLDGEERR RATTRANSYEMIRGVPFLINRAMMANMMDPVDDRHTTNPRDSYG KPLUNDTBAKGHPTURADVGTARGOGGTILK GNNPKLEDTYSASSEL	l			PCKEWITE TENERMISMI TENERMISMI TRANSCRIPTION TO THE STATE OF THE STATE
FARLEDCVILLATUVARGIGITMUGPKVGUVTHYQVRTSEITVYHES RTRARINGEISIMLIGEDDUINFKKIYNTIKKDEDITPLPPVGTK YMDVVKERIRLARQIEKSEYNFQACHNSWIEQAAAALEIELE EDMYKGGKADQGERRRQKGMKVLKKELRILLIGGUFTESGKTK YPTQSGKFPLUVSAPS KSESBAJGLSKGKKKKTKKPKEPQEDP OPSTSAN 5528 3 695 GPFLSACRWGACKVKVHDSLATISITLRRYLRIGATMAKSKFF YVRDPEADDTCLAHCWVVVRLDGRNFHRPAEKHNFAKRNDSRAL QLMTKCAQTVMEBLEDIVIAYGGSDEYSFVFKKRTWFKRRASK FMTHVASGASBAYSYTVFWADIGOGSDEYSFVFKKRTWFKRRASK FMTHVASGASBAYSYTVFWADIGOGSDEYSFVFKKRTWFKRRASK FMTHVASGASBAYSYTVFWADIGOGSDEYSFVFKKRTWFKRRASK FMTHVASGASBAYSYTVFWADIGOGSDEYSFVFKKRTWFKRRASK FMTHVASGASSYLTYMDYPPMRGTULIPGVDDAGGRIGGTIL AADKNSILDESFNINWINDPPMRRGTULIPGVDDAGGRIGGTIL AADKNSILDESFNINWINDPPMRRGTULIPGVDDAGGRIGGTIL LKUTLSWFLTSTVILLESFNINWINDPPMRRGTULIPGVDAGGRIGGTIL LKUTLSWFLTSTVILLESFSFNINWINDPPMRRGTULIPGVDAGGRIGGTIL LKUTLSWFLTSTVILLESFNINWINDPPMRRGTULIPGVDAGGRIGGTIL LKUTLSWFLTSTVILLESFNINWINDPPMRRGTULIPGVDAGGRIGGTIL LKUTLSWFLTSTVILLESFNINWINDPPMRRGTULIPGVDAGGRIGGTIL LKUTLSFFNINWINGSEGSBARGPRINGEVKMQVSGL 5529 48 640 TFREVSAHLKTRKLINPEAAERRWEDDBSGGRIGGKFW KEILE SVKMQRVSGL LSTLISTVILLESFNINWINDEPMRRGTULIPGVDAGGRIGGTIL LGCLREVTULLGSCLSBEGAARGPRINGEVKMQVSGLATTIPDPF KPRITLEELEVVSESCVEVGBINEESYLVIIRFTPTVPHCSLATIL GGLIRLVILLGCLDFRIKLEIVIJSEGTHSTEDINKQINKREV AAAMENPNLREIVEQCVLEPD 5530 4541 2606 AQIVHAISSVCHORDLKFERVYFFEKQGIVKLITDFGFSNK VCGGPFFCPARIDSSTLITMIMOCKTVVPSHVSKCKOLITTRNLOR POPKRRASICEIENHUNGLOKTVVPSHVSKCKOLITTRNLOR POPKRRASICEIENHUNGLOKTVVPSHVSKCKOLITTRNLOR POPKRASICEIENHUNGLOKTVVPSHVSKCKOLITTRNLOR POPKRASICEIENHUNGLOKTVVPSHVSKCKOLITTRNLOR POPKRASICEIENHUNGLOKTVVPSHVSKCKOLITTRNLOR POPKRASICEIENHUNGLOKTVVPSHVSKCKOLITTRNLOR POPKRASICEIENHUNGLOKTVVPSHVSKCKOLITTRNLOR POPKRASICEIENHUNGLOKTVVPSHVSKCKOLITTRNLOR POPKRASICEIENHUNGLOKTVVPSHVSKCKOLITTRNLOR POPKRASICEIENHUNGLOKTVVPSHVSKCKOLITTRNLOR POPKRASICEIENHUNGLOKTVVPSHVSKCKOLITTRNLOR POPKRASICEIENHUNGLOKTVVPSHVSKCKOLITTRNLOR POPKRASICEIENHUNGLOKTVVPSHVSKCKOLITTRNLOR POPKRASICEIENHUNGLOKTVVPSHVSKCKOLITTRNLOR POPKRASICEIENHUNGLOKTVVPSHVSKCKOLITTRNLOR POPKRASICEIENHUNGLOKTVPSHVANGANGANGANGANGANG	1		l '	MONTAVIDET KNEWIVETLIETKIHCETDEKDFYLYYFLMQYPG
RTARATNEGLSIMLIGEBOUINEKKIYKTIKKDEDIPLEPVOTK YMDVVKERTRIARGILESEVRNEQACLINNSWIEDDARALBIELE EDMYKGGKADQQERRRQKQMKVLKKELRHLLSQPLFTESQKTK YPTQSGKPPLLVSAFSKSESALSCLSKQKKKKTKKKEREPQEQQP QPSTSAN 5528 3 895 GPFISACRNWGGKVKVHDSLATISITLRKYLRIGATMAKSKFE YVRDFEADDTCLAHCWVVVRLDGRRHHFAEKKINFAKDMGRAL QLMYKCAQTVMEBLEDIVIAYGGSDEYSFVFKRKTNWFKRRASK FMTHVASQFASSYVFYWRYPEBOPLLYPBEFOGRVVYPENGT LKDYLSWRQADCHINNLYNTVFWALLOGSGLTPVQAQQRIGOTL AADKNBILESEFININYNNEPPWYRKGTVLIWQKVDEVMTKEIKL PTEMEGKRANTTRRTKPCKPSHLPRACLWIL 5529 48 640 TFRLVSAHLKTRKLTNPEAAERRWEDWSRQGWLSVKWQRVSGL LSWTLSRVLWLSGLSEPGAARQPRIMEEKALEVYDLIRTIRDPE KPHTLEELEVVSBSCVEVQBINEESYLVIIRFPTVPREGSLATL IGLCLRVKLQRCLEPFKKLEIVISEGTHSTEDINKQINDKERV AAMMENHIRIVEVQCULEPD 5530 4541 2606 AQIVHAISSYCHKLEIVGREDLKPENVYFEKQGLVKLTDFGFSNK FOPGKKLTTSCGSLAYSAPEILLGDEYDAPANDINSLGVLIFMU VCQGPPFQEANDSSTLTMIMDCKYTVPSHVSKCKDLITRMLQR DPKRRASLEEIENIPMLQGVDDSPATKYNIPLVSKNLSEBEHN SIIQMVLGDIADRDAIVALELTNRYNHITATYFLLARRILREK QEKEIOTRSASPSNIKAQPROSWPTKIDVPQDLEDDLTATPLSH ATTYOG PARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTV PASLKPTASGRKCLFRVEEDBEEDEBEDKKMBLSTQVVLRRKES VTNRLTSKKSAPVLNQIFESGSDDEPDMDENLPRKLSRLKMNI ASPGTVHKYHRKRSGGGGSGSSSETHTNGKDSGFSNKAGLGNSKGLUSSES ATTYOG PARAADSVLNGHRSKGLCDSAKKDDLESERRRUDSGG TYSWHRRDSSEGPPGSEGGGGGGSKPSNASGGVDKASPSRNNAG GSSPSSGGGMPTNTSGTTRRCAGPSNSMQLASRSAGELVESILK LMSLCLGSQLHGSTKYIIDPONGLSFSSVKVQEKSTMCSST GNAGQVPAVGGIKFFBDHMADTTTELERIKSNNLKONVLQLPLC EKTISVNIQNPKEGLLGASSPASCCUT SCHTIGTNINNPKEGLLGASSPASCCUT STURNINNPKEGLGASSPASCENT GSGPRAPPREDSWERPEPELIRGSWRAVSKSPLEEGTVLFARLF ALEPDLLELELPGYNCROPSSPEDCLSSPFFLDHIRKVMLVIDAAV TNVEDLSSLEEYLASIGRKHRAVGVKLUSFSTVGESLLYMLEKC LGFAFTPATRAANSQLYGGAVVQANSGRODGE SDMMVGGRKNITEDTETGGEELLHSVLJCKSVPDVLDGEERR RATTRANFYEMIRGVFFINRAMMANMMPVPDRRTTNPRDSYG KPLVLVRDRSELLYFADVCAGPGGFSEYVLWRKKMHAKGFGMTLK GPNDFKLEDTYSASSELFEPTYGGGGIDGGGTTPENISAFRN FULDNTDRKGWHFLMADGGFSEYGGRNLQELISCHLLCCFFIMA LSIVNTGGRFTIPFSVGLUVLLYCCFERVCLEFRYLE	1			RSDVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQRLRNLEQ
YMDVVKERIRLARQIEKSEYRNFQACLHNSWIEQAAAALBIELE E BMYKKGKADQOEBERROKQMKULKKEHRLLSQPLFTESQKTK YPTQSGKPPLLVSAPSKSESALSCLSKQKKKTKKTKPKEPQFEQP QPSTSAN SPISACRWWGACKVKHDSLATISITLRRYLRLGATMAKSKFE YVRDFEADDTCLAHCWVVVRLDGRNFHRPAEHNPAKENDSRAL QLMKKCAQTYMEELBELDIVIAVGQSDEYSFVFKKKTNWFKRRASK FMTHVASQPASSYVFYWRDYFEDQPLLYPPGFDGRVVVYPSNQT LKDYLSWRQADCHINNIYNTFWALIQQSGLTPVQAQGRLQGTL AADKNELIESSFPININNEPPMNEKGTVLIWGKDEVMTKEIKL PTEMEGKKMAVTRTRIKPCKPSHLPRAPCLRWI. 5529 48 640 TFRLVSAHLKTRKLINPEAAERRWRDWDSRQGWLSVKMQRVSGL LSWILSRVLWLSGLSBPGAARQPRIMEERALEVYDLIRTIRDPE KPRTLEELEVVSESCVEVQEINEERILTFFPTVPHCSLATL IGLCLEVKLQRCLPPKHKLEIYISCHSTERDENKQINDKERV AAAMENPNLRBIVECCVLEPD 5530 4541 2606 AQIVHAISYCHKLHVGRPDVFFFKQGLVKLTDFGFSNK FOPGKKLITSCGSLAYSAPEILLGDEYDAPAVDINSLGVILFML VCGQPFFGEANDSETLTMIMDCKYTVPSHVSKECKDLITRMLQR DFKRRASLEEIENHPWLQGVDDEPAKVANIPLVSYKNLSEEHN SIIQRWLGDLADRDAIVEALETNRYNHITATYFLLAERILREN GLEIQTRSASPSNIKAQFRQSWFTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVLNGHRSKGLOBAKKDDLPELAGPALSTVP PASLKETASGRKCLFRVEEDEEDEEDEKMPMSLSTQVVLRRKBS VTNRLTSRKSAPVLNGHRSKGLOBAKKDDLPELAGPALSTVP PASLKETASGRSGGGGSKPSNASGGVDKASPSSRCHVSISK ASPGTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRLINKDSGF TYSWHRRDSSBOPGSSGGGGGSKPSNASGGVDKASPSSRNAG GGSPSSGSGGNFTNTSTTRRCAGPSNAMGLASRSAGELVESLK LMSLCLGSGLIGSTKYTIDPQNGLSFSSWVQERSTRKMCISST GNAGQVPAVGGIKFFSHMADTTTELERIKKNILKNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI 65572 3395 1402 SDMWVGKRMITEDETERGESLHSVLQCKSVFDVLDGEEMR RARTRANPYENIRGVFFLNRAMKNANNDFVPDMFTNPRDS G KPLVKORREALLYPADVCAGPGGFSSYLVLNRKKWHAKGFGMTLK GPNDFKLEDFYSASSELFFPYYGGGILGGDLTRPENISAFRN FYLDNTRKGHFLKTPLTFFFTVVLVLRKKWHAKGFGMTLK GPNDFKLEDFYSASSELFFPYYGGGILGGDDLTRPENISAFRN FYLDNTRKGHFLKTPLTFFTFVVLVLYCCFRCYCKFRFTS	1			FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSEIYVHRSG
YMDVVKERIRLARQIEKSEYRNFQACLHNSWIEQAAAALBIELE E BMYKKGKADQOEBERROKQMKULKKEHRLLSQPLFTESQKTK YPTQSGKPPLLVSAPSKSESALSCLSKQKKKTKKTKPKEPQFEQP QPSTSAN SPISACRWWGACKVKHDSLATISITLRRYLRLGATMAKSKFE YVRDFEADDTCLAHCWVVVRLDGRNFHRPAEHNPAKENDSRAL QLMKKCAQTYMEELBELDIVIAVGQSDEYSFVFKKKTNWFKRRASK FMTHVASQPASSYVFYWRDYFEDQPLLYPPGFDGRVVVYPSNQT LKDYLSWRQADCHINNIYNTFWALIQQSGLTPVQAQGRLQGTL AADKNELIESSFPININNEPPMNEKGTVLIWGKDEVMTKEIKL PTEMEGKKMAVTRTRIKPCKPSHLPRAPCLRWI. 5529 48 640 TFRLVSAHLKTRKLINPEAAERRWRDWDSRQGWLSVKMQRVSGL LSWILSRVLWLSGLSBPGAARQPRIMEERALEVYDLIRTIRDPE KPRTLEELEVVSESCVEVQEINEERILTFFPTVPHCSLATL IGLCLEVKLQRCLPPKHKLEIYISCHSTERDENKQINDKERV AAAMENPNLRBIVECCVLEPD 5530 4541 2606 AQIVHAISYCHKLHVGRPDVFFFKQGLVKLTDFGFSNK FOPGKKLITSCGSLAYSAPEILLGDEYDAPAVDINSLGVILFML VCGQPFFGEANDSETLTMIMDCKYTVPSHVSKECKDLITRMLQR DFKRRASLEEIENHPWLQGVDDEPAKVANIPLVSYKNLSEEHN SIIQRWLGDLADRDAIVEALETNRYNHITATYFLLAERILREN GLEIQTRSASPSNIKAQFRQSWFTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVLNGHRSKGLOBAKKDDLPELAGPALSTVP PASLKETASGRKCLFRVEEDEEDEEDEKMPMSLSTQVVLRRKBS VTNRLTSRKSAPVLNGHRSKGLOBAKKDDLPELAGPALSTVP PASLKETASGRSGGGGSKPSNASGGVDKASPSSRCHVSISK ASPGTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRLINKDSGF TYSWHRRDSSBOPGSSGGGGGSKPSNASGGVDKASPSSRNAG GGSPSSGSGGNFTNTSTTRRCAGPSNAMGLASRSAGELVESLK LMSLCLGSGLIGSTKYTIDPQNGLSFSSWVQERSTRKMCISST GNAGQVPAVGGIKFFSHMADTTTELERIKKNILKNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI 65572 3395 1402 SDMWVGKRMITEDETERGESLHSVLQCKSVFDVLDGEEMR RARTRANPYENIRGVFFLNRAMKNANNDFVPDMFTNPRDS G KPLVKORREALLYPADVCAGPGGFSSYLVLNRKKWHAKGFGMTLK GPNDFKLEDFYSASSELFFPYYGGGILGGDLTRPENISAFRN FYLDNTRKGHFLKTPLTFFFTVVLVLRKKWHAKGFGMTLK GPNDFKLEDFYSASSELFFPYYGGGILGGDDLTRPENISAFRN FYLDNTRKGHFLKTPLTFFTFVVLVLYCCFRCYCKFRFTS	1	1		RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIPLFPVQTK
EDMYKGGKADQGEERRGKGMKULKKELRILLISQELFTESGKTK YPTOSGKPPLUVSAPSKSESALSCLSKKKKKKKKKKPEPQPEQP QPSTSAN 895 GPFLSACRWGRCKVKVHDSLATISTILRRYLRIGATMAKSKFE YVENPEADDTCLAHCWVVVRLDGRPFRRAEKHNEAKENDSRAL QLMTKCAQTVMEELBDIVIAYGQSDEYSFVFKRKTNWFKRRASK FMTHVASQPASSYVFYWRDYFEDQPLLYPPGDGRVVVYPSROGT LKDYLSWRQADCHINNLYNTVFMALIQGSGLPPVQAQGRLQGTL AADKNSILFSEPNINYNNEPPMYRKGTVLIWGKDEVMTKEIKL PTEMEKKMAVTRATKIPCKPSHIPALTQGSGLPPVQAQGRLQGTL AADKNSILFSEPNINYNNEPPMYRKGTVLIWGKDEVMTKEIKL PTEMEKKMAVTRATKIPCKPSHIPAPCLRHI 5529 46 640 TFRLVSAHLKTRKLINPEAAERRWRDWDSRQGWLSVKMQRVSGL LSWTLSRVLWLISGLSBEQAARQPRIMEERALBYVDLIRTITHDPE KPHTLEELEVVSESCVEVGGIINEELVIIRFTPYPHCSLATL IGLCLRVKLQRCLPPKIKLBIYISEGTHSTEEDINKQINDKERV AAAMENPILRSIVEQCVLEPD 5530 4541 2606 AQIVHAISYCHKLHVGERDLKPENVVFFEKQGLVKLTDFGFSNK FOPGKKLITTSCGSLAYSAPSILLIGDBYDAPADTWSLGVILFML VCGDPFOPANDSSTLIMIMCXYLVIIRFTPYPHCSLATL VCGDPFOPANDSSTLIMIMCXYLDYSHVSKKCKDLITRMLQR DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKKLSEBEIN SIIQRWVLGDIADRDAIVEALETNRYNHTATYFILAERILREK QEKEIGTRSSFSPNIKAQFRQSMFTIDVPQDLEDDIATPPLEH ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP PASLKPTASGRKCLFRVEEDDEEDEDKMENLEPKLSRVKNING SIIGRNVLGDIADRDAIVEALETNRYNHTATYFILAERILREK QEKEIGTRSSFSPNIKAQFRGSKSPNISTGVVKASPSENNAG GSSPSSGSGNPTNTSGTTRCAGPSNSMQLASRSAGEIDKSGF TYSWHRRINGSBGPPGSEDGGGGGSKSSNSNAGGVVKASPSENNAG GSSPSSGSGGNPTNTSGTTRCAGPSNSMQLASRSAGEIDVESLK LMSLCLGSQLHGSTKXIIDPQNLSFSSVVQKRSTKKMCISST GNAGQVPANGGIKFSPSHMADTTSLERIKSKNLKNNVLQLPLC EKTISVNIQRNPKBGLLCASSPSSCCHVI 5531 24 515 GSOFRAPRFRDSMERPEPELIRGSWRAVSRSPEHGTVLFARLP ALEPDLLPLFGYNCROPSSPENCLSSPEFLDHIRKVMLVIDAAV TNVEDLSSLESVLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPETPPATRAMSQULVARVQAMSRGWGB SDMWVGKRKMIIEDETFRGGELLHSVLQCKSVFDVLDGEEMR RARTRANSYENIRGVFFLNRAMKNANNDFVPDMFTNRDSVG KPLINTDRKGWHFLMADGGFSVEQGBNLQEILEKQLLCQFFLMA LSIVNTGGHFTCKTFDLFFFFSUCHVHRKXKMHASGFMTLK GPNDFKLEDFTYSASSELFFPYYGEGGIDGDGDTTRPNISAFRN FVLINNTDRKGWHFLMADGGFSVEQGBNLQEILEKQLLCQFFLMA LSIVNTGGHFTCKTFDLFFFFSUCHLYMCKCHMAGGFMTLK	1	İ		YMDVVKERIRLARQIEKSEYRNFQACLHNSWIEOAAAALEIELE
S528 3 895 GPFLSACRWIGACKVKVHDSLATISITLRRYLRLGATMAKSKFE YVRDPEADDTCLAHCWVVVRLDGROFHRPAERHNFAKPNDSRAL CLMMKCACTYMEELBUIJAGOGDEYSFVFRKRTNWFKRASK FMTHVASQPASSYVFYWRDYFEDQPLLYPPGFDGRVVVYPSNOT LKDYLSWRQADCHINNLYNTVFWALLQOSGLIPYQAQQRLQGTL AADKNELIESFENINNNEPPMHKGTVLIWGKVDEVMTKEIKL PTEMEGKKMAVTRTRTKPCKPSHLPRAPCLRWI. 5529 48 640 TFRLVSAHLKTRKLINPEAAERRWRDWDSRQWLSVKMQRVSGL LSWTLSRVLWLSGLSEPGAARQPRIMEERALEVYDLIRTIRDPE KPNTLEELBUVSESCVBVQBINEEYLVIIRFTPTVPHCSLATL IGLCLRVKLQRCLPFKHKLEIYISEGTHSTEDDINKQINKERV AAAMENPHLREIVSCVLLEPD 5530 4541 2606 AQIVHAISYCHKLHWGHRDLKPENVVFFEKQGLVKLTDFGFSNK FOEKKLTISGSLAYSAPEILLGDBYDAPAVDIWSLGVILFML VCGQPPFQEANDSETLTMIMDCKYTVPSHVSKECKDLITRMLQR DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKNISEBEHN SIIQRWVLGDIARDAIVEALETRNHTTATYFLLABRILREK QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVLNGHRSKGLCDSAKDDLPELAGPALSTVP PASLKETRASGRKCLFRVEEDEEBEDEKKPMSLSTOVLRKRES VTNKLTSRKSAPVLNQIFEBGESDDEFDMDENLPPKLSRLKMNI ASPGTVHKRYHRRKSQGRGSSCSSSTEDDSESRRELDKDSGF TYSWHRDSSEGPPGSBGDGGGSKPSNNSQGJVKASPSENNAG GGSPSSGSGGNFTNTSGTTRRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKYIIDPQNGLSFSSVVQEKSTWKNCISST GNAGQVPAVGGIKFFSDHMADTITELERIKSKNLKNNVLQLPLC EKTISVNIQRNYKBGLLCASSPASCCHVI 5531 24 515 GSGFRAPPRFDSMERPPEPLIRQSWRAVSRSPLEHGTVLFARLF ALEPDLLPLFQYNCRQFSSPECLLSSPFLDHIRKVMLVIDAAV TNVEDLSSLESYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGFATFPATRAMSQULGAVQAMRSRGMOGE 5532 3395 1402 SDWWVGKRKMIIEDETEPCGEELLHSVLQCKSVFPDVLDGEEMR RARTRANFYBNIRGVFFLNRAMMANNDFVFDMFTNPRDSYG KPLVKDRREALLYPADVCAGPGGFSSFVLNRKKWHAKGGMTLK GPNDFKLBDFFSASSELFPPYGEGGIDGDDITRPENISAFN FVLINTTGHFFICKTFTLFTFSVCVLYNKKWHAKGGFMTLK GPNDFKLBDFFSASSELFFRPYYGEGGIDGDDITRPENISAFN FVLINTTGHFFICKTFTLFTFSVCVLYNKKWHAKGGFMTLK GPNDFKLBDFFSASSELFFRPYYGEGGINGGDITRPENISAFN FVLINTTGHFFICKTFTLFTFSVCVLYNKKWHAKGGFMTLK GPNDFKLBDFFSASSELFFRPYYGEGGINGGDITRPENISAFN FVLINTTGHFFICKTFTLFTFFSVCVLYNKKWHAKGGFMTLK GPNDFKLBDFFLAGFFICKTFTLYTFSVCVLYNKKWHAKGGFMTLK GPNDFKLBDFFLAGFFICKTFTLYTFTFVCVLYNKKWHAKGGFMTLK GPNDFKLBDFFILMFTLMAGGFFTLKKGCCHCKFFT				EDMYKGGKADQQEERRROKOMKVLKKELRHLLSOPLFTESOKTK
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S528 3 895 GPFLSACRMWGACKVKVHDSLATISITLRRYLRIGATMAKSKFE YVRDFEADDTCLAHCWVWVRLDGRNFHRPARKHNFAKRNDSRAL OLMTKCAQTUMEELBUIVLAYDEWSFAPKKINMFKRKASK FMTHVASQPASSYVFWRDYFEDQPLLYPPGFDGRVVVYPSNGT LKDYLSWROADCHINNLYNTVFWALIQSGLTFVQAQGRQGTL AADKNEILFSEFNINYNNEPPWYRSTVLIMQKVDEWMKEIKL PTEMEGKKMAVTRTRKPCKPSHLPRAPCLEWIL TFRLVSAHLKTRKLINPEAAERRWRDDSRQWLSVKMQRVSGL LSWTLSRVLMLSGLSEPGAARQPRIMEEKALEVYDLIRTITDPE KPNTLEELEVVSESCVEVQEINEEEYLVIIRFTPTVPHCSLATL IGLCLPWKLQRCLPPKHKLEIYISEGTHSTREDINKQINDKERV AAMENPNLREIVECVLEPD AAAMENPNLREIVECVLEPD COMPANAMENPNLREIVECVLEPD COMPANAMENPNLREIVECVLEPD COMPANAMENPNLREIVECVLEPD COMPANAMENPNLREIVECVLEPD COMPANAMENPNLREIVECVLEPD COMPANAMENPNLREIVECVLEPD COMPANAMENPNLREIVECVLEPD COMPANAMENPNLREIVECVLEPD COMPANAMENPNLREIVECVLEPD COMPANAMENPNLREIVECVLEPD COMPANAMENPNLREIVECVLEPD COMPANAMENPNLREIVECVLEPD COMPANAMENPNLREIVECVLEPD COMPANAMENPNLREIVECVLEPD COMPANAMENPNLREIVECVLEPD COMPANAMENPNLREIVECVLEPD COMPANAMEN				OPSTSAN
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LKDYLSKRQADCHINNLYNTVEWALIQOSGLTPVQAQGRLQGTL AADKNEILFSEFNINYNNEPPMYRKGTVLIWQKVDEVMTKEIKI PTEMEGKKMAVTRITKPCKPSHLPRAPCLRWI 5529 48 640 TFRÜVSAHLKTRKLINPEAAERRWRDWDSRQGWLSVKMQRVSGL LSWTLSRVLMLSGLSBEQAARQPRIMEERALEVYDLIRTIRDPE KPNTLEELEVVSESCVEVQEINEERYLVILIRTPTPTVPHCSLATL IGLCLRVKLQRCLPFKHKLEIYISEGTHSTEEDINKQINDKERV AAAMENPNLREIVEQCVLEPD 5530 4541 2606 AQIVHAISYCHKLHVGHRDLKPENVVFFEKQGLVKLTDFGFSNK FOPGKKLITSCGSLAYSAPEILLGDEYDAPAVDINSLGVILFML VCGQPPFQEANDSETLTMIMDCKYTVPSHVSKECKDLIRMLQR DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKNLSEBEHN SIIQRMVLGDIADRDAIVEALETNRYNHITATYFLLAERILREK QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVLNGHRSKGLOSAKKDDLPELAGPALSTVP PASLKPTASGRKCLFRVEEDEBEEDEDKKMSLSTQVVLRRKES VTNRLTSRKSAPVLNQIFEGESDDEFDKMSMSTGVVLRRKES VTNRLTSRKSAPVLNQIFEGESDDEFDKMSMSTGVVLRRKES VTNRLTSRKSAPVLNQIFEGESDGGQSKPSNASGGVDKASPSENNAG GGSPSSGSGGNPTNTSGTTRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQEKSTWKNCISST TYSWHRRDSSEGPPGSSEDGGGQSKPSNASGGVDKASPSENNAG GGSPSSGSGGNPTNTSGTTRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQEKSTWKNCISST GNAGQVPAVGGIKFFSDHMADTTTELERIKSKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCIVI 5531 24 515 GSQFRAPRFDSMERPPPELIRQSWRAVSRSPLEHGTVLFARLF ALEPDLLPLFQVRCRPFSSPEDCLSSPEFLDHIRKVMLVIDAAV TNVEDLSSLEEYLASLGRKRRAVSVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGE 5532 3395 1402 SDMWVGKRKMITEDETEFGGEELLHSVLQCKSVFDVLDGEEMR RARTRANPYEMIRGVFFLNRAAMMAMMPVPDRMFTNPRDSYG KPLVKDRRAELLYFADVCAGPGGFSEVVLNRKKWHAKGFGMTLK GPNDFKLEDFYSASSELFPPYYGEGGIDGDDITRPENISAFRN FVLDNTDRKGVHFLMADGFSVEGQENLQEILSKQLLLCQFILMA LSIVRTGGHFICKTFDLFFFSVGLVVLLYCCFBRVCLFFRFITS				QLMTKCAQTVMEELEDIVIAYGQSDEYSFVFKRKTNWFKRRASK
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LSWTLSRVLWLSGLSBPGAARQPRIMEEKALEVYDLIRTIRDPE KPNTLEELEVVSESCUEVQEINEEGYLVIRFTPTVPHCSLATL IGLCLRVKLQRCLPFKHKLEIYISEGTHSTEEDINKQINDKERV AAAMENPNLREIVEQCVLEPD 5530 4541 2606 AQIVHAISYCHKLHVGHRDLKPENVVFFEKQGLVKLTDFGFSNK FQPGKKLTTSCGSLAYSAPEILLGDEYDAPAVDIWSLGVILFML VCGQPPFCPANDSETITMINDCKYTVPSHVSKECKDLITRMLQR DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKNLSEEEHN SIIQRMVLGDIADRDAIVEALETNRYNHHTATTFLLAERILREK QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVLNGHRSKGLCDSAKKODLPELAGPALSTVP PASLKPTASGRKCLFRVEEDBEEDBEDKKMMSLSTQVVLRRKPS VTNRLTSRKSAPVLNQIFEEGSDDEFDMDENLPPKLSRLKMNI ASPGTVHKRYHRKSGGRGSSCSSSETSDDDSESRRRLDKDGSF TYSWHRRDSSEGPPGSEGDGGGGSCSSSETSDDDSESRRRLDKDGSF TYSWHRRDSSEGPPGSEGDGGGGSCSSFRRLDKDSFRRLDKDGSF TYSWHRRDSSEGPPGSEGDGGGGSCSSFRRLDKDSFSRNLDKDGF GGSPSGGGGMPTNTGGTTRCAGPSNSMQLASRSAGELVBSLK LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQEKSTWKMCISST GNAGQVPAVGGIKFFSDHMADTTTELERIKSKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI 5531 24 515 GGPRAPRPRDSMERPEPELIRQSWRAVSRSPLEHGTVLFARLF ALEPDLLPLFQYNCRQFSS PEDCLSSPEFLDHIRKVMLVIDAAV TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRRAWSQLYGAVVQAMSRGMDGE 5532 3395 1402 SDMWVVGKRMIIEDETEFGGEELLHSVLQCKSVFDVLDGEEMR RATKRANPYEMIRGVFFLMRAAMMAMMDFVDRMFTNPRDSYG KPLVKDREAELLYFADVCAGPGGFSEVLWRKKWHAKGFGMTLK GPNDFKLEDFYSASSELFEPYYGGGGIDGGDITRPENISAFRN FVLDNTDRKGVHFLMADGGFSVEGQBNLQBEILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTFFSGLVLLLLCQFLMA LSIVRTGGHFICKTFDLFTFFSGLVLLLLCQFLMA	5529	48	640	TPRLVSAHLKTRKLINPEAAERRWRDWDSROGWLSVKMORVSGI.
KPNTLEELEVVSESCVEVQEINEEEYLVIIRFTPTVPHCSLATL IGLCRVKLQRCLPFKHKEIYISEGTHSTEEDINKQINDKERV AAAMENPRIREIVEQCVLEPD 5530 4541 2606 AQIVHAISYCHKLHVGHRDLKPENVVFFEKQGLVKLTDFGFSNK FQPSKKLITISCGSLAYSAPEILLGDEYDAPAVDIWSLGVILFML VCGQPPFQEANDSETLTMINDCKTTVPSHVSKECKDLITRMLQR DPKRRASLBEIENHPHLQGVDPSPATKYNIPLVSYKNLSEEEHN SILQRWVLGDIADRDAIVEALETRRYNHITATTFLLAERILREK QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP PASLKPTASGRKCLFEVEEDEEEDEEDEEDKKPMSLSTQVVLRRKPS VTNRLTSRKSAPVLNQIFEEGESDDEFDMDENLPPKLSRLKMNI ASPGTVHKRYHRRKSGGRGSSCSSSETSDDDSESRRRLDKDGGF TYSWHRRDSSEGPBGSGGGSKPSNAMGLASRSAGELVESLK LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQEKSTKMCISST GNAGQVPAVGGIKFFSDHMADTTTELERIKSKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI 5531 24 515 GSQPRAPRPRDSMERPEPPELIRGSWRAVSRSPLEHGTVLFARLF ALEPDLLPLFQYNCRQFSSPEDCLSSPSFLDHIRKVMLVIDAAV TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGE 5532 3395 1402 SDMMVVGKRMIIEDETEPGEEELLHSVLQCKSVFDVLDGEEMR RARTRANPYEMIRGVFFLNRAAMKMAMMDFVPDRMFTINPRDSYG KPLVKDREAELLYFADVCAGPGGFSEYVLWRKKWHAKGFGMTLK GPNDFKLEDFYSASSELFEPYGEGGIDGDGDITRPENISAFRN FVLDNTDRKGVHFIMADGGFSVEGQENLQEILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFRRVCLEFRJTS)		LSWTLSRVLWLSGLSRPGAAROPRIMEEKALEVVDLTPTTDDDD
IGLCLRVKLQRCLPFKHKLEIYISEGTHSTEEDINKQINDKERV AAAMENPNLREIVEQCVLEPD AQIVHAISYCHKLHVGHRDLKPENVVFFEKQGLVKLTDFGFSNK FQPGKKLTTSCGSLAYSAPEILLGDEYDAPAVDIWSLGVILFML VCGQPPFQEANDSETLTMIMDCKYTVPSHVSKECKDLITRMLQR DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKNLSEEBHN SIIQRWLGDIADRDAIVEALETNRYNHITATYFLLAERILREK QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP PASLKPTASGRKCLFRVEEDEEDEEDEKKPMSLSTQVVLRRKPS VTNRLTSRKSAPVLNQIFEEGESDDEFDMDENLPPKLSRLKMINI ASPGTVHKRYHRKSQGRGSSCSSSETSDDDSESRRRLDKDSGF TYSWHRRDSSEPPGSEGDGGGQSKPSNASGGVDKASPSENNAG GGSPSSGSGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKYIDPQNGLSFSSVKVQEKSTWKMCISST GNAGQVPAVGGIKFFSDHMADTTTELERIKSKNLKNNVLQLPLC EKTISVNIQRIPKEGLLCASSPASCCHVI 5531 24 515 GSQPRAPRPBDSMERPEPELIRQSWRAVSRSPLEHGTVLFARLF ALEPDLLPLFQYNCRQFSSPEDCLSSPEFLDHIRKVMLVIDAAV TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAMVGLYGLVGAVVQAMSRGWDGE 5532 3395 1402 SDWMVVGKRMISEDETEFGGEELLHSVLQCKSVFDVLDGEEMR RARTRANPYEMIRGVFFLNRAMKMANMDFVFDRMFTNERDSYG KPLVKDREAELLYFADVCAGPGGFSBYVLWRKKWHAKGFGMTLK GPNDFKLEDFYSASSELFBYYGEGGIDGDGITRPENISAFRN FVLDNTDRKGVHFLMADGGFSVEGQBNLQEILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTFFSVGLVYLLYCCFERVCLFKPITS		1		KPNTLEELEVVSESCVEVOETNEEEVLVIID DERDEVDUGGE AME
5530 4541 2606 AQIVHAISYCHKLHVGHRDLKPENVVFFEKQGLVKLTDFGFSNK FOPGKKLTTSCGSLAYSAPEILLGDEYDAPAVDIWSLGVILFML VCGQPPFCEANDSETTIMIMDCKYTVPSHVSKECKDLITRMLQR DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKNLSEEEHN SIIQRMVLGDIADRDAIVEALETINRYNHITATYFLLAERILREK QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP PASLKPTASGRKCLFRVEEDEEDEEDKKPMSLSTQVVLRRKPS VTNRLTGRKSAPVINQIFEEGESDDEFDMDENLPPKLSRLKMNI ASPGTVHKKYHRRKSQGSSCSSSETSDDDSESRRRLDKDSGF TYSWHRRDSSEGPPGSEGDGGGQSKPSNASGGVDKASPSENNAG GGSPSSGSGGNPTNTSGTTRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQEKSTWKMCISST GNAGQVPAVGGIKFFSDHMADTTTELERIKSKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI 5531 24 515 GSQFRAPRPRDSMERPEPELIRQSWRAVSRSPLEHGTVLFARLF ALEPDLLPLFQYNCRQFSSPEDCLSSPEFLDHIRKVMLVIDAAV TNVEDLSSLEEVLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGE 5532 3395 1402 SDWMVVGKRKNIIEDETEFCGEELLHSVLQCKSVFDVLDGEEMR RARTRANPYEMIRGVFFLNRAAMKNANMPVFPRMFTNPRDSYG KPLVKDREAELLYFADVCAGPGGFSBYVLWRKKWHAKGFGMTLK GPNDFKLEDFYSASSELFBPYYGEGGIDGDGITRPENISAFRN FVLDNTDRKGVHFLMADGGFSVEGQENLQEILSKQLLCQFLMA LSIVRTGGHFICKTFDLFTFFSVGLVYLLYCCFERVCLFKPITS		}		TCLCLDVVI ODCI DEVINI ETVI GEGMUCMEND TAVIO TODI
AQIVHAISYCHKLHVGHRDLKPENVVFFEKQGLVKLTDFGFSNK FQPGKKLTTSCGSLAYSAPEILLGDEYDAPAVDIWSLGVILFML VCGQPPFQEANDSETLHMIMDCKYTVPSHVSKECKDLITRMLQR DPKKRASLBEIENHPWLQGVDPSPATKYNIPLVSYKNLSEBEHN SIIQRMVLGDIADRDAIVEALETRRYNHTTATYFLLAERILREK QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP PASLKPTASGRKCLFRVEEDEEBEDEEDKKKPMSLSTQVVLRRKPS VTNRLTSRKSAPVLNQIFEEGESDDEFDMCBNLPPKLSRLKMNI ASPGTVHRYHRRKSQGRGSSCSSSETSDDDSESRRLDKDSGF TYSWHRRDSSEGPPGSEGDGGQQSKPSNASGGVDKASPSENNAG GGSPSSGSGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQEKSTWKMCISST GRAGQVPAVGGIKFFSDHMADTTTELERIKSKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI 5531 24 515 GSQFRAPRFDSMERPEPELIRQSWRAVSRSPLEHGTVLFARLF ALEPDLLPLFQYNCRQFSSPEDCLSSPEFLDHIRKVMLVIDAAV TNVEDLSSLEBYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAMSQLYGAVVQAMSRGWDGB 5532 3395 1402 SDWMVVGKRKMIIEDETEFCGEELLHSVLQCKSVFDVLDGEEMR RARTRANPYEMIRGVFFLNRAAMKMANMDFVPDRMFTNPRDSYG KPLVKDRRAELLYFADVCAGPGGFSEYVLWRKKWHAKGFGMTLK GPNDFKLGVHFLMADGGFSVEGQENLQEILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFSVGLVVLLYCCFRRVCLFKPITS		l i		TOLCHRYKLORCLPFKHKLEITISEGTHSTKEDINKQINDKERV
FOPGKKLTTSCGSLAYSAPEILLGDEYDAFAVDIWSLGVILFML VCGQPPFQEANDSETLTMIMDCKYTVPSHVSKECKDLITMLQR DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKNLSEEEHN SIIQRMVLGDIADRDAIVEALETRRYNHTTATYFLLAERILREK QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP PASLKPTASGRKCLFRVEEDEEDEEDKKRWSLSTQVVLRRKPS VTNRLTSRKSAPVLNQIFEEGESDDEFDMDENLPPKLSRLKMNI ASPGTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRLDKDSGF TYSWHRRDSSEGPPGSEGDGGGSKPSNASGGVUKASPSENNAG GGSPSSGSGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQEKSTWKMCISST GNAGQVPAVGGIKFFSDHMADTTTELERIKSKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI 5531 24 515 GSOPRAPRPDSMERPEPELIRGSWRAVSRSPLEHGTVLFARLF ALEPDLLPLFQYNCRQFSSPEDCLSSPEFLDHTRKVMLVIDAAV TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGMDGE 5532 3395 1402 SDWMVVGKRKMIIEDETEFCGEELLHSVLQCKSVFDVLDGEEMR RARTRAMPYEMIRGVFFLNRAAMKMANMDFVPDRMFTNPRDSYG KPLVKDREAELLYFADVCAGPGGFSEYVLWRKKWHAKGFGMTLK GPNDFKLEDFYSASSELFEPYYGEGGIDGDGITRPENISAFRN FVLDNTDRKGVHFLMADGGFSVEGQENLQEILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFRRVCLFKPITS	FF30			
VCGQPPFQEANDSETLTMIMDCKYTVPSHVSKECKDLITRMLQR DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKNISEEEHN SIIQRMVLGDIADRDAIVEALETNRYNHITATYFLLAERILREK QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP PASLKPTASGRKCLFRVEEDEEDEEDKKPMSLSTQVVLRRKPS VTNRLTSRKSAPVLNQIFEEGESDDEFDMDENLPPKLSRLKMNI ASPGTVHKRYHRRKSGCRGSSCSSSETSDDDSESRRRLDKDSGF TYSWHRRDSSEGPPGSEGDGGGQSKPSNASGGVDKASPSENNAG GGSPSSGSGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKXIIDPQNGLSFSSVKVQEKSTWKMCISST GNAGQVPAVGGIKFFSDHMADTTTELERIKSKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI 5531 24 515 GSQPRAPRPRDSMERPEPELIRQSWRAVSRSPLEHGTVLFARLF ALEPDLLPLFQYNCRQFSSPEDCLSSPEFLDHIRKVMLVIDAAV TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGE 5532 3395 1402 SDWMVVGKRKMIIEDETEFCGEELLHSVLQCKSVFDVLDGEEMR RARTRANPYEMIRGVFFLNRAAMKMANMDFVPDRMFTNPRDSYG KPLVKDREAELLYFADVCAGPGGFSEYVLWRKKWHAKGFGMTLK GPNDFKLEDFYSSELFEPYYGEGGIDGDDITRPNISAFRN FVLDNTDRKGVHFLMADGGFSVEGQENLQEILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFRRVCLFKPITS	5530	4541	2606 .	AQIVHAISYCHKLHVGHRDLKPENVVFFEKQGLVKLTDFGFSNK
DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKNLSEEEHN SIIQRWLGDIADRDAIVEALETTRYNHITATYFLLAERILREK QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP PASLKPTASGRKCLFRVEEDEEDEEDKKPMSLSTQVVLRRKPS VTNRLTSRKSAPVLNQIFEEGESDDEFDMDENLPPKLSRLKMNI ASPGTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRLDKDSGF TYSWHRRDSSEGPPGSEGDGGGQSKPSNASGGVDKASPSENNAG GGSPSSGSGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQEKSTWKMCISST GNAGQVPAVGGIKFFSDHMADTTTELERIKSKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI 5531 24 515 GSQPRAPRPSDSMERPEPELIRGSWRAVSRSPLEHGTVLFARLF ALEPDLLPLFQYNCRQFSSPEDCLSSPEFLDHIRKVMLVIDAAV TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGE 5532 3395 1402 SDWMVVGRRKMIIEDETEFCGEELLHSVLQCKSVFDVLDGEEMR RATRANPYEMIRGVFFLNRAAMKMANMDFVFDRHFTNPRDSYG KPLVKDREAELLYFADVCAGPGGFSEYVLWRKKWHAKGFGMTLK GPNDFKLEDFYSASSELFEPYYGEGGIDGDGDITRPENISAFRN FVLDNTDRKGVHFLMADGGFSVEGQBNLQEILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFRRVCLFKPITS				FQPGKKLTTSCGSLAYSAPEILLGDEYDAPAVDIWSLGVILFML
DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKNLSEEEHN SIIQRWLGDIADRDAIVEALETTRYNHITATYFLLAERILREK QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP PASLKPTASGRKCLFRVEEDEEDEEDKKPMSLSTQVVLRRKPS VTNRLTSRKSAPVLNQIFEEGESDDEFDMDENLPPKLSRLKMNI ASPGTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRLDKDSGF TYSWHRRDSSEGPPGSEGDGGGQSKPSNASGGVDKASPSENNAG GGSPSSGSGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQEKSTWKMCISST GNAGQVPAVGGIKFFSDHMADTTTELERIKSKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI 5531 24 515 GSQPRAPRPSDSMERPEPELIRGSWRAVSRSPLEHGTVLFARLF ALEPDLLPLFQYNCRQFSSPEDCLSSPEFLDHIRKVMLVIDAAV TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGE 5532 3395 1402 SDWMVVGRRKMIIEDETEFCGEELLHSVLQCKSVFDVLDGEEMR RATRANPYEMIRGVFFLNRAAMKMANMDFVFDRHFTNPRDSYG KPLVKDREAELLYFADVCAGPGGFSEYVLWRKKWHAKGFGMTLK GPNDFKLEDFYSASSELFEPYYGEGGIDGDGDITRPENISAFRN FVLDNTDRKGVHFLMADGGFSVEGQBNLQEILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFRRVCLFKPITS				VCGQPPFQEANDSETLTMIMDCKYTVPSHVSKECKDLITRMLOR
SIIQRWLGDIADRDAIVEALETNRYNHITATYFLLAERILREK QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGFALSTVP PASLKPTASGRKCLFRVEEDEEEDEKKPMSLSTQVVLRRKPS VTNRLTSRRSAPVLNQIFEEGESDDEFDMDENLPPKLSRLKMNI ASPGTVHKRYHRRKSQCRGSSCSSESTSDDDSESRRRLDKDSGF TYSWHRRDSSEGPPGSEGDGGQQSKPSNASGGVDKASPSENNAG GGSPSSGSGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKVIIDPQNGLSFSSVKVQEKSTWKMCISST GNAGQVPAVGGIKFFDHMADTTTELERIKSKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI 5531 24 515 GSQPRAPRPDSMERPEPELIRQSWRAVSRSPLEHGTVLFARLF ALEPDLLPLFQYNCRQFSSPEDCLSSPEFLDHIRKVMLVIDAAV TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGE 5532 3395 1402 SDWMVVGKRKMIIEDETEFCGEELLHSVLQCKSVFDVLDGEEMR RARTRANPYEMIRGVFFLNRAMKMANMDFVPDRMFTNPRDSYG KPLVKDREAELLYFADVCAGPGGFSEYVLWRKKWHAKGFGMTLK GPNDFKLEDFYSASSELFEPYYGEGGIDGDDITRPNISAFRN FVLDNTDRKGVHFIMADGGFSVEGQENLQEILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFRRVCLFKPITS				DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKNLSEERHN
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YRNLVSLGLVVSKPDLITPLEQRKEPWNVKSEBTVAIQPDVFSH YNKDLITEHCTEAS FQKVISRRHGS CDLENLHLRKKWKREECEG HNGCYDEKTFKYQDFDESSVESLFHQQILSSCAKSYNFDQYRKV FTHSSLLNQQEEIDIWGKHHIYDKTSVLFRQVSTLMSYRNYFIG EKNYHCNNSEKTLNQSSSPKNHQENYFLERQYKCKEFEEVFLQS MHGQEKQEQSYKCNKCVEVCTQSLKHIQHQTIHIRENSYSYNKY DKDLSQSSNLRKQIIHNEEKPYKCEKCGDSLNHSLHLTQHQIIP TEEKPYKWKECGKVFNLNCSLYLTKQQQIDTGENLYKCKACSKS FTRSSNLIVHQRIHTGEKPYKCKECGKAFRCSSYLTKHKRIHTG EKPYKCKECGKAFNRSSCLTQHQTTHTGEKLYKCKVCSKSYARS SNLIMHQRVHTGEKPYKCKECGKAFRCSSYLTKHKRIHTG KCKVCAKPFTCFSNLIVHERIHTGEKPYKCKECGKAFPYSSHLI RHHRIHTGEKPYKCKACSKSFSDSSGLTVHRTHTGEKPYTCKE CGKAFSYSSDVIQHRRIHTGGRPYKCEECGKAFNYRSYLTTHQR SHTGERPYKCEECGKAFNSRSYLTTHRRHTGERPYKCDECGKA FSYRSYLTTHRRSHSGERPYKCEECGKAFNSRSYLIAHQRSHTR EKL 5538 926 161 HSMMMKIPWGSIPVLMLLLLLGLIDISQAQLSCTGPPAIPGIPG GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAFSATRTI NVPLRRDQTIRFDHVITNMNNYSPRSGKFTCKVPGLYYFTYHA SSRCNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMEA 1258 1258 1258 1258 1258 1258 1258 125	5537	3	2391	
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CGKAFSYSSDVIQHRRIHTGQRPYKCEECGKAFNYRSYLTTHQR SHTGERPYKCEECGKAFNSRSYLTTHRRHTGERPYKCDECGKA FSYRSYLTTHRRSHSGERPYKCEECGKAFNSRSYLIAHQRSHTR EKL 161 HSMMMKIPWGSIPVLMLLLLLGLIDISQAQLSCTGPPAIPGIPG IPGTPGPDGQPGTPGIKGEKGLPGLAGDHGEFGEKGDPGIPGNP GKVGPKGPMGPKGGPGAPGAPGAKGESGDYKATQKIAFSATRTI NVPLRRDQTIRFDHVITNMNNYEPRSGKFTCKVPGLYYFTYHA SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMEA 1258 HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK				
SHTGERPYKCEECGKAFNSRSYLTTHRRHTGERPYKCDECGKA FSYRSYLTTHRRSHSGERPYKCEECGKAFNSRSYLIAHQRSHTR EKL 5538 926 161 HSMMMKIPWGSIPVLMLLLLLGLIDISQAQLSCTGPPAIPGIPG IPGTPGPDGQPGTPGIKGEKGLPGLAGDHGEFGEKGDPGIPGNP GKVGPKGPMGPKGGPGAPGPKGESGDYKATQKIAFSATRTI NVPLRRDQTIRFDHVITNMNNYEPRSGKFTCKVPGLYYFTYHA SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMEA 5539 38 1258 HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK	1	1		
FSYRSYLTTHRRSHSGERPYKCEECGKAFNSRSYLIAHQRSHTR EKL 5538 926 161 HSMMMKIPWGSIPVLMLLLLLGLIDISQAQLSCTGPPAIPGIPG IPGTPGPDGQPGTPGIKGEKGLPGLAGDHGEFGEKGDPGIPGNP GKVGPKGPMGPKGGPGAPGPKGESGDYKATQKIAFSATRTI NVPLRRDQTIRFDHVITNMNNYEPRSGKFTCKVPGLYYFTYHA SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMEA 5539 38 1258 HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK				
EKL 5538 926 161 HSMMMKIPWGSIPVLMLLLLLGLIDISQAQLSCTGPPAIPGIPG IPGTPGPDGQPGTPGIKGEKGLPGLAGDHGEFGEKGDPGIPGNP GKVGPKGPMGPKGGPGAPGAPGHKGESGDYKATQKIAFSATRTI NVPLRRQQTIRFDHVITNMNNYEPRSGKFTCKVPGLYYFTYHA SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMEA 5539 38 1258 HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK	i			SHTGERPYKCEECGKAFNSRSYLTTHRRRHTGERPYKCDECGKA
EKL 5538 926 161 HSMMMKIPWGSIPVLMLLLLLGLIDISQAQLSCTGPPAIPGIPG IPGTPGPDGQPGTPGIKGEKGLPGLAGDHGEFGEKGDPGIPGNP GKVGPKGPMGPKGGPGAPGAPGHKGESGDYKATQKIAFSATRTI NVPLRRQQTIRFDHVITNMNNYEPRSGKFTCKVPGLYYFTYHA SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMEA 5539 38 1258 HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK				FSYRSYLTTHRRSHSGERPYKCEECGKAFNSRSYLIAHORSHTR
5538 926 161 HSMMMKIPWGSIPVLMLLLLLGLIDISQAQLSCTGPPAIPGIPG IPGTPGPDGQPGTPGIKGEKGLPGLAGDHGEFGEKGDPGIPGNP GKVGPKGPMGPKGGPGAPGAPGAPGKGESGDYKATQKIAFSATRTI NVPLRRDQTIRFDHVITNMNNYEPRSGKFTCKVPGLYYFTYHA SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMEA 1258 HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK	1	[
IPGTPGPDGQPGTPGIKGEKGLPGLAGDHGEFGEKGDPGIPGNP GKVGPKGPMGPKGGPGAPGPKGESGDYKATQKIAFSATRTI NVPLRRDQTIRPDHVITMMNNIYERSGKFTCKVPGLYYFTYHA SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMEA 1258 HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK				
GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAFSATRTI NVPLRRDQTIRFDHVITNMNNYEPRSGKFTCKVPGLYYFTYHA SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMEA 5539 38 1258 HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK	5538	926	161	
NVPLRRDQTIRFDHVITNMNNYEPRSGKFTCKVPGLYYFTYHA SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMEA 5539 38 1258 HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK	1	· ·		
NVPLRRDQTIRFDHVITNMNNYEPRSGKFTCKVPGLYYFTYHA SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMEA 5539 38 1258 HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK	1	f		GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAFSATRTI
SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMEA 5539 38 1258 HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK	1	(1	
GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMEA 5539 38 1258 HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK	1	1	(
5539 38 1258 HRGPSGAAAPGCALPRGQALBGPRSCRRPQPMARRYDELPHYPG IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK	1	1		
IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK	1	1		
IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK	5539	38	1258	HRGPSGAAAPGCALPRGQALBGPRSCRRPQPMARRYDELPHYPG
	1	1		
I DETIGHTHE LIGHT COLUMN COLUM	1	1	1	
AN		i		
SDSFNEDIAAFAKQVRSERPLPSSNPELDNLVIQAIQVLRFHLL	_	L	.1	SUSFNEDTAAFAKQVRSERPLFSSNPELDNLVTQATQVLRFHLL

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			ELEKVHDLCDNFCHRYITCLKGKMPIDLVIBDRDGGCREDFEDY
			PASCPSLPDQNNMWIRDHEDSGSVHLGTPGPSSGGLASQSGDNS
	ì		SDQGDGLDTSVASPSSGGEDEDLDQERRRNKKRGIFPKVATNIM
			RAWLFQHLSHPYPSEEQKKQLAQDTGLTILQVNNWFINARRRIV
			QPMIDQSNRTGQGAAFSPEGQPIGGYTETQPHVAVRPPGSVGMS
5540			LNLEGEWHYL
5540	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG
1			PSGAAAPGCALPRGQALBGPRSCRRPQPMARRYDELPHYPGIVD
			GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI
t			YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE
)			KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED
			SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED
}			EDLDQEPRRNKKRGIPPKVATNIMRAWLFQHLSHPYPSEEQKKQ
			LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG
1			QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5541	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG
			PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD
1			GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI
			YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
1			FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE
			KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED
			EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ
			LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG
		•	QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5542	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG
			PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD
			GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI
	1		YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
			FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE
ł			KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED
			SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ
1			LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG
		•	QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5543	2405	665	RWVREQPWPLRTSEAVKTPALRPFPGPRGVSPFPKPDWGKSPAP
1			KRPFSDSGAFWSPERRPGVLEAPRRRPVPASFRAVPPKPTRVHG
			SSASRDRVLARTMIVADSECRABLKDYLRFAPGGVGDSGPGEEQ
ł i	ì		RESRARRGPRGPSAFIPVEEVLREGAESLEQHLGLEALMSSGRV
			DNLAVVMGLHPDYFTSFWRLHYLLLHTDGPLASSWRHYIAIMAA
1			ARHQCSYLVGSHMAEFLQTGGDPEWLLGLHRAPEKLRKLSEINK
}			LLAHRPWLITKEHIQALLKTGEHTWSLAELIQALVLLTHCHSLS
			SFVFGCGILPEGDADGSPAPQAPTPPSEQSSPPSRDPLNNSGGF
1 1			ESARDVEALMERMOQLQESLLRDEGTSQEEMESRFELEKSESLL
			VTPSADILEPSPHPDMLCFVEDPTFGYEDFTRRGAQAPPTFRAQ
1 1		•	DYTWEDHGYSLIQRLYPEGGQLLDEKFQAAYSLTYNTIAMHSGV
			DTSVLRRAIWNYIHCVFGIRYDDYDYGEVNQLLERNLKVYIKTV ACYPEKTTRRMYNLFWRHFRHSEKVHVNLLLLEARMQAALLYAL
[RAITRYMT
5544	1895	514	LGGLLGRQRLLLRMGAGRLGAPMERHGRASATSVSSAGEQAAGD
			PEGRRQEPLRRRASSASVPAVGASAEGTRRDRLGSYSGPTSVSR
			QRVESLRKKRPLFPWFGLDIGGTLVKLVYFEPKDITAEEBEEEV
ļ			ESLKSIRKYLTSNVAYGSTGIRDVHLELKDLTLCGRKGNLHFIR
			FPTHDMPAFIQMGRDKNPSSLHTVPCATGGGAYKFEQDFLTIGD
}			LQLCKLDELDCL1KGILYIDSVGFNGRSQCYYFENPADSEKCQK
	1		LPFDLKNPYPLLLVNIGSGVSILAVYSKDNYKRVTGTSLGGGTF
			FGLCCLLTGCTTFEEALEMASRGDSTKVDKLVRDIYGGDYERFG
]			LPGWAVASSFGNMMSKEKREAVSKEDLARATLITITNNIGSIAR
	ĺ	İ	MCALNENINQVVFVGNFLRINTIAMRLLAYALDYWSKGQLKALF SEHEGYFGAVGALLELLKIP
L	L		PRINCE TO ANY OF MANAGEMENT IN

	C 5	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning		Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H-Histidine, I-Isoleucine, K-Lysine,
	location	corresponding	
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
5545	802	131	GAMWSAGRGGAAWPVLLGLLLALLVPGGGAAKTGAELVTCGSVL
		i	KLLNTHHRVRLHSHDIKYGSGSGQQSVTGVEASDDANSYWRIRG
	(GSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPLSNNQEV
			SAFGEDGEGDDLDLWTVRCSGQHWEREAAVRFQHVGTSVFLSVT
Ì			GEOYGSPIRGOHEVHGMPSANTHNTWKAMEGIFIKPSVEPSAGH
ł		ì	DEL
	1502	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVFT
5546	1592	146	RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKNSLKDCVAVAGP
{			
j			LGVTHFLILSKTETNVYFKLMRLPGGPTLTFQVKKYSLVRDVVS
]			SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMATMFQNLFPSI
1	1		NVHKVNLNTIKRCLLIDYNPDSQELDFRHYSIKVVPVGASRGMK
			KLLQEKFPNMSRLQDISELLATGAGLSESEAEPDGDHNITELPQ
J			AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS
1		1	FVSKTEEELQAILEAKEKKLRLKAQRQAQQAQNVQRKQEQREAH
ļ		}	RKKSLEGMKKARVGGSDEEASGIPSRTASLELGEDDDEQEDDDI
!		1	EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGRL
1			CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRGRFGKRVA
5547	1592	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVFT
		1	RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKNSLKDCVAVAGP
1			LGVTHFLILSKTETNVYFKLMRLPGGPTLTFQVKKYSLVRDVVS
{			SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMATMFQNLFPSI
	į		NVHKVNLNTIKRCLLIDYNPDSQELDFRHYSIKVVPVGASRGMK
1	1	1	KLLQEKFPNMSRLQDISELLATGAGLSESEAEPDGDHNITELPQ
1			AVAGRGNMRAQOSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS
((1	FVSKTEEELQAILEAKEKKLRLKAQRQAQQAQNVQRKQEQREAH
}		}	RKKSLEGMKKARVGGSDEEASGIPSRTASLELGEDDDEQEDDDI
(EYFCOAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGRL
			·
			CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRGRFGKRVA DOTGPPETIAFTFPRSTMEPLCPLLLVGFSLPLARALRGNETTA
5548	1	2153	DOTGPPETIAFTFPRSTMEPECPELEVGFSEPEARALRGNETIA
	1	1	
ļ			DSNETTTTSGPPDPGASQPLLAWLLLPLLLLLVLLLAAYFFRF
			RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI
			RKORKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN
			RKORKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK
			RKORKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY
			RKORKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK
			RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC
			RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR
			RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC
			RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ
			RKORKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK
			RKORKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQBTVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVBDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMLAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLBEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR
			RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQBTVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVBDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFFFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLBEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW
			RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLBEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQBREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG
			RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHACPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLBEEFRKLTNVRIMKEMMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL
			RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHACPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLBEEFRKLTNVRIMKEMMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ
			RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGFIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLBEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILBRVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK
5549	915	256	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQBREQDKCYQWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQTGNHPITVHCSAGAGRTGTFIAL SNILBRVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK
5549	915		RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FTAAQGPKQBTVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQBREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQTGNHPITVHCSAGAGRTGTFIAL SNILBRVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFTDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME
5549	915		RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLBEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQBREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPTERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF
5549	915		RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLBEEFRKLTNVRIMKEMMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQBREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQTGNHPITVHCSAGAGRTGTFIAL SNILBRVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAPKMAGTARHDREMAIQAKKKLTTATDPIERIRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD
	*	256	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHACPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLBEEFRKLTNVRIMKEMMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQBREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL
5549	915		RKORKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLBEEFRKLTNVRIMKEMMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHPKYQNGEWSEEQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL
	*	256	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRWVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGFIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLBEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATOGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG SNILBRVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHPKYQNGEWSEEQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMTAWKL RKRKVFLKMRRLNRKKTLSLVKELDAFFKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI
	*	256	RKORKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLBEEFRKLTNVRIMKEMMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHPKYQNGEWSEEQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL
	*	256	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRWVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGFIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLBEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATOGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG SNILBRVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHPKYQNGEWSEEQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMTAWKL RKRKVFLKMRRLNRKKTLSLVKELDAFFKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI
	*	256	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRWVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLBEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQBREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILBRVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHPKYQNGEWSEEQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL RKRKVFLKMRRLNRKKTLSLVKELDAFFKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAETMVASADGLVYEPTVFDLSPQQKEWQ
	*	256	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLBEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQBREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FFATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPTERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMTTAWKL RKRKVFLKMRRLNKKTLSLVKELDAFFKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAETMVASADGLVYEPTVFDLSPQQKEWQ RMLQLIQSRLQEEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN
	*	256	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEEFRKLTNVRIMKEMMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQBREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERIRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL RKRRVFLKMRRLNRKKTLSLVKELDAFFRVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAETMVASADGLVYEPTVFDLSPQQKEWQ RMLQLIQSRLQBEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRIHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVNHESYN
	*	256	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHACPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLBEEFRKLTNVRIMKEMMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQBREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHPKYQNGEWSEEQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL RKRKVFLKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAETMVASADGLVYEPTVFDLSPQQKEWQ RMLQLIQSRLQEEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVNHESYN FSHRIDHLSFGELVPAIINFLDGTEKIAIDHNQMFQYFITVVPT KLHTYKISADTHQFSVTERERIINHAAGSHGVSGIFMKYDLSSL
	*	256	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLBEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPABGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHPKYQNGEWSEEQVFRKFLD NFDSPYDKDGLVTPEEFMYYAGVSASIDTDVYFIIMMRTAWKL RKRKVFLKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAETMVASADGLVYEPTVFDLSPQQKEWQ RMLQLIQSRLQBEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRIHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVNHESYN FSHRIDHLSFGELVPAIINPLDGTEKIAIDHNQMFQYFITVVPT KLHTYKISADTHQFSVTERBRIINHAAGSHGVSGIFMKYDLSSL MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC
	*	256	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHACPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLBEEFRKLTNVRIMKEMMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQBREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHPKYQNGEWSEEQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL RKRKVFLKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAETMVASADGLVYEPTVFDLSPQQKEWQ RMLQLIQSRLQEEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVNHESYN FSHRIDHLSFGELVPAIINFLDGTEKIAIDHNQMFQYFITVVPT KLHTYKISADTHQFSVTERERIINHAAGSHGVSGIFMKYDLSSL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
J	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid sequence	sequence	Codon, /=possible nucleotide deletion,
ļ ———	sequence		\=possible nucleotide insertion)
			WFVFRRYAEFDKLYNTLKKQFPAMALKIPAKRIFGDNFDPDFIK QRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSDPSEDE
1	1	ĺ	DERSSQKLHSTSQNINLGPSGNPHAKPTDFDFLKVIGKGSFGKV
1			LLAKRKLDGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKNVKH
	[PFLVGLHYSFQTTEKLYFVLDFVNGGELFFHLQRERSFPEHRAR
}		ļ	FYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVVLTDFGLC
			KEGIAISDTTTTPCGTPEYLAPEVIRKQPYDNTVDWWCLGAVLY
			EMLYGLPPFYCRDVAEMYDNILHKPLSLRPGVSLTAWSILEELL
1			EKDRQNRLGAKEDFLEIQNHPFFESLSWADLVQKKIPPPFNPNV
İ			AGPDDIRNFDTAFTEETVPYSVCVSSDYSIVNASVLEADDAFVG
5552	2748	930	FSYAPPSEDLFL
	2,40	330	LGPAAGAAMGKKHKKHKAEWRSSYEDYADKPLEKPLKLVLKVGG SEVTELSGSGHDSSYYDDRSDHERERHKEKKKKKKKKKSEKEKHL
]			DDEERRKRKEEKKRKREREHCDTEGEADDFDPGKKVEVEPPPDR
			PVRACRTQPAENESTPIQQLLEHFLRQLQRKDPHGFFAFPVTDA
ļ	,		IAPGYSMI IKHPMDFGTMKDKIVANEYKSVTEFKADFKLMCDNA
			MTYNRPDTVYYKLAKKILHAGFKMMSKQAALLGNEDTAVEEPVP
1 .			EVVPVQVETAKKSKKPSREVISCMFEPEGNACSLTDSTAEEHVL
			ALVEHAADEARDRINRFLPGGKMGYLKRNGDGSLLYSVVNTAEP
1			DADEEETHPVDLSSLSSKLLPGFTTLGFKDERRNKVTFLSSATT
			ALSMQNNSVFGDLKSDEMELLYSAYGDETGVQCALSLQEFVKDA
(GSYSKKVVDDLLDQITGGDHSRTLFQLKQRRNVPMKPPDEAKVG DTLGDSSSSVLEFMSMKSYPDVSVDISMLSSLGKVKKELDPDDS
			HLNLDETTKLLQDLHEAQAERGGSRPSSNLSSLSNASERDQHHL
			GSPSRLSVGEQPDVTHDPYEFLQSPEPAASAKT
5553	74	1095	LGREAVYLVSRMDGPVAEHAKQEPFHVVTPLLESWALSQVAGMP
			VFLKCENVQPSGSFKIRGIGHFCQEMAKKGCRHLVCSSGGNAGT
1 1	}		AAAYAARKLGIPATIVLPESTSLQVVQRLQGEGAEVOLTGKVWD
Į (EANLRAQELAKRDGWENVPPFDHPLIWKGHASLVQELKAVLRTP
1 1	}		PGALVLAVGGGGLLAGVVAGLLEVGWQHVPIIAMETHGAHCFNA
1 [AITAGKLVTLPDITSVAKSLGAKTVAARALECMQVCKIHSEVVE DTEAVSAVQQLLDDERMLVEPACGAALAAIYSGLLRRLQAEGCL
1			PPSLTSVVVIVCGGNNINSRELQALKTHLGOV
5554	166	2318	CSGRTGGRGSLRPAENVCLTCKLSGAETRGLLCPALRTWIMKVL
1 1			GRSFFWVLFPVLPWAVQAVEHEEVAQRVIKLHRGRGVAAMQSRQ
} }			WVRDSCRKLSGLLRQKNAVLNKLKTAIGAVRKDVGLSDEEKLFQ
] [VHTFEIFQKELNESENSVFQAVYGLQRALOGDYKDVVNMKESSR
1		- (-	QRLEALREAAIKEETEYMELLAABKHQVEALKNMQHQNQSLSML
1 1			DEILEDVRKAADRLEEBIEEHAFDDNKSVKGVNFEAVLRVEEEE
1 1	1		ANSKQNITKREVEDDLGLSMLIDSQNNQYILTKPRDSTIPRADH
]]			HFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPSGLN SIKSIVQVETLGEFGVFFTLFLVGLEFSPEKLRKVWKISLQGPC
! [YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSLSSTPLVSRFLM
	}		GSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQAGAS
			ASSSIVVEVLRILVLIGQILFSLAAVFLLCLVIKKYLIGPYYRK
			LHMESKGNKEILILGISAFIFLMLTVTELLDVSMELGCFLAGAL
			VSSQGPVVTEEIATSIEPIRDFLAIVFFASIGLHVFPTFVAYEL
	Ì		TVLVFLTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV
	i		SEFSFVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI
5555	212	1425	TRCVPRPERRSSL
		1472	LSLRTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPONISTECLILI VI IGAVIAGEDEVKII GVIDGA GTVATK
			GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY
] }		ļ	DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQQDRNIPR
1			GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE
			MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD
[]	GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV
	l		TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL
			PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK
5556	5835		VYNGLQGY
	3033	3346	RTRGMSKNCVPMEFEEYLLRMFQGTFYLLQKITKDNNAHTVKSR

	Predicted	Predicted end	Amino acid segment containing signal peptide
1	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i I	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
, ,	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
, ,	sequence	acquence	\=possible nucleotide insertion)
	sequence		LEELDESYIEKFTDFLRLFVSVHLRRIESYSQFPVVEFLTLLFK
1			YTFHOPTHEGYFSCLDIWTLFLDYLTSKIKSRLGDKEAVLNRYE
{ }			DALVLLLTEVLNRIQFRYNQAQLEELDDETLDDDQQTEWQRYLR
]			QSLEVVAKVMELLPTHAFSTLFPVLQDNLEVYLGLQQFIVTSGS
1			GHRLNITAENDCRRLHCSLRDLSSLLQAVGRLAEYFIGDVFAAR
1 1			FNDALTVVERLVKVTLYGSQIKLYNIETAVPSVLKPDLIDVHAQ
1			SLAALQAYSHWLAQYCSEVHRQNTQQFVTLISTTMDAITPLIST
			KVODKLLLSACHLLVSLATTVRPVFLISIPAVQKVFNRITDASA
1	!		LRLVDKAQVLVCRALSNILLLPWPNLPENEQQWPVRSINHASLI
ļ ļ			
l i			SALSRDYRNLKPSAVAPQRKMPLDDTKLIIHQTLSVLEDIVENI
1			SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFFL
J Ł			TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGCR
j [VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERPS
1 1			PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENEP QFSAIMQAFGQSFLQPDIHLFKQNLFYLETLNTKQKLYHKKIFR
, 1)	TAMLFQFVNVLLQVLVHKSHDLLQEEIGIAIYNMASVDFDGFFA
1			AFLPEFLTSCDGVDANQKSVLGRNFKMDRVRRERGRAKRRAEWA
1 1			RKPGTCAARRGHIEASGRGLCPPCSLAAAHEMPADLVL
		491	VILGAGLEDKDMWIPVVGLPRELELSALAGAGRECILGSEAATR
5557	1712	491	KHLPARNHCGLSDSSPOLWPEPDFRNPPRKASKASLDFKRYVTD
{ }			RRLAETLAOIYLGKPSRPPHLLLECNPGPGILTOALLEAGAKVV
])	ALESDKTFIPHLESLGKNLDGKLRVIHCDFFKLDPRSGGVIKPP
			AMSSRGLFKNLGIEAVPWTADIPLKVVGMFPSRGEKRALWKLAY
1 1			DLYSCTSIYKFGRIBVNMFIGEKEFQKLMADPGNPDLYHVLSVI
1			WOLACEIKVLHMEPWSSFDIYTRKGPLENPKRRELLDQLQQKLY
1			LIOMIPRONLFTKNLTPMNYNIFFHLLKHCFGRRSATVIDHLRS
1 1		į	
1 1			LTPLDARDILMQIGKQEDEKVVNMHPQDFKTLFETIERSKDCAY KWLYDETLEDR
	1509	96	RAGCTHPQVPADLGAPAEPRRPQKTCVCLLQPQPGGQRGPTTMI
5558	1509	30	TGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRS
1 1		Ì	LLKLKMVOVVFRHGARSPLKPLPLEEQVEWNPQLLEVPPQTQFD
{			YTVTNLAGGPKPYSPYDSOYHETTLKGGMFAGQLTKVGMQQMFA
1		1	LGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLA
1 1			GLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTA
1 1			SLOPGISEDLKKVKDRMGIDSSDKVDFFILLDNVAAEQAHNLPS
1 1		ĺ	CPMLKRFARMIEORAVDTSLYILPKEDRESLQMAVGPFLHILES
] [•	ľ	NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPP
1			FAVDLTMELYOHLESKEWFVOLYYHGKEQVPRGCPDGLCPLDMF
1			LNAMSVYTLSPEKYHALCSQTQVMEVGNEE
	150	1983	PLAATAHFAKMSRVAKYRROVSEDPDIDSLLETLSPEEMEELEK
5559	150	1,703	ELDVVDPDGSVPVGLRORNOTEKQSTGVYNREAMLNFCEKETKK
			LMOREMSMDESKOVETKTDAKNGEERGRDASKKALGPRRDSDLG
1 1			KEPKRGGLKKSFSRDRDEAGGKSGEKPKEEKIIRGIDKGRVRAA
1			VDKKEAGKDGRGEERAVATKKEERKKGSDRNTGLSRDKDKKREE
[MKEVAKKEDDEKVKGERRNTDTRKEGEKMKRAGGNTDMKKEDEK
1			VKRGTGNTDTKKDDEKVKKNEPLHEKEAKDDSKTKTPEKQTPSG
1		}	PTKPSEGPAKVEEEAAPSIFDEPLERVKNNDPEMTEVNVNNSDC
1			ITNEILVRFTEALEFNTVVKLFALANTRADDHVAFAIAIMLKAN
1			KTITSLNLDSNHITGKGILAIFRALLONNTLTELRFHNORHICG
]			GKTEMEIAKLLKENTTLLKLGYHFELAGPRMTVTNLLSRNMDKQ
] 1		1	ROKRLOEORQAQEAKGEKKDLLEVPKAGAVAKGSPKPSPQPSPK
1			PSPKNSPKKGGAPAAPPPPPPPPLAPPLIMENLKNSLSPATQRKM
		}	1
1		 	GDKVLPAQEKNSRDQLLAAIRSSNLKQLKKVEVPKLLQ
5560	9	921	SSVVEFSALSVSMACLSPSQLQKFQQDGFLVLEGFLSAEECVAM
1 1			QQRIGEIVAEMDVPLHCRTEFSTQEEEQLRAQGSTDYFLSSGDK
1			IRFFFEKGVFDEKGNFLVPPEKSINKIGHALHAHDPVFKSITHS
1 1			FKVQTLARSIGLQMPVVVQSMYIFKQPHFGGEVSPHQDASFLYT
		1	EPLGRVLGVWIAVEDATLENGCLWFIPGSHTSGVSRRMVRAPVG
1		1	CARDOMORI GOODA DOMOS WITHOUT CONCESS OF THE THORNESS OF THE
			SAPGTSFLGSEPARDNSLFVPTPVQRGALVLIHGEVVHKSKQNL
5561	2175	1775	SAPGTSFLGSEPARDNSLFVPTPVQRGALVLIHGEVVHKSKQNL SDRSRQAYTPHLMEASGTTWSPENWLQPTAELPFPQLYT CYFIFQFFSSPYPGLHPHQTPAPLPNPGLYPPPVSMSPGQPPPQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning		
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
j	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1		1	· ·
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	1		QLLAPTYFSAPGVMNFGNPSYPYAPGALPPPPPPHLYPNTQAPS
l	1	1	QVYGGVTYYNPAQQQVQPKPSPPRRTPQPVTIKPPPPEVVSRGS
i	ì	ì	S
	ļ <u>.</u>		
5562	342	1385	SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCETLEDLKLH
1		1	LQSTDYGNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP
	ì	1	LASFLDFITYSYMIDNVILLITGTLHQRSIAELVPKCHPLGSFE
1	i		QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNIEI
1		1	IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT
1	ļ.		
[Į.	Į.	INSFGTELSKEDRAKLFPHCGRLYPEGLAQLARADDYEQVKNVA
}			DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNQFHF
			GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF
5563	342	1385	SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCETLEDLKLH
-2	1	1	LQSTDYGNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP
Į	1	1	LASFLDFITYSYMIDNVILLITGTLHORSIABLVPKCHPLGSFE
	1	į.	QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNIEI
1	!		IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT
1	}	Į.	INSFGTELSKEDRAKLPPHCGRLYPEGLAQLARADDYEQVKNVA
			DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNQFHF
Ì	ł		GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF
	 	ļ	RVRRDKRAVWTARGRRRCGDSMSGGWMAOVGAWRTGALGLALLL
5564	3	914	
1	l .	1	LLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRTSGLC
1	ł	ł	VPLTWRCDRDLDCSDGSDEEECRIEPCTQKGQCPPPPGLPCPCT
ì	ı		GVSDCSGGTDKKLRNCSRLACLAGELRCTLSDDCIPLTWRCDGH
1		1	PDCPDSSDELGCGTNEILPEGDATTMGPPVTLESVTSLRNATTM
1			GPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLV
1	Ì		
	1		TATLLLLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP
5565	993	138	RWNSPNPARAGSISRPQRAPGSVSAVAMTAAVFFGCAFIAFGPA
	ļ	i	LALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIID
[l	1	NKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSIN
1			PGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLGPGTVGIH
1	-	ł	
į.	ļ	j	GDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVL
1		}	LTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRS
	j) ·	LKLCLLCQDKNFLLYNQRSR
5566	2043	1232	SHIOHHGRGAQAPVKMVSWMISRAVVLVFGMLYPAYYSYKAVKT
		}	KNVKEYVRWMMYWIVFALYTVIETVADQTVAWFPLYYELKIAFV
			IWLLSPYTKGASLIYRKFLHPLLSSKEREIDDYIVQAKERGYET
1			1
1			MVNFGRQGLNLAATAAVTAAVKSQGAITERLRSFSMHDLTTIQG
1	1	1	DEPVGQRPYQPLPEAKKKSKPAPSESAGYGIPLKDGDEKTDEEA
	1		EGPYSDNEMLTHKGPRRSQSMKSVKTTKGRKEVRYGSLKYKVKK
t		1	RPQVYF
5567	1554	233	EFLGSGVSPDLANEDGLTALHQCCIDDFREMVQQLLEAGANINA
1	-55.	1	CDSECWTPLHAAATCGHLHLVELLIASGANLLAVNTDGNMPYDL
1			
l			CDDEQTLDCLETAMADRGITQDSIEAARAVPELRMLDDIRSRLQ
1	1		AGADLHAPLDHGATLLHVAAANGFSEAAALLLEHRASLSAKDQD
1	Ī		GWEPLHAAAYWGQVPLVELLVAHGADLNAKSLMDETPLDVCGDE
		1	EVRAKLLELKHKHDALLRAQSRQRSLLRRRTSSAGSRGKVVRRV
1	1		SLTORTDLYRKOHAGEAIVWOOPPPTSPEPPEDNDDROTGAELR
1	1		PPPPEEDNPEVVRPHNGRVGGSPVRHLYSKRLDRSVSYQLSPLD
1		1	
1	J	J	STTPHTLVHDKAHHTLADLKRQRAAAKLQRPPPEGPESPETAEP
	. <u></u>		GLPGDTVTPQPDCGFRAGGDPPLLKLTAPAVEAPVERRPCCLLM
5568	1731	587	AEDROPASRRGAGTTAAMAASGPGCRSWCLCPEVPSATFFTALL
			SLLVSGPRLFLLQQPLAPSGLTLKSEALRNWQVYRLVTYIFVYE
1			NPISLLCGAIIIWRFAGNFERTVGTVRHCFFTVIFAIFSAIIFL
1		1	
1		1	SFEAVSSLSKLGEVEDARGFTPVAFAMLGVTTVRSRMRRALVFG
1		1	MVVPSVLVPWLLLGASWLIPQTSFLSNVCGLSIGLAYGLTYCYS
1		1	IDLSERVALKLDQTFPFSLMRRISVFKYVSGSSAERRAAQSRKL
1			NPVPGSYPTQSCHPHLSPSHPVSQTQHASGQKLASWPSCTPGHM
1		1	PTLPPYQPASGLCYVQNHFGPNPTSSSVYPASAGTSLGIQPPTP
1	1	1	VNSPGTVYSGALGTPGAAGSKESSRVPMP
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5569	22	835	QTPCPLAWERGSRSEDISVPGQKPPTCSSFSGMDVGPSSLPHLG

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to first amino acid residue of amino acid residue of amino acid amino acid amino acid sequence ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, (-possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide insertion) LKLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL				
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residue of anino acid sequence (Codon, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible deletion, A-po				
amino acid sequence Codom, /=possible nucleotide deletion, /-possible nucleotide insertion) LKILLILLILIPEGONTOCYGI POMPGIPGAPGROPOLIGOP MGPEGIPATPO REPROGROGREDIACHOROGYMOG POMPGYGA PMGIPGAPGEGENKOKOGOSPUTTROTTOPARSLIERNAYI. TNPOGDYTTSTEKTRICKYRGIYYEVIRGHOROGYMOG PMGYGA PMGIPGAPGEGENKOKOGOSPUTTROTTOPARSLIERNAYI. TNPOGDYTTSTEKTRICKYRGIYYEVIRGHOROGYMOGOSPUTTROTTOPARSLIERNAYI. TNPOGDYTTSTEKTRICKYRGIYYEVIRGHOROGYMOGOSPUTTROTTOTTOPARSLIERNAYI. TNPOGDYTTSTEKTRICKYRGIYYEVIRGHOROGYMOGOSPUTTROTTOTTOPARSLIERNAYI. SSSYSPEGPLIPPO BORROGYMATSTEEDARPRAPGEGGGOVGOTORGREERGGGDY PYEGGYMKVAVLDEDHYP KSPSIGPOWGOTORGREERGGGDY PYEGGYMKVAVLDEDHYP KSPSIGPOWGOTORGREERGGGDY MSSSSPEGRAMDTOVALTECALARY PRI DELAGDAAMTIH RPEKENGAMATATATECALKGEGEOTORGSSESSANSSISPSED ADDMEL SSSYSPERAPPARAPGEGGGOVGOTORGREERGGGDY PYEGGYMKVAVLDEDHYP KSPSIGPOWGOTORGRERGGGDY PYEGGYMKVAVLDEDHYP KSPSIGPOWGOTORGRERGGGDY PYEGGYMKVAVLDEDHYP KSPSIGPOWGOTORGRERGGGDY PYEGGYMKVAVLDEDHYP KSPSIGPOWGOTORGRERGGGDY PYEGGYMKVAVLDEDHYP KSPSIGPOWGOTORGRERGGGDY PYEGGYMKVAVLDEDHYP KSPSIGPOWGOTORGRERGGGDY PYEGGYMKVAVLDEDHYP KSPSIGPOWGOTORGRERGGGDY MSSSPEROMENDIA PROTTEGEN TO SINCE THE COLLEGA AMTILM RPEKTOKATATULTINITY SSSIPLOLING THE COLLEGA AMTILM RPEKTOKATATULTINITY SSSIPLOLING THE COLLEGA AMTILM RPEKTOKATATULTINITY SSSIPLOLING THE COLLEGA AMTILM RPEKTOKATATULTINITY SSSIPLOLING THE COLLEGA AMTILM RPEKTOKATATULTINITY SSSIPLOLING THE COLLEGA AMTILM RPEKTOKATATULTINITY SSSIPLOLING THE COLLEGA AMTILM RPEKTOKATATULTINITY THE SSSIPLOLING THE COLLEGA AMTILM RPEKTOKATATULTINITY THE SSSIPLOLING THE COLLEGA AMTILM RPEKTOKATATULTINITY THE SSSIPLOLING THE COLLEGA AMTILM RPEKTOKATATULTINITY THE SSSIPLOLING THE COLLEGA AMTILM RPEKTOKATATULTINITY THE SSSIPLOLING THE COLLEGA AMTILM RPEKTOKATATULTINITY THE SSSIPLOLING THE COLLEGA AMTILM REGISTANT THE COLLEGA AMTILM REGISTANT THE COLLEGA AMTILM REGISTANT THE COLLEGA AMTILM REGISTANT THE COLLEGA AMTILM REGISTANT THE COLLEGA AMTILM REGISTANT THE COLLEGA AMTILM REGISTANT THE COLLEGA AMTILM REGISTANT THE COLLEGA AMTILM REGISTANT THE COLLEGA AMTILM				
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RWGRRGLGAGAGAGESPATSLERMKKRDFSLEQLRQYDGSRNP RILLAVNGKVPDVTKGSKFYGPAGPYGTAGRDASRGLATFCLD KDALRDEYDDLSDLNAVQMSSVERWEMGPKEKTYDYVGRLLKPGE EPSEYTDEEDTKDHNKQD VPARTPNAEDQGPEARAATATPCQSGGRERAGEAAEDGVKMAAF SEMGVMPELAQAVEMDWLLPTDIQAESIPLILGGDVLMAAET GSCKTGAFSIPVIQIVVETLKDQQECKKGKTTIKTGASVLINKMQ MNYPDBGSAFATGSDGLCQSREVHGGCATKGLMKGKHYYE VSCHDQGLCRVGWSTMQASLDLGTDKFGFGFGGTGKKSHNKQFD NYGEBFTMHDTIGCYLDIDKGHVKFSKNKKDLGLAFEIPPHMKN QALPPACVLKNAELKFNFGEEEFKFPFKDGFVALSKABEDGYIVN SQHSGRAQVTDTKFLDPAAPKALIVEPSRELARGTLINNIKOPKKY SQHSGRAQVTDTKFLDPAAPKALIVEPSRELARGTLINNIKOPKKY IDNPKLRELLIIGGVAARDQLSVLENGVDTVVGTPGRLDDLVST GKINLSQVRFLVLDEADGLLSQGYSDFINRHNQIPQVTSDGKK LQVIVCSATLHSFDVKKLSKIMHPFTWOLKGEDSVPDTVHHV VVPVNPKTDRLWERLGKSHIRTDDVAAKDNTRPGANSPEMMSEA IKILKGBYAVARAIKEHMMQAIIFCRTKIDCUNLEQYFIQQGGG PDKKGHGFSCVCLHGDRKPHERKQNLERFKKGVFFLICTDVAA RGIDIHGVPYVINVTLPDEKQNYVHRIGRVGRARRMGLAISLVA RGIDHGVPYVINVTLPDEKQNYVHGIGRVGRARRMGLAISLVA RGIDHGVPYVINVTLPDEKQNYVHGIGRVGRARRMGLAISLVA RGIDHGVPYVINVTLPDEKQNYVHGIGRVGRARRMGLAISLVA RGIDHGVPYVINVTLPDEKQNYVHGIGRVGRARRMGLAISLVA RGIDHGVPYVINVTLPDEKQNYVTYGQKRAAGGGSYKGHVDIL APTVQELAALEKEAQTSFLHLGFLUPNDLFRTF 5574 1731 952 NEGLEVFKRQELQPEDKGAVFEDASTERSAMSLGLQLVGYILG LLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMMECATHS TGTTQCDIYSTLLGLPADIQAAMVTTSAISLACIISVVGM RCTVFCQESRAKDRVAVAGGVFFILGGLLGFIPVAMMLHGILRD FYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSCQRN RNYDAVQAQPLATRSSRPRQPPKVKSERNSVLTGVV SPLTGCSCCQRN RNYDAVQAQPLATRSSRPRQPPKVKSERNSVLTGVV LLGAMLLTASFSAQAHKSLLKGNDPLLSQCAVGCLEALLDYLDAR SPDIGRNSPHYLMFP 5575 456 766 LLMADFCPPFTAAAVLLSSTGIMELLEKMLALITLAKADSSPTTAL LCSAMLLTASFSAQAHKSLLKGNHVLDLLILEAMNNLRDSNPKLQIRAPBA QTLPSINQSCLPGFYTPAELKPVMSLORSGLGFLFFPBECV DKFRRFRPHLKSLUSRKHVHLDLILEAMNNLRDSNPKLQIRAPBA QTLPSINQSCLPGFYTPAELKPVMSCLRFRGFBDTISTPBECV DKFRRFRPHLKSLUSRKHVHLDLILEAMNNLRDSRPKLQIRAPBA QTLPSINQSCLPGFYTPAELKPVVSCRIGSGPTRPPECV DKFRRFRCPPLATTSUIVFNHRAMSTLLPTVYSVLHTTPAILLK EITLUDDASTEEHLKELBGYVKQLGVVRVXVRQERRKGLITARL LGASVAQAEVLTFILDAHCECFHGWLEPLLARIBERKTVVVSPDI VTIDLNTFFFAKPVQRGRVHSRGNEPWSLTTGWSTLPPHEKQRF	5572	2802	2085	
RILLAVNGKVPDVTKGSKKYQPAGPYGIFAGRDASRGLATFCLD KDALRDBYDDLSDLNAVQMESVREWMQFKKYDYVGRLLKPGE EPESYTDEBDTKDHNKQD VPARTPNAEDQGPEARAATATFCQSGGRERAGEAAEDGVKMAAF SEMGVMPEIAQAVERDMILLPPDTQABSIPLILGGGDVLMAAET GSGKTGAFSIPVIQIVYETLKDQQEGKKGKTTIKTGASVLNKKQ MNYDBGSAFAIGSDGLCCQSREVKEHHGCATKGLMKGHYYE VSCHQGQLCRVUWSTMQASLDLFNFOFGFGFGFKSKHNKQFD NYGEBFTMHDTIGCYLDIDKGHVKFSKNGKDLGLAFEIPHMKN QALFPACVLKNAELKFNFGEEFKFPFKDGFVALSKAPDGYIVK SQHSGAAQVTQTKFLPNAPKALIVEPSRELAEQTLNNIKQFKKY IDMPKLRELLIIGGVAARDQLSVLENGGVDIVVGTPGRLDDLVST GKLNLGQVKFLVLDBADGLLSGGYSDFINNHNQIPQVTSDGKR LQVIVCSATLHSPDVKKLSEKIMHFPTWVDLKGEDSVPDTVHHV VVPVNRKTDRLMERLGKSHIRTDDVHAKDNTRPGANSPEWMSEA IKILKGSYAVRAIKEHMVDQAITFCRTNIDDDHSQYFIQGGG PDKKGROFSCVCLHGDRKPHERKQNUERFKKGDVFLILCTDVAA RGIDHGVPYVINVTLPDEKQNTVYHRIGRVGRAERGGLAISLVA TEKEKWYHVSSRGKGCYNTRLKEDGGCTIWNEMQLLSEIBE HLNCTISQVEPDIKVPVDBFDGKTYGQKRAAGGGSYKGHVDIL APTVQELAALEKEACOTSLHLAJDQLFRTP 5574 1731 952 NEGLEVFKEQELQPEDKGAVPEDASTERSAMASLGLQLVGYILG LLGLLGTLVAMLLPSWKTSSYVGASIVTAUGFSKGLWECATHS TGTQCDIYSTLLGJLAPDIQAAQAMMTYSGAISLAGIISVVSM RCTYFCQESRAKDRVAVAGGVFFILGGLLGFIPVANNLHGILRD FYSPLVPDSMKFEIGEALYLGIISLFLGFILGFILFVSCM RCTYFCQESRAKDRVAVAGGVFFILGSLLGFIPVANNLHGILRD FYSPLVPDSMKFEIGEALYLGIISLFLGFILGFILFVSCCRN RSNYYDAYQAQLATRSSPRFQQPKVKSEFNSYSLTGVV LCSAWLLTASFSAQQHKGSLQXDPLLSQACVGCLEALLDYLDAR SPDIGRNSPHYLMFF 5576 249 2146 RSNGAPWFRIKELLERRIMPLRLAWVGGAPVFLFLFLHRDVSSR EEATBERPHLKSLVSKROHVLDHLEAMNILRDSMPKLQTRAPPA QQTLFSINQSCLPGFYTPAELKFMFRPQDPNAPGADGKAFQK SKMTPLETQEKEGYKKICFHAFASDRISLGREIGFDTRPECV DOKFRRCPPLATTSVILVPHMEAMSTLLERTJSVLYLTHTPAILLK EILUDDASTEPHLKENLBGVYKQLQVVRVURQEERKGLITARL LGASVAQAEVLTFLDAHCECFHGWLEPLLARTABSDTVJVSPDI VTIDLNTFFFAKPUQGGRUNSRGFFDBSLTFGGWETLPPHEKGRR				
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EPSEYTDEEDTKDHHKOD VPARTPNAEDQGPEARAATATPCQSGGRERAGEAAEDGVKMAAF SEMGVMPEIAQAVEEMDHILDTDIQAESIPLILGGGDVLMAAET GSGKTGAFSIPVIQIVYETLKDQQEGKKGKTIKTGASVLINKWQ MNFYDRGSAFAIGSDGLCQSREVKEWHGCRATKGIMKGKHYYE VSCHDQGLCRVWSTMQASLDLGTDKFOFGFGGTGKKSHNKQFD NYGEEFTMHDTIGCYLDIDKGHVKFSKNGKDLGLAFEIPPHMKN QALFPACVLKNAELKFNFGEEFKFPPKDGFVALSKAPDGYIVK SQHSGAQAVQTYKFLPNAPKALIVEPSRELAEQTLNNIKQFKKY IDMFKLRELLIIGGVAARDQLSVLENGYDIVVGTPGRLDDLVST GKLNLSQVRFLVLDEADGLLSQGYSDFINRMHNQIPQVTSDGKR LQVIVCSATLHSFDVKKLSEKIMHFPTWVDLKGEDSVPDTVHHV VVPVNPKTDRLWERLGKSHIRTDDVHAKDYTRFQANSPEMMSEA IKILKGSYAVRAIKEHKMDQAIIFCTKKIDCDNLEQYFIQQGG PDKKGHOFSCVCLHGDRKPHEKKONLEFKKGDVRFLICTDVAA RGIDIHGVPYVINVTLPDEKONYVHRIGRVGRAERMGLLSILVA TEKEKVWYHVCSSRGKGCYNTRLKEDGGCTIWYNEMQLLSEIEE HLKCTISQVEPDIKVPVDEFFDGKVTYGQKRAAGGGSYKGHVDIL APTVQELAALEKEAGTSFIHLGVLPNQLFRFF 5574 1731 952 NEGLEVFKEQELQPEDKGAVPEDASTERSAMASLGLQLVGYILG LGLLGTLVAMLLPSWKTSSVVGASIVTAVGFSKGLMMECATHS TGITQCDIVSTLLGLPADIQAAQAMMTSSAISSLACIISVVGM RCTVFCQESRAKDRVAVAGGVFFILGGLLGPIPVANNLHGILRD FYSPLVPDSMKFEIGEALYLGIISSLFSLILGIILCFSCSCQRN RSNYYDAYQAQFLATRSSPRFQQPFKVKSEFNSYSLTGVV LUMALPCPPPTAAAVLLSSTGLMELLEKMLALTLAKADSPRTAL LCSAMLLTASFSAQQHKGSLQKDPLLSQACVGCLEALLDYLDAR SPDIGRNSPHYLMFP 5576 249 2146 RSWGAPWFWRMELERRRMPLRLAMVGCAFVLFIFLLHRDVSR EEATEKPMLKSLVSKKOHVUDLMLEAMNNLRDSMPKLQIRAPEA QQTLFSINGSCLPGFYTFAELKPERPPPDPAAGAGKAFQK SKWTPLETQEKEEGYKKHCFNAFASDRISLGRSLGPDTRPPECV DOKFRECPPLATISVIIVFNHEAMSTLLRTVYSVLHTTPAILLK EIILVDDASTEBHLKEKLBQVVKQLQVVRVQCEERKGLITARL LGASVAQAEVLTFLDAHCECFHGWLEBPLLARIABBCKTVVVSPDI VTIDLNTFFFAKPVQRGRVHSRGMFDWSLTFGGWETLPPHEKKRR				RILLAVNGKVFDVTKGSKFYGPAGPYGIFAGRDASRGLATFCLD
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SEMGVMPEIAQAVEEMDWLLPTDIQAESIPLILGGGDVLMAAET GSCKTGAFSIPVIQIVYETLKDQQECKKGKTITKTASVINKWQ MNYPDRGSAFAIGSDGLCCQSREVKEWHGCRAFKGLMKKCHYYE VSCHDQGLCRVGWSTMQASLDLGTDKFGPGFGGTGKKSHNKQFD NYGEETMHDTIGCYLDIDKGHVFSKNGKDLGLAFEIPPHMRN QALPPACVLKNAELKENFGGEFEKFPPKDGFVALSKAPDGYIVK SQHSGNAQVTQTKFLPNAPKALIVEPSRELAEQTLNNIKQFKKY IDNPKLRELLIIGGVAARDQLSVLENGVDIVVGTPGRLDDLVST GKLNLSQVRFLVLDEAGGLLSQGYSDFINRMHNQIPQVTSDGKR LQVIVCSATLHSFDVKKLSEKIMHPPTWVDLKGEDSVPDTVHHV VVPVNFKTDRLMERLGKSHIRTDDVHAKDNTRPGANSPEMMSEA AIKILKGGSYAVARIKEHKMDQAIIFCRTKTLDCDNLSQYFIQGGG PDKKGHOFSCVCLHGDRKPHERKQNLERFKKGDVRFLICTDVAA RGIDIHGVPYVINVTLPDEKQNYVHRIGRVGRAERGLAISLVA TEKEKWYHVGSSRGKGCVNTRILKEDGGCTIWNEMQLLSEIEE HLNCTISQVEPDIKVPVDEFDGKVTYGQKRAAGGGSYKGHVDIL APTVQELAALEKEAQTSFHLHGVLENDLPRTF JEGLEVFKSEGLOFEDKGAVPEDASTERSMASLGLQLVGYILG LGGLEVFKSEGLOFEDKGAVPEDASTERSMASLGLQLVGYILG LGGLEVFKSEGLOFEDKGAVPEDASTERSMASLGLICLVVGM RCTVFCQESRAKDRVAVAGGVFILGGLLGFTPAVANHLGILRD FYSPLVPDSMKFEIGBALYLGIISSLFSLIAGIILCFSCSCQRN RSNYDAYQAQVLATTASSPRGQPPKVKSEFNSYSLTGVV SSTYLDAYQAQVLATTASSPRGQPPKVKSEFNSYSLTGVV LCSAWLLTASFSAQQHKGSLQKDPLLSQACVGCLEALLDYLDAR SPDIGRNSPHYLMFP SPDIGRNSPHYLMFP SPDIGRNSPHYLMFP SPDIGRNSPHYLMFP SPDIGRNSPHYLMFP SPDIGRNSPHYLMFP SPDIGRNSPHYLMFP SPDIGRNSPHYLMFP SPDIGRNSPHYLMFP SSWGAPWFWRMRLLRRRHMPLRLAMVGCAFVLFLFLLHRDVSSR EEATEKPHLKSLVSRKDHVLDLMLEAMNNLRDSMPKLQIRAPEA QQTLFSINGSCLFGFYTPAELKFFMERPPQDPNAPGADGKAPCK SKWTPLETQEKEGGYKKHCFNAFASDRISLQRSLGPDTRPPECV DOKFRCPPLATTSVIIVFNBRASSTLLRTVSVSUHTTPAILLK EIILVDDASTEEHLKRLBCYVCDLGVVRVVRQEERKGLITARL LGASVAQAEVLFILDAHCECFHGWLEPLLARIBDKTVVVSPDI VTIDLNTFEFAKFVQRGRVHSRSNPTWSSTFGWETLPPHEKQRR		4.00	4.5	EPSEYTDEEDTKDHNKQD
GSGKTGAFSIPVIQIVYETLKDQQEGKKGKTTIKTGASVLNKWQ MNYYDRGSAFAIGBGLCQSREVKEWIGGCRATKGLMKGKHYYE VSCHDQGLGKWGSTMQASJDLGTDKFGFGFGTGKKSKNKKQFD NYGEEFTMHDTIGCYLDIDKGHVKFSKNGKDLGLAFEIPPHMKN QALFPACVLKNAELKFFFGEEFFKFPFDGFVALSKAPDGYIVK SQHSGNAQVJOTKFLPHAPKALIVEPSRELABQTLNNIKQFKKY IDNPKLRELLIIGGVAARDQLSVLENGVDIVVGTFGRLDDLVST GKLNLSQVRFLVLDEADGLLSQGYSDFINRHNQIPQVTSDGKR LQVIVCSATLHSFDVKKLSEKIMHPFTWVDLKGEDSVPDTVHHV VVPVNRTDRLWERLGKSHIRTDDVHAKDNTRPGANSPEMMSEA IKILKGBYAVRAIKEHKMDQAIIFCRTKIDCDNLBQYFIQQGG PDKKGHQFSCVCLHGDRKPHERKQNLERFKKGDVRFLICTDVAA RGIDIHGVPVINVTLPDEKQNYVHRIGRVGRAERMGLAISLVA RGIDIHGVPVINVTLPDEKQNYVHRIGRVGRAERMGLAISLVA TEKEKWYHVCSSRGKGCYNTRLKEDGGCTIHYNBMQLLSEIEE HLNCTISQVEPDIKVPVDEFFDKVTYGQKRAAGGGSYKGHVDIL APPTVGLAALEKEAQTSFHLIGVLPNOLPRTF 5574 1731 952 NEGLEVFKEQELQPEDKGAVPEDASTERSAMASLGLQLVGYILG CLGLLGTLVAMLLPSWKTSSYVGASAISSLACIISVVGM RCTVFCQESRAKDRVAVAGGVFFLIGGLLGFIPVAWNLHGILRD FYSPLVPDSMKFFLIGBALYIGIISSLFSLIAGIILGFSCSCQRN RSNYYDAYQAQPLATRSSPRGQPPKVKSEFNSYSLTGYV 5575 456 766 LLMALPCPPPTAAAVLLSSTGLMELLEKMLALITLAKADSPRTAL LCSAWLLTASFSAQOHKGSLQKDPLLSQACVGCLEALLDYLDAR SPDIGRNSPHYLMFP 5576 249 2146 RSWGAPWFWEMELLRREHMPLRLAWVGCAFVLFLFLLHRDVSSR EEATEKPWLKSLVSRKDHVLDLMLEAMNNLRDSMPKLQIRAPEA QQTLFSINGSCLPGFYTPAELKPFWERPPQDPNAPGADGKARQK SKMTPLETGEKEGSYKYNFARPASDRISLGRSLGPDTRPPECV DOKFRRCPPLATTSVIIVFHNEAWSTLLRTYYSVLHTTPAILLK EIILVDDASTEEHLKEKLBQYVKQLQVVRVQRQERKGLITARL LGASVAQAEVLTFLDAHCECFHGWLEPLLARIABBKTVVVSPDI VTIDLNTFFFAKPVQRGRVHSRGNFDMSLTFGMSTLPPHEKQRR	5573	2562	219 .	VPARTPNAEDQGPEARAATATPCQSGGRERAGEAAEDGVKMAAF
MNFYDRGSAFAIGSDGLCCQSREVKEWHGCRATKGLMKGKHYYE VSCHDQGLCRVGWSTMQASLDLGTDKFGFGFGGTCKKSHNKQFD NYGEBFTMHDTIGCYLDIDKGHVKFSKNGKDLGLAFEIPPHMKN QALFPACVLKNAELKFNFGEEEFKFPPKDGFVALSKAPDGYIVK SQHSGNAQVTQTKFLPNAPKALIUFSRELABQTINNIKQFKKY IDMPKLRELLIIGGVARADQLSVLENGYDIVVGTFGRIDDLVST GKLNLSQVRFLVLDEADGLLSQGYSDFINRHNQIPQVTSDGKR LQVIVCSATLHSFDVKKLSEKIMHFPTWDLKGBDSVPDTVHHV VVPVNPKTDFLWERLGSKINTEDDVHAXDNTRPGANSPBMWSEA IKILKGEYAVRAIKEHKMDQAIIFCRTKIDCDNLEQYFIQQGGG PDKKGHOFSCVCLHGDRKPHERKGNLERFKKSDVSFLICTDVAA RGIDIHGVPVINVTLPBEKQNYVHRIGRVGRAERMGLAISLVA TEKEKVWYHVCSSRGKGCYNTRLKEDGGCTIWYNEMQLLSEIEE HLNCTISQVSPDIKVPVDEFDGKVTYGQKRAAGGGSYKGHVDIL APTVQELAALEKAQTSFLHLGYLPNQLPRTF 5574 1731 952 NEGLEVFKEQELQPEDKGAVPEDASTERSAMASLGLQLVGYILG LGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMMECATHS TGITQCDIYSTLLGLPADIQAAQAMMVTSASISSLACIISVVGM RCTVFCQESRAKDRVAVAGGVFFILGGLLGFIPVAWNLHGILRD FYSSLVPDSNKFEIGEALYLGIISSLFSLIAGIILCFSCSCQRN RSNYYDAYQAQPLATRSSPRPQOPPKVKSEPNSYSLTGYV LCSAWLLTASFSAQQHKGSLQKDPLLSQACVGCLEALLDYLDAR SPDIGRNSPHYLMFF 5576 249 2146 RSNKAPPFWARVLLRRRRMPDRLAMVGCAFVLFLFLLHRDVSSR EEATEKPWLKSLVSRKDHVLDLMLEAMNNLRDSMPKLQIRAPEA QQTLFSINGSCLPGFYTPAELKPWBRPPQDPNAPGADGKARQK SKMTPJETQEKEEGYKKHCANFASDRISLQRSLGPDTRPPECV DOKFRRCPPLATTSVIIVFINEAMSTLLRTYYSVLHTTPAILLK EIILVDDASTEEHLKEKLBQYVKQLQVVVVQRGERKGLITARL LGASVAQAEVLTFLDAHCECFHGWLEPLLARIABBCKTVVVSPDI VTIDLNTFETAKPVQRGRVHSRGNFDMSLTFGWSTLPPHEKQRR		1		SEMGVMPEIAQAVEEMDWLLPTDIQAESIPLILGGGDVLMAAET
VSCHDQGLCRVGWSTMQASLDLGTDKFGFGFGGTGKKSHNKQFD NYGEFFTMHDTIGCYLDIDKGHVKFSKNGKLDLGLAFFLTPHHKN QALFPACVLKNAELKFNFGEEBFKFPP KDGFVALSKAPDGYIVK SQHSGNAQVTQTKFLPNAPKALIVEPSRELABQTLNNIKQFKKY IDMFKLRELLIIGGVAARDQLSQUSDFINRHHNQIPQVTSDGKR GKLNLSQVRFLVLDBADGLLSQGYSDFINRHHNQIPQVTSDGKR LQVIVCSATLHSFDVKKLSEKIMHFPTWVDLKGBDSVPDTVHHV VVPVNPKTDRLMERLGKSHIRTDDVRAKDNTRPGANSPEMWSEA IKILKGSYAVRAIKEHKNDQAIIFCRTKJDCDNLEQYFIQQGG PDKKGHOFSCVCLHGDRKPHERKQNLERFKKGDVFLICTDVAA RGIDIHGVPYVINVTLPDBKQNYVHRIGRVGRAERGGSYKGHVDIL APTVQELAALEKEAQTSFLHLGYLPNQLPRTF 5574 1731 952 NEGLEVFKCQELQPEDKGAVPEDDASTERSAMASLGLQLVGYILG LLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGMMECATHS TGTTQCDIYSTLLGLPADIQAAQAMWYTSSAISSLACTISVVGM RCTVFCQESRAKDRVAVAGGVFFILGGLLGPIPVAWNLHGILRD FYSFLYDDSMKFEIGEALYLGIISSLFSLLAGIILCFSCSCQN RSNYYDAYQAQPLATRSSPRFGQPPXVKSEFNSYSLTGYV 5575 456 766 LLWALPCPPPTAAAVLLSSTGIMELLEKMLALTLAKADSPRTAL LCSAWLLTASFSAQQHKGSLQKDPLLSQACVGCLEALLDYLDAR SPDIGRNSPHYLMFP 5576 249 2146 RSWGAPWFWRRLLRRRRMPLRLAMVGCAFVLFLFLLHRDVSSR EEATEKPMLKSLVSRKDHVLDLMLEAMNNLRDSMPKLQIRAPEA QQTLFSINQSCLPGFYTPAELKFMERPPDRADGAGKAFQK SKMTPLETQEKEEGYKKHCFNAFASDRISLQRSLGPDTRPPECV DQKFRCPPLATTSVIIVFHNEAWSTLLRTVYSVLHTTPAILLK EIILVDDASTEEHLKEKLBQYVKQLQVVRVVRQEERRGLITARL LGASVAQAEVLTFLDAHCECFHGWLEPLLARIABDKTVVVSPDI VTIDLNTFEFAKFVQRGRVHSRGNFDWSLTFGMETLPPHEKQRR				GSGKTGAFSIPVIQIVYETLKDQQEGKKGKTTIKTGASVLNKWQ
NYGEEFTMHDTIGCYLDIDKGHVKFSKNGKDLGLAFEIPPHMKN QALPPACULKNAELKFNFGEEBEFKFPF KOGFVALSKAPDGYIVK SQHSGNAQVOTTKFLPNAPKALLVEPSRELABGYLINIKQFKKY IDNPKLRELLIIGGVAARDQLSVLENGVDIVVGTPGRLDDLVST GKLNLSGVRFLVLDEADGLLSGGYSDFINRMHNQIPQVTSDGKR LQVIVCSATLHSFDVKKLSEKIMHFPTWVDLKGEDSVPDTVHHV VVPVNPKTDRLWERLGKSHIRTDDVARKDNTRPGANSPEMWSEA IKILKGEYAVRAIKEHKMDQAIIFCRTKIDCDNLEQYFIQQGGG PDKKGHOFSCVCLHGDRKPHERKQNLEFFKKGDVRFLICTDVAA RGIDIHGVPYVINVTLPDEKQNYVHRIGRVGRAERMGLAISLVA TEKEKWYHVCSSRGKGGYNTRLKEDGGCTIWYMEMGLLSEIEE HLNCTISQVEPDIKVPVDBFDGKVTVGQKRAAGGGSYKGHVDIL APTVQELAALEKEAQTSFLHLGYLPNQLFRTF 5574 1731 952 NEGLEVPFEQBLQPEDKGAVPEDASTERSAMASLGLQLVGYILG LLGLLGTLVANLLPSWKTSSYVGASIVTAVGFSKGLMMECATHS TGITOCDIYSTLLGJPADIQAQAMMYTSSAISSLACTISVVGM RCTVFCQESRAKDRVAVAGGVFFILGGLLGFIPVAWNLHGILRD FYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSCQRN RSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV 5575 456 766 LLWALPCPPPTAAAVLLSSTGLMELLEKMLALTLAKADSPRTAL LCSAWLLTASFSAQQHKGSLQKDPLLSQACVGCLEALLDYLDAR SPDIGRNSPHYLMFF 5576 249 2146 RSWGAPWFWRMLLRRRHMPLRLAMVGCAFVLFLFLLHRDVSSR EEATEKFWLKSLVSRKDHVLDLMLEAMNNLRDSMPKLQIRAPEA QQTLFSINQSCLPGFYTPAELKPERPPQDPNAPGADGKAFQK SKMTPLETGEKEEGYKKHCFNAFASDRISLQRSLGPDTRPPECV DQKFRCPPLATTSVIIVFHNEAWSTLLRTVYSVLHTTPAILLK EIILVDDASTEEHLKEKLBGYVKQLQVVRQVVRQVERGERGLITARL LGASVAQAEVLTFLDAHCECFHGWLEPLLARIABDKTVVVSPDI VTIDLNTFEFAKPVQRGRVHSSRUFDWSLTFGWBTLPPHEKQRR			1	MNPYDRGSAFAIGSDGLCCQSREVKEWHGCRATKGLMKGKHYYE
QALPPACVLKNAELKFNFGEEEFKFPP KDGFVALSKAPDGYIVK SQHSGNAQVTOTKFLPNAPKALIVEPSRELABGOTLNNIKQFKKY IDNPKLRELLI IGGVAARDQLSVLENGVDIVVGTPGRLDDLVST GKLNLSQVRFLVLDEADGLLSQGYSDFINRMINQIPQVTSDCKR LQVIVCSATLHSFDVKKLSEKIMHPPTWVDLKGEDSVPDTVHHV VVPVNPKTDRLWERLGKSHIRTDDVHAKDNTRPGANSPEMWSEA IKILKGSYAVRAI KEHKMDQAIIFCRTKIDCUNLBQYFIQQGGG PDKKGHQFSCVCLHGDRKPHERKQNLERFKKGDVRFLICTDVAA RGIDIHGVPYVINVTLPDEKQNYVHRIGRVGRAERMGLAISLVA TEEKKVWHVCSSRGGGYTNTRLKEDGGCTIWYNEMGLLSEIEE HLNCTISQVEPDIKVPVDEFDGKVTYGQKRAAGGGSYKGHVDIL APTVQELAALEKEAQTSFLHLGYLPNQLFRTF 1731 952 NEGLEVFKEQELQPEDKGAVPEDASTERSAMASLGLQLVGYILG LLGLLGTLVANHLPSKKTSSYVGASIVTAVGFSKGLWMECATHS TGITQCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGM RCTVFCQESRAKDRVAVAGGVFFILGGLLGFIPVAWHLHGILRD FYSPLVPDSMKFEIGEALYGIISSLFSLIAGIILCFSCSCQRN RSNYYDAYQAQPLATRSSRPGQPPKVKSEFNSYSLTGVV 5575 456 766 LLWALPCPPPTAAAVILSSTGLMELLEKMLALTLAKADSPRTAL LCSAWLLTASFSAQHKGSLQKDPLLSQACVGCLEALLDYLDAR SPDIGRNSPHYLMFP 5576 249 2146 RSWGAPWFWRMLLRRRHMPLRLAMVGCAFVLFLFLLHRDVSSR EEATEKPWLKSLVSRKDHVLDLMLEAMMNLRDSMPKLQIRAPEA QQTLFSINQSCLPGFYTPAELKFFWERPPQDPNAPGADGKAFQK SKMTPLETGEKEEGYKKHCFNAFASDRISLQSSLGFDTRPPECV DQKFRRCPPLATTSVIIVPHNEAWSTLLRTVYSVLHTTPAILLK EIILVDDASTEEHLKEKLBGYVKQLGVVRVVQGEEKRGLITARL LGASVAQAEVLTFLDAHCECFFIGWLEPILLARIABDKTVVVSVPDI VTIDLNTFEFAKPVQRGRVHSRGNFDWSLTFGWETLPPHEKQRR				VSCHDQGLCRVGWSTMQASLDLGTDKFGFGFGGTGKKSHNKQFD
SQHSGNAQVTQTKFLPNAPKALIVEPSRELAEQTLNNIKQFKKY IDMPKLRELLIIGGVAARDQLSVLENGVDIVVGTPGRLDDLVST GKLNLSQVRFLVLDEADGLLSQGYSDFINRMHNQIPQVTSDGKR LQVIVCSATLHSFDVKKLSEKIMHPFTWYDLKGEDSVPDTVHHV VVPVNPKTDRLWERLGKSHIRTDDVHAKDNTRPGANSPEMWSEA IKILKGSYAVRAIKEHKMDQAIIFCRTKIDCDNLEQYFIQQGG PDKKGHQFSCVCLHGDRKPHERKQNLERFKKGDVRFLICTDVAA RGIDIHGVPYVINVTLPDEKQNYVHRIGRVGRAERMGLAISLVA TEKEKVWHVCSSRGKGCYNTRLKEDGGCTIWYNEMQLLSEIEE HLNCTISQVEPDIKVPVDEFDGKVTYGQKRAAGGGSYKGHVDIL APPTVQELAALEKEAQTSFLHLGYLPNQLFRTF LLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHS TGITQCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGM RCTVFCQESRAKDRVAVAGGVFFILGGLLGFIPVAWNLHGILRD FYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSCQRN RSNYDAYQAQOPLATRSSRPGQPPKVKSEFNSYSLTGYV 5575 456 766 LLWALPCPPTAAAVLLSSTELMELLEKMLAITLAKADSPRTAL LCSAWLLTASFSAQOHKGSLQKDPLLSQACVGCLEALLDYLDAR SPDIGRNSPHYLMFP 5576 249 2146 RSWGAPWFWRRLLRRRHMPLRLMWGCAFVLFLFLLHRDVSSR EEATEKPHLKSLVSRKDHVLDLMLEAMMNLRDSMPKLQIRAPEA QQTLFSINQSCLPGFYTPABLKPFWERPPQDPNAPGADGKAFQK SKMTPLBTQEKEEGYKKHCFNAFASDRISLQRSLGFDTRPPECV DQKFRCCPPLATTSVIIVFHNEAWSTLLRTVYSVLHTTPAILLK EIILVDDASTEEHLKEKLBGVYKQLGVVRVQCEEKKGLITARL LGASVAQAEVLTFLDAHCECFHGWLEPLLARIABDKTVVVSPDI VTIDLNTFEFAKKPVQRGRVHSRGNFDMSLTFGWBTLPPHEKQRR				NYGEEFTMHDTIGCYLDIDKGHVKFSKNGKDLGLAFEIPPHMKN
IDNPKLRELLIIGGVAARDQLSVLENGVDIVVGTPGRLDDLVST GKKNLSQVRFLVLDEADGLLSGGYSDFINRMINQIPQVTSDSKR LQVIVCSATLHSFDVKKLSEKIMHFPTWVDLKGEDSVPDTVHHV VVPVNPKTDRLWERLGKSHIRTDDVHAKDNTRPGANSPEMMSEA IKILKGEYAVRAIKEHKMDQAIIFCRTKIDCDNLEQYFIQQGGG PDKKGHOFSCVCLHGDRKPHERKQNLERFKKGDVRFLICTDVAA RGIDIHGVPYVINVTLPDEKQNYVHRIGRVGRARGGGSYKGHVDIL AFTVQELAALEKEAQTSFLHLGYLPNQLFRTF HLNCTISQVEPDIKVPVDEFDGKVTYGQKRAAGGGSYKGHVDIL APTVQELAALEKEAQTSFLHLGYLPNQLFRTF LLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHS TGITQCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGM RCTVFCQESRAKDRVAVAGGVFFILGGLLGFIPVAWNLHGILRD FYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSCQRN RSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV 5575 456 766 LLWALPCPPPTAAAVLLSSTGLMELLEKMLALTLAKADSPRTAL LCSAWLLTASFSAQQHKGSLOKDPLLSQACVGCLEALLDYLDAR SPDIGRNSPHYLMFP 5576 249 2146 RSWGAPMFWRMELLRRRHMPLRLAMVGCAFVLFLFLLHRDVSSR EEATEKPNLKSLVSRKDHVLDIMLEAMNNLRDSMPKLQIRAPEA QQTLFSINQSCLPGFTTPAELKPFWRRPPQDPNAPGADGKAFQK SKWTPLETQEKEEGYKKHCFNAFASDRISLQRSLGPDTRPPECV DOKFRCPPLATTSVIIVFHNEAWSTLLRTVYSVLHTTPAILLK EIILVDDASTEEHLKEKLEQVYKQLQVVRVVRQEERKGLITARL LGASVAQAEVLTFLDAHCECFHGWLEPLLARIABDKTVVVSPDI VTIDLNTFEFAKPVQRGRVHSRGNFDWSLTFGWETLPPHEKQRR				QALFPACVLKNAELKFNFGEEEFKFPPKDGFVALSKAPDGYIVK
GKLNLSQVRFLVLDEADGLLSQGYSDFINRMHNQIPQVTSDGKR LQVIVCSATLHSFDVKKLSEKIMHPPTWVDLKGEDSVPDTVHHV VVPVNPKTDRLWERLGKSHIRTDDVHAKDNTRPGANSPEMWSEA IKILKGBVAVRAIKEHKMDQAIIFCRTKIDCDNLEQYFIQQGGG PDKKGHQFSCVCLHGDRKPHERKQNLERFKKGDVRFLICTDVAA RGIDIHGVPYVINVTLPDEKQNYVHRIGRVGRAERMGLAISLVA TEKEKVWYHVCSSRGKGCYNTRLKEDGGCTIWYNEMQLLSEIEE HLNCTISQVEPDIKVPVDEFDGKVTYGQKRARGGGSYKGHVDIL APTVQELAALEKEAQTSFLHLGYLPNQLFRTF 5574 1731 952 NEGLEVFKQELQPEDKGAVPFDASTERSAMASLGLQLVGYILG LLGLLGTLVAMLLPSWKTSSVGASIVTAVGFSKGLWMECATHS TGITQCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGM RCTVFCQESRAKDRVAVAGGVFFILGGLLGFIPVAWNLHGILRD FYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSCQRN RSNYYDAYQAQPLATRSSPREQPPKVKSEFNSYSLTGYV 5575 456 766 LLWALPCPPPTAAVLLSSTGLMELLEKMLALTLAKADSPRTAL LCSAWLLTASFSAQQHKGSLQKDPLLSQACVGCLEALLDYLDAR SPDIGRNSPHYLMFP 5576 249 2146 RSWGAPFFWRMELLRRHMPLRLAMVGCAFVLFLFLLHRDVSSR EEATEKPWLKSLVSRKDHVLDLMLEAMNNLRDSMPKLQIRAPEA QQTLFSINGSCLPGFYTPAELKPFWBRPPQDPNAPGADGKAFQK SKWTPLETQEKEEGYKKHCFNAFASDRISLQRSLGPDTRPPECV DQKFRCPPLATTSVIIVFHNEAWSTLLRTVYSVLHTTPAILLK EIILVDDASTEEHLKEKLBQTVKQLQVVRVVRQEERKGLITARL LGASVAQAEVLFFLDAHCECFHGWLEPLLARIABDKTVVVSPDI VTIDLNTFEFAKPVQRGRVHSRGNFDWSLTFGWBTLPPHEKQRR)		}	SQHSGNAQVTQTKFLPNAPKALIVEPSRELAEQTLNNIKQFKKY
LQVIVCSATLHSFDVKKLSEKIMHPPTWVDLKGEDSVPDTVHHV VVPVNPKTDRLWERLGKSHIRTDDVHAKDNTRPGANSPEMWSEA IKILKGEYAVRAIKEHKMDQAIIFCRTKIDCDNLEQYFIQQGG PDKKGHQFSCVCLHGDRKPHERKQNLERFKKGDVRFLICTDVAA RGIDIHGVPYVINVTLPDEKQNYVHRIGRVGRAERMGLAISLVA TEKEKVWYHVCSSRGKGCYNTRLKEDGGCTIWYNEMQLLSEIEE HLNCTISQVEPDIKVPVDEFDGKVTYGQKRAEAGGSYKGHVDIL APTVQELAALEKEAQTSFLHLGYLPNQLPRTF 5574 1731 952 NEGLEVFKREGLQFEDKGAVYEDASTERSAMASLGLQLVGYILG LLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHS TGITQCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGM RCTVFCQESRAKDRVAVAGGVFFILGGLLGFIPVAWNLHGILRD FYSPLVPDSMKFEIGSALYGIISSLFSLIAGIILCFSCSCQRN RSNYYDAVQAQPLATRSSPRPGQPPKVKSEFNSVSLTGYV 5575 456 766 LLWALPCPPPTAAAVLLSSTGLMELLEKMLALTLAKADSPRTAL LCSAWLLTASFSAQQHKGSLQKDPLLSQACVGCLEALLDYLDAR SPDIGRNSPHYLMFP 5576 249 2146 RSWGAPWFWRMRLLRRRHMPLRLAMVGCAFVLFLFLLHRDVSSR EEATEKPHLKSLVSRKDHVLDLMLEAMNNLRDSMPKLQIRAPEA QQTLFSINQSCLPGFYTPAELKPFWERPPQDPNAPGADGKAFQK SKWTPLETQEKEEGYKKHCFNAFASDRISLQRSLGPDTRPPECV DQKFRRCPPLATTSVIIVFHNEAWSTLLRTVYSVLHTTPAILLK EIILVDDASTEEHLKEKLBQYVKQLQVVRVVRQEERKGLITARL LGASVAQAEVLTFLDAHCECFHGWLEPLLARIABDKTVVVSPDI VTIDLNTFEFAKPVQRGRVHSRGNFDWSLTFGWETLPPHEKQRR				IDNPKLRELLIIGGVAARDQLSVLENGVDIVVGTPGRLDDLVST
VVPVNPKTDRLWERLGKSHIRTDDVHAKDNTRPGANSPEMWSEA IKILKGEYAVRAIKEHKMDQAIIFCRTKIDCDNLEQYFIQQGG PDKKGHQFSCVCLHGDRKPHERKQNLERFKKGDVRFLICTDVAA RGIDIHGVPYVINVTLPDEKQNYVHRIGRVGRAERMGLAISLVA TEKEKVWYHVCSSRGKGCYNTRLKEDGGCTIWYNEMQLLSEIEE HLNCTISQVEPDIKVPVDEFFGKVTVGQKRAAGGSYKGHVDIL APTVQELAALEKEAQTSFLHLGYLPNQLFRTF 5574 1731 952 NEGLEVFKEQELQPEDKGAVPEDASTERSAMASLGLQLVGYILG LLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHS TGITQCDIYSTLLGBLPADIQAAQAMMVTSSAISSLACIISVVGM RCTVFCQESRAKDRVAVAGGVFFILGGLLGFIPVAWNLHGILRD FYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSCQRN RSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV 5575 456 766 LLWALPCPPPTAAAVLLSSTGLMELLEKMLALTLAKADSPRTAL LCSAWLLTASFSAQAHKGSLQKDPLLSQACVGCLEALLDYLDAR SPDIGRNSPHYLMFP 5576 249 2146 RSWGAPWFRMRLLRRHMPLRLAMVGCAFVLFLFLLHRDVSSR EEATEKPWLKSLVSRKDHVLDLMLEAMNNLRDSMPKLQIRAPEA QQTLFSINQSCLPGFYTPAELKPFWERPPQDPNAPGADGKAFQK SKWTPLETQEKEEGYKKHCFNAFASDRISLQRSLGPDTRPPECV DQKFRRCPPLATTSVIIVFHNEAWSTLLRTVYSVLHTTPAILK EIILVDDASTEEHLKEKLBQYVKQLQVVRQVRVVRQEERKGLITARL LGASVAQAEVLTFLDAHCECFHGWLEPLLARLAEDKTVVVSPDI VTIDLNTFEFAKPVQRGRVHSRGNFDWSLTFGWETLPPHEKQRR			1	GKLNLSQVRFLVLDEADGLLSQGYSDFINRMHNQIPQVTSDGKR
IKILKGEYAVRAIKEHKMDQAIIFCRTKIDCDNLEQYFIQQGG PDKKGHQFSCVCLHGDRKPHERKQNLERFKKGDVRFLICTDVAA RGIDIHGVPYVINVTLPDEKQNYVHRIGRVGRAERMGLAISLVA TEKEKVWYHVCSSRGKGCYNTRLKEDGGCTIWYNEMQLLSEIEE HLNCTISQVEPDIKVPVDEFFGKVTYQQKRAAGGSYKGHVDIL APTVQELAALEKEAQTSFLHLGYLPNQLFRTF 5574 1731 952 NEGLEVFKEQELQPEDKGAVPEDASTERSAMASIGLQLVGYILG LLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHS TGITQCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGM RCTVFCQESRAKDRVAVAGGVFFILGGLLGFIPVAWNLHGILRD FYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSCQRN RSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV 5575 456 766 LLWALPCPPPTAAAVLLSSTGLMELLEKMLALTLAKADSPRTAL LCSAWLLTASFSAQAHKGSLQKDPLLSQACVGCLEALLDYLDAR SPDIGRNSPHYLMFP 5576 249 2146 RSWGAPWFMRMTLLRRHMPLRLAMVGCAFVLFLFLLHRDVSSR EEATEKPWLKSLVSRKDHVLDLMLEAMNNLRDSMPKLQIRAPEA QQTLFSINQSCLPGFYTPAELKPFWERPPQDPNAPGADGKAFQK SKWTPLETQEKEEGYKKHCFNAFASDRISLQRSLGPDTRPPECV DQKFRRCPPLATTSVIIVFHNEAWSTLLRTVYSVLHTTPAILLK EIILVDDASTEEHLKEKLBQYVKQLQVVRVVRQEERKGLITARL LGASVAQAEVLTFLDAHCECFHGWLEPLLARLAEDKTVVVSPDI VTIDLNTFEFAKPVQRGRVHSRGNFDWSLTFGWETLPPHEKQRR				LQVIVCSATLHSFDVKKLSEKIMHFPTWVDLKGEDSVPDTVHHV
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LGASVAQAEVLTFLDAHCECFHGWLEPLLARIABDKTVVVSPDI VTIDLNTFEFAKPVQRGRVHSRGNFDWSLTFGWBTLPPHEKQRR	[
VTIDLNTFEFAKPVQRGRVHSRGNFDWSLTFGWBTLPPHEKQRR		}		
KDETYPIKSPIFAGGLFSISKSYFEHIGTYDNQMEIWGGENVEM				
	L	L	J	ADETIFICATION AGGLESISKSYFEHIGTYDNOMETWGGENVEM

	I Book Market	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	beginning	_	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
Ì	location	corresponding	
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
j	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
}	sequence	i	\=possible nucleotide insertion)
	 		SFRVWQCGGQLEIIPCSVVGHVFRTKSPHTFPKGTSVIARNQVR
ł			LAEVWMDSYKKIFYRRNLQAAKMAQEKSFGDISERLQLREQLHC
1		Ì	HNFSWYLHNVYPEMFVPDLTPTFYGAIKNLGTNOCLDVGENNRG
1	{	1	GKPLIMYSCHGLGGNQYFEYTTQRDLRHNIAKQLCLHVSKGALG
1		j	LGSCHFTGKNSQVPKDEEWBLAQDQLIRNSGSGTCLTSQDKKPA
{			MAPCNPSDPHQLWLFV
	 	1275	RNSDCSCGEISVHCLPWVLFILDLKVESSMFCPLKLILLPVLLD
5577	3	12/5	
1	1		YSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTL
1	l .		SPGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLL
1	1	į.	QDVQEADQGTYICEIRLKGESQVFKKAVVLHVLPEEPKELMVHV
1	l		GGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKLRM
1			SVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCS
			IHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIV
			GIVCATILLLPVLILIVKKTCGNKSSVNSTVLVKNTKKTNPEIK
1	J		EKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPV
	1	·	WPSLRSDRNNSLEKKSGGGMPKTQQAF
5578	3	783	AVESMASPGAGRAPPELPERNCGYREVEYWDQRYQGAADSAPYD
55.5		1	WFGDFSSFRALLEPELRPEDRILVLGCGNSALSYELFLGGFPNV
1			TSVDYSSVVVAAMOARYAHVPOLRWETMDVRKLDFPSASFDVVL
1			EKGTLDALLAGERDPWTVSSEGVHTVDQVLSEVSRVLVPGGRFI
			SMTSAAPHFRTRHYAQAYYGWSLRHATYGSGFHFHLYLMHKGGK
		i	LSVAQLALGAQILSPPRPPTSPCFLQDSDHEDFLSAIQL
		1010	RNSGLARGASALARHGGGLAGGVGWDCGACASRCOGVMEGLLTR
5579	3	1540	
[CRALPALATCSRQLSGYVPCRFHHCAPRRGRRLLLSRVFQPQNL
}	1		REDRVLSLQDKSDDLTCKSQRLMLQVGLIYPASPGCYHLLPYTV
	1	Ì	RAMEKLVRVIDQEMQAIGGQKVNMPSLSPAELWQATNRWDLMGK
}	}		ELLRLRDRHGKEYCLGPTHEEAITALIASQKKLSYKQLPFLLYQ
i	1		VTRKFRDEPRPRFGLLRGREFYMKDMYTFDSSPEAAQQTYSLVC
1		ł	DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEFQLPVDIGEDRLA
1		i	ICPRCSFSANMETLDLSQMNCPACQGPLTKTKGIEVGHTFYLGT
i			KYSSIFNAQFTNVCGKPTLAEMGCYGLGVTRILAAAIEVLSTED
1		1	CVRWPSLLAPYQACLIPPKKGSKEQAASELIGQLYDHITEAVPQ
	1	1	LHGEVLLDDRTHLTIGNRLKDANKFGYPFVIIAGKRALEDPAHF
1		Į.	EVWCQNTGEVAFLTKDGVMDLLTPVQTV
5580	1681	450	ADAGTRCIPGFVVPSGAGYSAPAORGRRSSGRMRAAAAPGLTAP
7000	1001	1 730	WRLLOCCELEAGELGMAVPAAAMGPSALGOSGPGSMAPWCSVSS
1		1	GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG
1		1	SPDKTASVFLLEKDRLVKENNYRGHGDSVDOLCWHPSNPDLFVT
1			
1		ì	ASGDKTIRIWDVRTTKCIATVNTKGENINICWSPDGQTIAVGNK
		1	DDVVTFIDAKTHRSKAEEQFKFEVNEISWNNDNNMFFLTNGNGC
		1	INILSYPELKPYQSINAHPSNCICIKFDPMGKYFATGSADALVS
		1	LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA
1		1	EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR
	1		EAGTVKLFGLPNDS
5581	54	947	GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS
	1		CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA
1	}		YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG
	1	1	TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY
		1	SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH
			TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL
	1	1	TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW
5582	5775	2739	
3302	1	1 2/33	EKGLOFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ
1		1	ALVOYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY
1	1		
1	1	1	EKALEDSEKALGLDSES IRALFRKARALNELGRHKEAYECSSRC
1	1		SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG
1	1		TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF
1	1		PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL
1			VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP
			ASFGLVMDPSKKLAASVLDALDPPGPTLDPLDLLPYSETRLDAL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Í	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
			DSFGSTRGSLDKPDSFMEETNSQDHRPPSGAQKPAPSPEPCMPN
			TALLIKNPLAATHEFKQACQLCYPKTGPRAGDYTYREGLEHKCK
l	1		RDILLGRLRSSEDQTWKRIRPRPTKTSFVGSYYLCKDMINKQDC
) .		KYGDNCTFAYHQEEIDVWTEBRKGTLNRDLLFDPLGGVKRGSLT
{	İ		IAKLLKEHQGIFTFLCEICFDSKPRIISKGTKDSPSVCSNLAAK
}	}		HSFYNNKCLVHIVRSTSLKYSKIRQFQEHFQFDVCRHEVRYGCL
1	[REDSCHFAHSFIELKVWLLQQYSGMTHEDIVQESKKYWQQMEAH
	1		AGKASSSMGAPRTHGPSTFDLQMKFVCGQCWRNGQVVEPDKDLK
	ļ		YCSAKARHCWTKERRVLLVMSKAKRKWVSVRPLPSIRNFPQQYD
1	1		LCIHAQNGRKCQYVGNCSFAHSPEERDMWTFMKENKILDMQQTY
ĺ			DMWLKKHNPGKPGEGTPISSREGEKQIQMPTDYADIMMGYHCWL
ł	ł		CGKNSNSKKQWQQHIQSEKHKEKVFTSDSDASGWAFRFPMGEFR
			LCDRLQKGKACPDGDKCRCAHGQEELNEWLDRREVLKQKLAKAR
			KDMLLCPRDDDFGKYNFLLQEDGDLAGATPEAPAAAATATTGE
5583	3	1265	SSGCROGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE
1			IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD
	ļ		QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV
			HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL
1			CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC
1			SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDOEPELEPGDVI
1			IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
1			LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIOFLVIF
			PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEON
<u> </u>	·		WRQHREAYEEDEDGPQAGVQCQTA
5584	3	1265	SSGCROGRPGRSDRPRPPPPRRHKMVKETRYYDILGVKPSASPEE
} /			IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD
			QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV
1 (HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL
		·	CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC
			SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI
1 1			IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
1 1	ſ		LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLRKGILIIQPLVIF
1 1			PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN
5585	2619	915	WRQHREAYEEDEDGPQAGVQCQTA
1	2017	212	LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM
j			YHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQMLCQRHRRKS
[i	-	İ	SVTDSFSSLVNRPTLGQFTEEEIHAEVCYAKCLLQRAALTFLQD
1 1			ENMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG
l i	•	į	VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEEAEKLLKPYLNR
) [1	,	YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM
1 1	ļ		CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL
	1	}	SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS
[l	ŀ	RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK
	[ſ	AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS
	}		ISANEKKIKYDHYLIPNALLELALLIMEQDRNEEAIKILESAKQ
	1		NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL
5586	2619	915	LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM
			YHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQMLCQRHRRKS
1	1	- 1	SVTDSFSSLVNRPTLGQFTEEEIHAEVCYAKCLLQRAALTFLQD
		į	ENMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG
1	1		VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS
]	GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEEAEKLLKPYLNR
		1	YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM
		1	CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL
		[SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS
	1	į	RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK
			AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS
	ł	1	ISANEKKIKYDHYLIPNALLELALLLMEODRNEEAIKLLESAKO
			NYKNYSMESRTHFRIQAATLOAKSSLENSSRSMVSSVSL
5587	1768	148	SSAVPDGAVGRPVAVAVGGPPHSCRCRPCCLMAAIGVHLGCTSA
			THE CHARLES OF THE CLIP AND THE

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	ļ	\=possible nucleotide insertion)
			CVAVYKDGRAGVVANDAGDRVTPAVVAYSENEEIVGLAAKQSRI
	}	1	RNISNTVMKVKQILGRSSSDPQAQKYIAESKCLVIEKNGKLRYE IDTGEETKFVNPEDVARLIFSKMKETAHSVLGSDANDVVITVPF
			DFGEKQKNALGEAARAAGFNVLRLIHEPSAALLAYGIGODSPTG
•			KSNILVFKLGGTSLSLSVMEVNSGIYRVLSTNTDDNIGGAHFTE
	ļ	1	TLAOYLASEFORSFKHDVRGNARAMMKLTNSAEVAKHSLSTLGS
		Ĭ	ANCFLDSLYEGODFDCNVSRARFELLCSPLFNKCIEAIRGLLDO
			NGFTADDINKVVLCGGSSRIPKLQQLIKDLFPAVELLNSIPPDE
			VIPIGAAIEAGILIGKENLLVEDSLMIECSARDILVKGVDESGA
		1	SRFTVLFPSGTPLPARRQHTLQAPGSISSVCLELYESDGKNSAK
			EETKFAQVVLQDLDKKENGLRDILAVLTMKRDGSLHVTCTDQET
)	į	GKCEAISIEIAS
5588	3	589	TPPPPEQAMVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGK
	1	1	LVSLEKYRGSVSLVVNVASECGFTDQHYRALQQLQRDLGPHHFN
]		}	VLAFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
			AHPAFKYLAQTSGKEPTWNFWKYLVAPDGKVVGAWDPTVSVEEV
		L	RPQITALVRKLILLKREDL
5589	1884	553	LRQAWHEGGIGQTDKERGAAALPGEEGDPTRGRSLGRASWESGS
			PRRPRSPFSSFLPRPICLSLEARPCSIEDRRNWSLIGRPGAPAS
		}	GLNRSSGLWLGPDRCRPRSRCSCRVMENPSPAAALGKALCALLL
			ATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPLF
			RPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEAWALM KEIEAAGEALOSVHAVFSAPAVPSGTGOTSAELEVORRHSLVSF
			VVRIVPSPDWFVGVDSLDLCDGDRWREQAALDLYPYDAGTDSGF
	ļ		TFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARV
1			TLLRLRQSPRAFIPPAPVLPSRDNEIVDSASVPETPLDCEVSLW
1		-	SSWGLCGGHCGRLGTKSRTRYVRVQPANNGSPCPELEEEABCVP
	,		DNCV
5590	72	896	LCSSGALRLLPAMVAWRSAFLVCLAFSLATLVQRGSGDFDDFNL
			EDAVKETSSVKQPWDHTTTTTTNRPGTTRAPAKPPGSGLDLADA
			LDDQDDGRRKPGIGGRERWNHVTTTTKRPVTTRAPANTLGNDFD
			LADALDDRNDRDDGRRKPIAGGGGFSDKDLEDIVGGGEYKPDKG
		Ì	KGDGRYGSNDDPGSGMVAEPGTIAGVASALAMALIGAVSSYISY
Į			QQKKFCFSIQQGLNADYVKGENLEAVVCEEPQVKYSTLHTQSAE
			PPPPPBPARI
5591	68	1494	AGSSRRAAAERLLVSAGCRSLAGRASGVLLLPAELLPGEEEAMA
1			LRVTRNSKINAENKAKINMAGAKRVPTAPAATSKPGLRPRTALG
			DIGNKVSEQLQAKMPMKKEAKPSATGKVIDKKLPKPLEKVPMLV PVPVSEPVPEPEPEPEPEPVKEEKLSPEPILVDTASPSPMETSG
1			CAPAEEDLCQAFSDVILAVNDVDAEDGADPNLCSEYVKDIYAYL
			ROLEEEQAVRPKYLLGREVTGNMRAILIDWLVOVOMKFRLLOET
			MYMTVSIIDRFMONNCVPKKMLOLVGVTAMFIASKYEEMYPPEI
ļ			GDFAFVTDNTYTKHQIRQMEMKILRALNFGLGRPLPLHFLRRAS
(KIGEVDVEQHTLAKYLMELTMLDYDMVHFPPSOIAAGAFCLALK
Į.	1		ILDNGEWTPTLOHYLSYTEESLLPVMQHLAKNAAMVNOGLTKHM
			TVKNKYATSKHAKISTLPQLNSALVQDLAKAVAKV
5592	242	924	YGESKDWNQKDLLSALVLTTVNCLPTPIMAKSAEVKLAIFGRAG
			VGKSALVVRFLTKRFIWEYDPTLESTYRHQATIDDEVVSMEILD
			TAGQEDTIQREGHMRWGEGFVLVYDITDRGSFEEVLPLKNILDE
1	1		IKKPKNVTLILVGNKADLDHSRQVSTEEGEKLATELACAFYECS
			ACTGEGNITEIFYELCREVRRRRMVQGKTRRRSSTTHVKQAINK
			MLTKISS
5593	3	1113	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH
			SSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLDRDAB
			DVDLNHYRIGKIEGFEVLKKVKTLCLRQNLIKCIENLEELQSLR
			BLDLYDNQIKKIENLEALTELEILDISFNLLRNIEGVDKLTRLK
	1	I	KLFLVNNKISKIENLSNLHOLOMLELGSNRIRAIENIDTLTNLE
1	ł .		1
			SLFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIEGLQNLVNLR
			SLFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIEGLQNLVNLR ELYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTELQ EFWMNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
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NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
110:			Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding		L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
{	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			MLALPSVRQIDATFVRF
5594	3	1113	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH
			SSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLDRDAE
			DVDLNHYRIGKIEGFEVLKKVKTLCLRQNLIKCIENLEELQSLR
	1		ELDLYDNQIKKIENLEALTELEILDISFNLLRNIEGVDKLTRLK
			KLFLVNNKISKIENLSNLHQLQMLELGSNRIRAIENIDTLTNLE
1)		SLFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIEGLQNLVNLR
1			ELYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTELQ
1	1		EFWMNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKV
1_			MLALPSVRQIDATFVRF
5595	3	1476	ARWNGRWVQVPAWPGPGCGTNASGERQRQLPRAWRPVGRTLGSE
1	1		PIALAWSPPLYLFPIPLPSWAVSQPTPTLGTMFADLDYDIEEDK
1			LGIPTVPGKVTLQKDAQNLIGISIGGGAQYCPCLYIVQVFDNTP
1			AALDGTVAAGDEITGVNGRSIKGKTKVEVAKMIQEVKGEVTIHY
			NKLQADPKQGMSLDIVLKKVKHRLVENMSSGTADALGLSRAILC
			NDGLVKRLEELERTAELYKGMTEHTKNLLRAFYELSQTHRAFGD
]	}		VFSVIGVREPQPAASEAFVKFADAHRSIEKFGIRLLKTIKPMLT
			DLNTYLNKAIPDTRLTIKKYLDVKFEYLSYCLKVKEMDDEEYSC
1			IALGEPLYRVSTGNYEYRLILRCRQEARARFSQMRKDVLEKMEL
j			LDQKHVQDIVFQLQRLVSTMSKYYNDCYAVLRDADVFPIEVDLA
			HTTLAYGLNQEEFTDGEEEEEEEDTAAGEPSRDTRGAAGPLDKG
1			GSWCDS
5596	698	219	GAVLAPSSLPAAELAAQGESQSLEDLSNTSRPTSEVYKISFIFP
İ			NGDKYDGDCTRTSSGIYERNGIGIHTTPNGIVYTGSWKDDKMNG
	[FGRLEHFSGAVYEGQFKDNMFHGLGTYTFPNGAKYTGNFNENRV
			KGEGEYTHIQGTRMDVVTFHFTSCSQT
5597	3	731	ISCKMAADGQSSLPASWRSVTLTHVEYPAGDLSGHLLAYLSLSP
			VFVIVGFVTLIIFKRELHTISFLGGLALNEGVNWLIKNVIQEPR
			PCGGPHTAVGTKYGMPSSHSQFMWFFSVYSFLFLYLRMHQTNNA
			RFLDLLWRHVLSLGLLAVAFLVSYSRVYLLYHTWSQVLYGGIAG
			GLMAIAWFIFTQEVLTPLFPRIAAWPVSEFFLIRDTSLIPNVLW
			FEYTVTRAEARNRQRKLGTKLQ
5598	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL
			VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG
1			DAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMMSQLELLSGG
	Į		EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE
	}		IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR
			GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD
1			QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR
			LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL
			SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK
	1		NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM
			ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS
1	1		TNOPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS
1	[SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL
1	1		YGSYVFGDRNGNFLTLQQSPVTKQWQBKPLCLGTSGSCRGYFSG
1			HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE
	1		CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG
5599	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL
j	1		VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG
	1		DAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMMSQLELLSGG
1	<u> </u>		EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE
1	Į		IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR
1			GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKOVRGPASNYLD
	1		QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR
}	}	1	LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL
1			SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK
1			NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM
1	1		ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS
1			TNOPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS

No:	ريمد ا			
Nucleotide location	TID		Predicted end	Amino acid segment containing signal peptide
Cocation Corresponding Cofired Corresponding Cofired C				(A=Aranine, C=Cysteine, D=Aspartic Acid, E=
Leleucine, M-Methionine, N-Asparagine, enisties amino acid residue of amino acid residue of amino acid sequence S-Serine, T-Threonine, V-Valine, S-Serine, T-Threonine, V-Valine, w-residue of amino acid sequence S-Serine, T-Threonine, V-Valine, w-residue of amino acid sequence S-Serine, T-Threonine, V-Valine, w-residue of w-res	NO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of severine, T-Threonine, V-Valine, amino acid amino acid amino acid amino acid sequence		1		H=H18Cldine, I=1801eucine, K=Lysine,
amino acid residue of amino acid sequence solvent, Y-Tyrcophan, Y-Tyrcoshen, X-Unknown, **stop Codon, /-possible nucleotide deletion, /-possible nucleotide insertion)	1		l.	L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence Codon, /-possible nucleotide deletion, /-possible nucleotide insertion codon, /-possible nucleotide insertion codon, /-possible nucleotide insertion codon, /-possible nucleotide insertion codon, /-possible nucleotide insertion codon, /-possible nucleotide insertion codon, /-possible nucleotide insertion codon, /-possible nucleotide insertion codon, /-possible nucleotide insertion codon, /-possible nucleotide insertion codon, /-possible nucleotide insertion codon, /-possible nucleotide insertion codon, /-possible nucleotide insertion codon, /-possible nucleotide insertion codon, /-possible nucleotide insertion codon, /-possible nucleotide codon,	1		i e	P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence Codon, /-possible nucleotide deletion,	J		*	S=Serine, T=Threonine, V=Valine,
Sequence A-possible nucleotide insertion		1	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
SARILOTIKGNYESPSILEPPPSNOFLVGGFYVRGCGSERL VGSVYPGDBNOFITLOGGPYTKOGCGNETHGGGROFTSGERCYPS HILGFGDBLGEVYILSSKSMTOTHNGKLYKLVDPKRPLMPEE CRATVOPAQTITSECSRLCRNGYCTPTCKCCCSPGNBGDPCRTG SLRVLSGHLMGTRDLVOPPKRSFKFVTLNGGECAYHHEPEE CRATVOPAQTITSECSRLCRNGYCTPTCKCCCSPGNBGDPCRTG SLRVLSGHLMGTRDLVOPPKRSFKFVTLNGGCAYHHEISPCA BUMPSBMKPVNQTAASMKGLRGLLHPQOLHLLSQLEDDNGSF SNABMSELSVAQKQREKLLERCKWPACKNGBCCAYHHEISPCA AVAPPAPPSSSQLCRYPPACKMBCCPFHHYSRITUSPKP AVAPPAPPSSSQLCRYPPACKMBCPFHHYGRIPVDCTRPDC TPYMPTINVPRHALMKIRPGTSB 5601 1977 1244 SLRVLSGHLMGVTRDLVOPPKBASPKFVTLLGGVPSPPGYMSDGE EDMCFBGMKPVNQTAASNKGLRGLLHPQOLHLLSQLEDDNGSF SNABMSELSVAQKPEKLLERCKWBCPFHYHGRIPVDSPKP AVAPPAPPSSQLCRYPPACKKMBCPFHYHGRIPVDSPKP AVAPPAPPSSQLCRYPPACKKMBCPFHYHGRIPVDSPKP AVAPPAPPSSQLCRYPPACKKMBCPFHYHGRIPVDSPKP AVAPPAPPSSQLCRYPPACKKMBCPFHYHGRIPVDSPKP AVAPPAPPSSQLCRYPPACKKMBCPFHYHGRIPVDSPKP AVAPPAPPSSQLCRYPPACKKMBCPFHYHGRIPVDSPKP AVAPPAPPSSQLCRYPPACKKMBCPFHYHGRIPVDSPKP AVAPPAPPSSQLCRYPPACKKMBCPFHYHGRIPVDSPKP THYPTINVPPRHALMKIRTPGTSB 5602 246 766 YHTSCTWWRTAKEALENTEVPVGCLMVYNNBVVGKGRNEWOTK NATHABMWAJDAVLKTPYNGCBSKSPSPVFHHYNGTVLTVTVEPCIMC AAALRIMKIPLVVGCOMERFGGCGSVLNIASADLPNTGRPQC IFGYRABEAVERMLTFYNGCBPAPAPSKVKHTVLVYTVEPCIMC AAALRIMKIPLVVGCOMERFGGGGSVLNIASADLPNTGRPQC IFGYRABEAVERMLTFYNGCBPAPAPSKVKHTULLYTVTBCIMC AAALRIMKIPLVVGCOMERFGGGGSVLNIASADLPNTGRPQC IFGYRABEAVERMLTFYNGCBPAPAPSKVKHTULLYTVERCIMC AAAARHKIPLVVGGERFGGGGSSCSPSPVFHRGMDDGGAPAR TULVGSTKERKNNISIVLRDLEFSTGYTVCNVENSCHMUHHMEQVQ RLDGGLLHPTTLSTVANGKARTULLTPTSSC CGGGDGGGGGGGGGGGGGCGCCDCGGGAPAT TULVGSTKERKNNISIVLRDLEFSTGYTVCNVENSCHMUHHMEQVQ RLDGJLSSTIIJIGGNYGTDFAGGGGGFGCDTVGDV VUDGNSAASHVLHQDSGLGYNDLDLIFCDBLRSGGFGTVDDV VUDGNSAASHVLHQDSGLGYNDLDLIFCDBLRSGGFGTVDDV VUDGNSAASHVLHQDSGLGYNDLDLIFCDBLRSGGFGTVDDV VUDGNSAASHVLHQDSGLGYNDLDLIFCDBLRSGGFGTVDDV VUDGNSAASHVLHQDSGLGYNDLDLIFCDBLRSGGGGGGCGCGGGCGGGCGGGGGGGGGGGGGGGGGGGG		amino acid	sequence	Codon, /=possible nucleotide deletion,
S600 1977 1244 SIRVISGEMENT SECRIFICATION OF THE PROPERTY OF T	1	sequence	ì	\=possible nucleotide insertion)
HILGFGEBELGEVILLSSEKSMTOTHINGKLYKLTUPKRYDMEG CRATVOPAOTITSSCRILCHGYCYPTUKCCSPGWBEDPCRT6 SIRVISGHLMOTRGLUQFDKPASPKFIVTLDGVPSPFGYMSDGE SIRVISGHLMOTRGLUQFDKPASPKFIVTLDGVPSPFGYMSDGE EDMCFBGMKPYWOTIAASIKGLRGLLHPQQLIBLLSKQLEDPIGSF SIRVISGHLMOTRGLUQFDKCKTDAKCTKRDCPFTHYSRITPUSPKD AVAPPAPPSSGLCRYPPACKWBCCFTHYHGRITPUSPKDAVAPPAPPSSGLCRYPPACKWBCCFTHYHGRITPUSPKD AVAPPAPPSSGLCRYPPACKWBCCFTHYHGRITPUSPKDAVAPPAPPSSGLCRYPPACKWBCCFTHYHGRITPUSPKDAVAPPAPPSSGLCRYPPACKWBCFTHYHGRITPUSPKDAVAPPAPPSSGLCRYPPACKWBCFTHYHGRITPUTCTRPDC TYMPTINVPRHALKHIRPQTSE SIRVISGHLMGVTROLUQPDKASPKFIVTLDGVPSPPGYMSDQE EDMCFBGMKPWNQTAASNKGLRGLLHPQQLHLLSQLEDPIGSF SIRVISGHLMGVTROLUQPDKASPKFIVTLDGVPSPPGYMSDQE EDMCFBGMKPWNQTAASNKGLRGLHPQQLHLLSQLEDPIGSF SARMSELSVAQKPERLLBECKYWPACKWBCPFYHPKHCRYNTCCTRPDC TYMPTINVPPRHALKHIRPQTSE AVAPPAPPSSSCLCRYPPACKWBCPFYHPKHCRYNTCCTRPDC TYMPTINVPPRHALKHIRPQTSE AVAPPAPPSSSCLCRYPPACKWBCPFYHPKHCRYNTCTRPDC TYMPTINVPPRHALKHIRPQTSE AVAPPAPPSSSCLCRYPPACKWBCPFYHPKHCRYNTCTRPDC TANTAHABWWAJDQVLDWCROSGKSPSEVFHHVLIVYIVPECIMC AAALRIMKTPILVYIGCQMERGGCGSVLNIASADLPHTGRPQC INTSCLUWENTAKEALENTEVPVGCLMVYNNEVVGKGRRIVNTGTK AAALRIMKTPILVYIGCQMERGGCGSVLNIASADLPHTGRPQC INTSCLUWENTAKEALENTEVPVGCLMVYNNEVVGKGRRIVNTGTK AAALRIMKTPILVYYIGCQMERGGCGSVLNIASADLPHTGRPQC INTSCLUWENTAKEALENTEVPVGCLMVTNNEVVGKGRRIVNTGTK AAALRIMKTPILVYYIGCQMERGGCGSVLNIASADLPHTGRPQC CCFEBLHFRYTYNSBAPKILLBEGTVTVNNEKSDFRYTLKDDRI TUKSTKEKRNITSII SILLDFLTSSDTGKYTCHVKNFKSDFRYTLKDDRI TUKSTKEKRNITSII SILLDFLTSSDTGKYTCHVKNFKSDFRYTLKDDRI TUKSTKEKRNITSII SILLDFLTSSDTGKYTCHVKNFKSDFRYTLKDDRI TUKSTKEKRNITSII SILLDFLTSSDTGKYTCHVKNFKSDFRYTLMCQVQ RILDGILSTTIIGGNYTGHTLKAPYQVGWCNSDFMSLI SILLSINSGGNYULHQDSGLQYKDLDLIFCQBFTXCWNNEVQPVDAVANGAVARADLPHTAMEQVQ RILDGILSTDTGKNATTHITLGAVYGTCHVNDSDRMSLI SILSINSGGNYULHQDNICSTURGPTTLTKTRPEIRGGGC CHANILLUARGHENTORHHITTHETURGACHARGATTHERPEIRGGC GARPHALRSLLHINNIVLTRHQDANTHYNVRLHWYDDF VWANGSTNFRDFRAGGGRAPPHLLCNITHTWKLHWODF VWANGSTNFRDFRAGGGRAPPHLCNITHTWKHHWODF				SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCOSERL
HILGFGEBELGEVILLSSEKSMTOTHINGKLYKLTUPKRYDMEG CRATVOPAOTITSSCRILCHGYCYPTUKCCSPGWBEDPCRT6 SIRVISGHLMOTRGLUQFDKPASPKFIVTLDGVPSPFGYMSDGE SIRVISGHLMOTRGLUQFDKPASPKFIVTLDGVPSPFGYMSDGE EDMCFBGMKPYWOTIAASIKGLRGLLHPQQLIBLLSKQLEDPIGSF SIRVISGHLMOTRGLUQFDKCKTDAKCTKRDCPFTHYSRITPUSPKD AVAPPAPPSSGLCRYPPACKWBCCFTHYHGRITPUSPKDAVAPPAPPSSGLCRYPPACKWBCCFTHYHGRITPUSPKD AVAPPAPPSSGLCRYPPACKWBCCFTHYHGRITPUSPKDAVAPPAPPSSGLCRYPPACKWBCCFTHYHGRITPUSPKDAVAPPAPPSSGLCRYPPACKWBCFTHYHGRITPUSPKDAVAPPAPPSSGLCRYPPACKWBCFTHYHGRITPUTCTRPDC TYMPTINVPRHALKHIRPQTSE SIRVISGHLMGVTROLUQPDKASPKFIVTLDGVPSPPGYMSDQE EDMCFBGMKPWNQTAASNKGLRGLLHPQQLHLLSQLEDPIGSF SIRVISGHLMGVTROLUQPDKASPKFIVTLDGVPSPPGYMSDQE EDMCFBGMKPWNQTAASNKGLRGLHPQQLHLLSQLEDPIGSF SARMSELSVAQKPERLLBECKYWPACKWBCPFYHPKHCRYNTCCTRPDC TYMPTINVPPRHALKHIRPQTSE AVAPPAPPSSSCLCRYPPACKWBCPFYHPKHCRYNTCCTRPDC TYMPTINVPPRHALKHIRPQTSE AVAPPAPPSSSCLCRYPPACKWBCPFYHPKHCRYNTCTRPDC TYMPTINVPPRHALKHIRPQTSE AVAPPAPPSSSCLCRYPPACKWBCPFYHPKHCRYNTCTRPDC TANTAHABWWAJDQVLDWCROSGKSPSEVFHHVLIVYIVPECIMC AAALRIMKTPILVYIGCQMERGGCGSVLNIASADLPHTGRPQC INTSCLUWENTAKEALENTEVPVGCLMVYNNEVVGKGRRIVNTGTK AAALRIMKTPILVYIGCQMERGGCGSVLNIASADLPHTGRPQC INTSCLUWENTAKEALENTEVPVGCLMVYNNEVVGKGRRIVNTGTK AAALRIMKTPILVYYIGCQMERGGCGSVLNIASADLPHTGRPQC INTSCLUWENTAKEALENTEVPVGCLMVTNNEVVGKGRRIVNTGTK AAALRIMKTPILVYYIGCQMERGGCGSVLNIASADLPHTGRPQC CCFEBLHFRYTYNSBAPKILLBEGTVTVNNEKSDFRYTLKDDRI TUKSTKEKRNITSII SILLDFLTSSDTGKYTCHVKNFKSDFRYTLKDDRI TUKSTKEKRNITSII SILLDFLTSSDTGKYTCHVKNFKSDFRYTLKDDRI TUKSTKEKRNITSII SILLDFLTSSDTGKYTCHVKNFKSDFRYTLKDDRI TUKSTKEKRNITSII SILLDFLTSSDTGKYTCHVKNFKSDFRYTLMCQVQ RILDGILSTTIIGGNYTGHTLKAPYQVGWCNSDFMSLI SILLSINSGGNYULHQDSGLQYKDLDLIFCQBFTXCWNNEVQPVDAVANGAVARADLPHTAMEQVQ RILDGILSTDTGKNATTHITLGAVYGTCHVNDSDRMSLI SILSINSGGNYULHQDNICSTURGPTTLTKTRPEIRGGGC CHANILLUARGHENTORHHITTHETURGACHARGATTHERPEIRGGC GARPHALRSLLHINNIVLTRHQDANTHYNVRLHWYDDF VWANGSTNFRDFRAGGGRAPPHLLCNITHTWKLHWODF VWANGSTNFRDFRAGGGRAPPHLCNITHTWKHHWODF				
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EDMCFEGMKPYNGUTASNIKGLRGLHPQCHLLISFIDEDNGSF SNAEMSELSVAQKPKILLERCKYMPACKNOBECAYHIP1SPCKA FPNCKFAEKCLFVHPNCKYDAKCTKPDCPFTHVSRRIPVLSPKP AVAPPAPPSSSQLCRYPPACKNOBECAYHIP1SPCKA FPNCKFAEKCLFVHPNCKYDAKCTKPDCPFTHVSRRIPVLSPKP AVAPPAPPSSSQLCRYPPACKNOBCPYHPRICKPTTQCTRPDC TPYHPTINVPRHALKHIRQTSE EDMCFEGMKPWONTAASNIKGLRGLHPQCHHLISRQLEDDNGSF SNAEMSELSVAQKPKLLERCXYMPACKNOBECAYHHP1SPCKA FPNCKFAEKCLFVHPNCKYDAKCTKPDCPFTHVSRRIPVLSPKP AVAPPAPPSSSQLCRYPPACKKM2CPFYHFRICKFTNTQCTRPDC TFYHPTINVPPRHALKHIRQTSE 5602 246 766 7156 7157 7157 7157 7157 7157 7157	5600	1977	1244	SIRVI SCHI MOTEDI VODDE DAS DE EL VEL DOVDE DOCUMEDOS
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QRNLGPALSRTLSQLYCSYGPLT	1		(VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL
5606 3 1099 GRSRCPGFGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK	5606	3	1099	
LSSVGSISBEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA	I			
IEECQYQFRNRRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSA		1	1	1 - 1
GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG			1	
VAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTHMRVEC				
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KCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRRVG				
SSRALVPRNAQFKPHTDEDLVYLEPSPDFCBQDMRSGVLGTRGR				
TCNKTSKAIDGCELLCCGRGFHTAQVELAERCSCKFHWCCFVKC				···
	L	L		RQCQRLVELHTCR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
75		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning		
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i			
ſ	amino acid	sequence	Codon, /=possible nucleotide deletion,
· ·	sequence		\=possible nucleotide insertion)
5607	521	141	PPVCNPAEAMPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRV
			QQRKESKKPPAKLQPRALAGWLRPEDGGQAEGAEDELEVRFNAP
1	1		FDVGIKLSGVQYQQHSQALGKFLQDILWERAKEAPADK
5608	2	983	WFQSPLRQADPGPPRHTLFMDFVAGAIGGVCGDAVGYPLDTVKV
		ľ	RIQTEPKYTGIWHCVRDTYHRBRVWGFYRGLLLPVCTVSLVSSE
ļ	į		VFGTYRHCLAHICRLRFGNPDAKPTKADITLSGCASGLVRVFLT
l	1	Į.	SPTEVAKVRLOTOTOAOKOORRLSASGPLAVPPMCPVPPACPEP
1	i	į.	KYRGPLHCLATVAREEGLCGLYKGSSALVLRDGHSFATYFLSYA
1	ļ ·		
1		1	VLCEWLSPAGHSRPDVPGVLVAGGCAGVLAWAVATPMDVIKSRL
		ŧ	QADGQGQRRYRGLLHCMVTIVREEGPRVLFKGLVLNCCRAFPVN
	1		MVVFVAYBAVLRLARGLLT
5609	1628	304	AKGVWVLPSPPPRPGRGALVSGSGLRRGRSGTSWRPRRMNHKSK
5509	1 2020	1	KRIREAKRSARPELKDSLDWTRHNYYESFSLSPAAVADNVERAD
	1]	
1	1	1	ALQLSVEEFVERYERPYKPVVLLNAQEGWSAQEKWTLERLKRKY
1	1		RNQKFKCGEDNDGYSVKMKMKYYIEYMESTRDDSPLYIFDSSYG
1		1	EHPKRRKLLEDYKVPKFFTDDLFQYAGEKRRPPYRWFVMGPPRS
į.	1	ł	GTGIHIDPLGTSAWNALVQGHKRWCLFPTSTPRELIKVTRDEGG
Ī		1	NOODEAITWFNVIYPRTOLPTWPPEFKPLEILOKPGETVFVPGG
l .	1		1
	1	1	WWHVVLNLDTTIAITQNFASSTNFPVVWHKTVRGRPKLSRKWYR
1	i		ILKQEHPELAVLADSVDLQESTGIASDSSSDSSSSSSSSSSDSD
l .	1		SECESGSEGDGTVHRRKKRRTCSMVGNGDTTSQDDCVSKERSSS
1		l	R
5610	54	1196	LERTPASADMAWTKYOLFLAGLMLVTGSINTLSAKWADNFMAEG
3610	3*	1130	CGGSKEHSFQHPFLQAVGMFLGEFSCLAAFYLLRCRAAGOSDSS
		1	
		1	VDPQQPFNPLLFLPPALCDMTGTSLMYVALNMTSASSFQMLRGA
1	Ī		VIIFTGLFSVAFLGRRLVLSQWLGILATIAGLVVVGLADLLSKH
		}	DSQHKLSEVITGDLLIIMAQIIVAIQMVLEEKFVYKHNVHPLRA
	1	1	VGTEGLFGFVILSLLLVPMYYIPAGSFSGNPRGTLEDALDAFCQ
	1		VGQQPLIAVALLGNISSIAFFNFAGISVTKELSATTRMVLDSLR
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	}	1	TVVIWALSLALGWEAFHALQILGFLILLIGTALYNGLHRPLLGR
1	1		LSRGRPLAEESEQERLLGGTRTPINDAS
5611	2	577	FVLPNRLGIPGSTFRGPGACASSSSLAASAKPGAGGSPALAMSG
		1	ELSNRFOGGKAFGLLKAROERRLABINREFLCDOKYSDEENLPE
	l.	1	WE BE DESCRIBED THE OFFICE AND THE OWN OFFICE OF THE OWN OFFICE OF THE OWN OF THE OWN OFFI OWN OWN OF THE OWN OWN OWN OWN OWN OWN OWN OWN OWN OWN
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		,	KLTAFKEKYMBFDLNNEGEIDLMSLKRMMEKLGVPXTHLBMKKM
1			ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP
Ĺ			ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP
5612	1	721	ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP
5612	1	721	ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP
5612	1	721	ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA
5612	1	721	ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL
5612	1	721	ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET
5612	1	721	ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS
5612	1	721	ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLLGPVGS
5612	1 115	721	ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS
	·		ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLLGPVGS RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD
	·		ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLITLENLILNEFSYTATEARRLYLQRKTVPSALLVQLTQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLLGPVGS RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFHMFFDST
	·		ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLLGPVGS RGVDPALRRÆKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFHMFFDST AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIFTAF
	·		ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLLGPVGS RGVDPALRREKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD KTSRNLFFFLCINLSFAFVELLYGIWSNCLGLISDSFHMFFDST AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIFTAF FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKHGGH
	·		ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLLGPVGS RGVDPALRRÆKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFHMFFDST AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIFTAF
	·		ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLLGPVGS RGVDPALRREKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD KTSRNLFFFLCINLSFAFVELLYGIWSNCLGLISDSFHMFFDST AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIFTAF FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKHGGH
	·		ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA EEDCIKQGWILDGIPETRRQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLLGPVGS RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD KTSRNLFFFLCINLSFAFVELLYGIWSNCLGLISDSFHMFFDST AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIFTAF FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKHGGH GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH
	·		ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLLGPVGS RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFIMFFDST AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIFTAF FIFSEGVERALAPPDVHERLLLVSILGFVVNLIGIFVFKHGGH GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH AHGHGHFHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI ASAIMMQNFGLMIADPICSILIAILIVVSVIPLLRESVGILMQR
	·		ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLTQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLLGPVGS RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFHMFFDST AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIPTAF FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKGGH GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH AHGHGHFHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI ASAIMMQNFGLMIADPICSILIAILIVVSVIPLRESVGILMQR TPPLLENSLPQCYQRVQQLQGVYSLQEQHFWTLCSDVYVGTLKL
5613	115	1279	ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLITLENLILNEFSYTATEARRLYLQRTTVPSALLVQLTQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLLGPVGS RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFHMFFDST AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIPTAF FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKHGGH GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH AHGHGHFHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI ASAIMMQNFGLMIADPICSILIAILIVVSVIPLLRESVGILMQR TPPLLENSLPQCYQRVQQLQGVYSLQEQHFWTLCSDVYVGTLKL IVAPDADARWILSQTHNIFTQAGVRQLYVQIDFAAM
	·		ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLTQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLLGPVGS RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFHMFFDST AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIPTAF FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKGGH GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH AHGHGHFHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI ASAIMMQNFGLMIADPICSILIAILIVVSVIPLRESVGILMQR TPPLLENSLPQCYQRVQQLQGVYSLQEQHFWTLCSDVYVGTLKL
5613	115	1279	ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLITLENLILNEFSYTATEARRLYLQRTTVPSALLVQLTQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLLGPVGS RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFHMFFDST AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIPTAF FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKHGGH GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH AHGHGHFHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI ASAIMMQNFGLMIADPICSILIAILIVVSVIPLLRESVGILMQR TPPLLENSLPQCYQRVQQLQGVYSLQEQHFWTLCSDVYVGTLKL IVAPDADARWILSQTHNIFTQAGVRQLYVQIDFAAM
5613	115	1279	ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLTQERLA EEDCIKQGWILDGIPETREQALRIQTIGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLLGPVGS RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFHMFFDST AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIPTAF FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKHGGH GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH AHGHGHFHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI ASAIMMQNFGLMIADPICSILIAILIVVSVIPLLRESVGILMQR TPPLLENSLPQCYQRVQQLGGVYSLQECHFWTLCSDVYVGTLKL IVAPDADARWILSQTHNIFTQAGVRQLYVQIDFAAM LLSRNEHACPLQAGLGLTQRKPKAIRGREGRATNQGQGETQNER APWGARQRLGVMAELQQLQEFEIPTGREALRGNHSALLRVADYC
5613	115	1279	ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQKTVPSALLVQLIQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLLGPVGS RGVDPALRRÆKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFHMFFDST AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIPTAF FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKHGGH GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH AHGHGHFHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI ASAIMMQNFGLMIADPICSILIAILIVVSVIPLLRESVGILMQR TPPLLENSLPQCYQRVQQLGVYSLQEQHFWTLCSDVYVGTLKL IVAPDADARWILSQTHNIFTQAGVRQLYVQLDFAAM LLSRNBHACPLQAGLGLTQRKPKAIRGREGRATNQGQGETQNER APWGARQRLGVMAELQQLQEFEIPTGREALRGNHSALLRVADYC EDNYVQATDKRKALEETMAFTTQALASVAYQVGNLAGHTLRMLD
5613	115	1279	ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLLGPVGS RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFIMFFDST AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIFTAF FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKHGGH GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH AHGHGHFHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI ASAIMMQNFGLMIADPICSILIAILIVVSVIPLLRESVGILMQR TPPLLENSLPQCYQRVQQLQGVYSLQEGHFWTLCSDVYVGTLKL IVAPDADARWILSQTHNIFTQAGVRQLYQUFDFAAM LLSRNEHACPLQAGGLTQRKPKAIRGREGRATNQGQETQNER APWGARQRLGVMAELQQLQEFEIPTGRBALRGNHSALLRVADYC EDNYVQATDKRKALEETMAFTTQALASVAYQVGNLAGHTLRMLD LQGAALRQVEARVSTLGQMVNMHMEKVARREIGTLATVQRLPPG
5613	115	1279	ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLLGPVGS RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD KTSRNLFFFLCLINLSFAFVELLYGIWSNCLGLISDSFIMMFPDST AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIFTAF FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKHGGH GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH AHGHGHFHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI ASAIMMQNFGLMIADPICSILIAILIVVSVIPLLRESVGILMQR TPPLLENSLPQCYQRVQQLQGVYSLQEQHFWTLCSDVYVGTLKL IVAPDADARMILSQTHNIFTQAGVRQLYVQIDFAAM LLSRNEHACPLQAGGLTQRKPKAIRGREGRATNQGGGETQNER APWGARQRLGVMAELQQLQEFEIPTGREALRGNHSALLRVADYC EDNYVQATDKRKALEETMAFTTQALASVAYQVGNLAGHTLRMLD LQGAALRQVEARVSTLGQMVNMHMEKVARREIGTLATVQRLPPG QKVIAPENLPPLTPYCRRPLNFGCLDDIGHGIKDLSTQLSRTGT
5613	115	1279	ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLLGPVGS RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFIMFFDST AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIFTAF FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKHGGH GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH AHGHGHFHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI ASAIMMQNFGLMIADPICSILIAILIVVSVIPLLRESVGILMQR TPPLLENSLPQCYQRVQQLQGVYSLQEGHFWTLCSDVYVGTLKL IVAPDADARWILSQTHNIFTQAGVRQLYQUFDFAAM LLSRNEHACPLQAGGLTQRKPKAIRGREGRATNQGGETQNER APWGARQRLGVMAELQQLQEFEIPTGRBALRGNHSALLRVADYC EDNYVQATDKRKALEETMAFTTQALASVAYQVGNLAGHTLRMLD LQGAALRQVEARVSTLGQMVNMHMEKVARREIGTLATVQRLPPG
5613	115	1279	ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLLGPVGS RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD KTSRNLFFFLCLINLSFAFVELLYGIWSNCLGLISDSFIMMFPDST AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIFTAF FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKHGGH GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH AHGHGHFHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI ASAIMMQNFGLMIADPICSILIAILIVVSVIPLLRESVGILMQR TPPLLENSLPQCYQRVQQLQGVYSLQEQHFWTLCSDVYVGTLKL IVAPDADARMILSQTHNIFTQAGVRQLYVQIDFAAM LLSRNEHACPLQAGGLTQRKPKAIRGREGRATNQGGGETQNER APWGARQRLGVMAELQQLQEFEIPTGREALRGNHSALLRVADYC EDNYVQATDKRKALEETMAFTTQALASVAYQVGNLAGHTLRMLD LQGAALRQVEARVSTLGQMVNMHMEKVARREIGTLATVQRLPPG QKVIAPENLPPLTPYCRRPLNFGCLDDIGHGIKDLSTQLSRTGT
5613	115	1279	ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQRRTVPSALLVQLTQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLLGPVGS RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFHMFFDST AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIFTAF FIFSEGVERALAPPDVHHERLLLVSLLGFVVNLIGIFVFKHGGH GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH AAGHGHFHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI ASAIMMQNFGLMIADPICSILIAILIVVSVIPLLRESVGILMQR TPPLLENSLPQCYQRVQQLQGVYSLQEQHFWTLCSDVYVGTLKL IVAPDADARWILSQTHNIFTQAGVRQLYVQIDFAAM LLSRNBHACPLQAGLGTGRKPKAIRGREGRATNQGQGETQNER APWGARQRLGVMAELQQLQEFEIPTGREALRGNHSALLRVADYC EDNYVQATDKRKALEETMAFTTQALASVAYQVGNLAGHTLRMLD LQGAALRQVEARVSTLGQMVNMHMEKVARREIGTLATVQRLPPG QKVIAPENLPPLTPYCRRPLNFGCLDDIGHGIKDLSTQLSRTGT LSRKSIKAPATPASATLGRPPRIPEPVHLPVVPDGRLSAASSAS SLASAGSAEGVGGAPTPKGQAAPPAPPLPSSLDPPPPPAAVEVF
5613	115	1279	ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLLGPVGS RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFHMFFDST AILAGLASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIFTAF FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKHGGH GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH AGGHGHFHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI ASAIMMQNFGLMIADPICSILIAILIVVSVIPLRESVGILMQR TPPLLENSLPQCYQRVQQLQGVYSLQEQHFWTLCSDVYVGTLKL IVAPDADARMILSQTHNIFTQAGVRQLYVQIDFAAM LLSRNEHACPLQAGLGLTQRKPKAIRGREGRATNQGQETQNER APWGARQRLGVMAELQQLQEFEIPTGREALRGNHSALLRVADYC EDNYVQATDKRKALEETMAFTTQALASVAYQVGNLAGHTLRMLD LQGAALRQVEARVSTLGGMVNMHMEKVARREIGTLATVQRLPPG QKVIAPENLPPLTPYCRRPLNFGCLDDIGHGIKDLSTQLSASSAS

SEQ	Predicted	Predicted end	Limino agid domest control
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	bequence	\=possible nucleotide insertion)
<u> </u>	- Dequence		SDGWCEGVSSEGTGFFPGNYVEPSC
5615	<u> </u>	1558	
3013]	1550	ALGRRRPGDPREMEAAATPAAAGAARREELDMDVMRPLINEONF
			DGTSDEEHEQELLPVQKHYQLDDQEGISFVQTLMHLLKGNIGTG
			LLGLPLAIKNAGIVLGPISLVFIGIISVHCMHILVRCSHFLCLR
ļ			FKKSTLGYSDTVSFAMEVSPWSCLQKQAAWGRSVVDFFLVITQL
l			GFCSVYIVFLAENVKQVHEGFLESKVFISNSTNSSNPCERRSVD
ţ			LRIYMLCFLPFIILLVFIRELKNLFVLSFLANVSMAVSLVIIYQ
1			YVVRNMPDPHNLPIVAGWKKYPLFFGTAVFAFEGIGVVLPLENQ
1			MKESKRFPQALNIGMGIVTTLYVTLATLGYMCFHDEIKGSITLN
			LPQDVWLYQSVKILYSFGIFVTYSIQFYVPAEIIIPGITSKFHT
			KWKQICEFGIRSFLVSITCAGAILIPRLDIVISFVGAVSSSTLA
i]		LILPPLVEILTFSKEHYNIWMVLKNISIAFTGVVGPLLGTYITV
5616			EEIIYPTPKVVAGTPQSPFLNLNSTCLTSGLK
2010	1	719	DDFVRCGPQSAAMGASARLLRAVIMGAPGSGKGTVSSRITTHFE
			LKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIPDDVMTRLAL
			HELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV
			IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDD
			KPETVIKRLKAYEDQTKPVLEYYQKKGVLETFSGTETNKIWPYV
5637	156		YAFLQTKVPQRSQKASVTP
5617	176	765	PWRGRGSRPRGAGAMAEEQVNRSAGLAPDCEASATAETTVSSVG
	ļ		TCEAAGKSPEPKDYDSTCVFCRIAGRQDPGTELLHCENEDLICF
	Ì		KDIKPAATHHYLVVPKKHIGNCRTLRKDQVELVENMVTVGKTIL
ļ			ERNNFTDFTNVRMGFHMPPFCSISHLHLHVLAPVDQLGFLSKLV
			YRVNSYWFITADHLIEKLRT
5618	3	1692	YLNYINLKSENKLSGKEDLWEKLQYLWKSTLNLPEDLLRVPDES
1	İ		LFLNSGGDSLKSIRLLSEIEKLVGTSVPGLLEIILSSSILEIYN
1			HILQTVVPDEDVTFRKSCATKRKLSNINQERASGTSLHQKAIMT
			FTCHNEINAFVVLSRGSQILSLNSTRFLTKLGHCSSACPSDSVS
1.			QTNIQNLKGLNSPVLIGKSKDPSCVAKVSEEGKPAIGTQKMELH
1			VRWRSDTGKCVDASPLVVIPTFDKSSTTVYIGSHSHRMKAVDFY
1			SGKVKWEQILGDRIESSACVSKCGNFIVVGCYNGLVYVLKSNSG
1			EKYWMFTTEDAVKSSATMDPTTGLIYIGSHDQHAYALDIYRKKC
1			VWKSKCGGTVFSSPCLNLIPHHLYFATLGGLLLAVNPATGNVIW
1			KHSCGKPLFSSPQCCSQYICIGCVDGNLLCFTHFGEQVWQFSTS
			GPIFSSPCTSPSEQKIFFGSHDCFIYCCNMKGHLQWKFETTSRV
			YATPFAFHNYNGSNEMLLAAASTDGKVWILESQSGQLQSVYELP
F.C. 2			GEVFSSPVVLESMLIIGCRDNYVYCLDLLGGNQK .
5619	2160	1477	DSPVLPTSGNVISTAQPAQPWSAVEAALRSLGSPPGAGRGCPCP
			AQSLHSHQLAAWDPLKPSLRSYPPHLLQHPQLRSLTASSGHLGR
			RSCPQPRPLEELLRAGSSTRPQPLTSSCCGMSCMYSFLGHCSVL
ì			LWGTKGRGSGSPSSPGCCLHPPAQHSQDLPLVHVDVGWQPPLGP
			TVGLRPGLLGERQRGALRAGDPQCQCPLPATVREDLGVPSPWAA
FC20	<u></u>		ECSPPATP
5620	930	182	PLPPPTLAMFLTRSEYDRGVNTFSPEGRLFQVEYAIEAIKLGST
•			AIGIQTSEGVCLAVEKRITSPLMEPSSIEKIVEIDAHIGCAMSG
			LIADAKTLIDKARVETQNHWFTYNETMTVESVTQAVSNLALQFG
			EEDADPGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFVQCDAR
			AIGSASEGAQSSLQEVYHKSMTLKEAIKSSLIILKQVMEEKLNA
-		*	TNIELATVQPGQNFHMFTKEELEEVIKDI
5621	3	819	VVEFVEYTATDANVKNESLSSVQQLGIKMTVRYGKFLSLLKDGA
			ENDLTWVLKHCERFLKQQQTSIKSSLLCLQGNYAGHDWFVSSLF
			MIMLGDKEKTFQFLHQFSRLLTSAFLWLPRLHISSYLPNDTVES
			GIHPVYFCSTHYIEMLLKAELPLVFSAFHMSGFAPSQICLQWIT
			QCFWNYLDWIEICHYIATCVFLGPDYQVYICIAVFKHLQQDILO
			HTQTQDLQVFLKEEALHGFRVSDYFEYMEILEQNYRTVLLRDMR
			NIRLQST
5622	1122	456	AASTKDAVSRKRSHSASEKSGTGTSISKRLNMNPQIRNPMKAMY
			PGTFYFQFKNLWEANDRNETWLCFTVEGIKRRSVVSWKTGVFRN
			QVDSETHCHAERCFLSWFCDDILSPNTKYQVTWYTSWSPCPDCA
L			GEVAEFLARHSNVNLTIFTARLYYFQYPCYQEGLRSLSQEGVAV

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	
	amino acid		P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
i			EIMDYEDFKYCWENFVYNDNEPFKPWKGLKTNFRLLKRRLRESL
			Q
5623	3	954	FLPFFIRAPKISRNGQWLFTFTTPFPFANKALPGWEGIVPACFW
1			RKKILTPSTGTMELLQVTILFLLPSICSSNSTGVLEAANNSLVV
			TTTKPSITTPNTESLQKNVVTPTTGTTPKGTITNELLKMSLMST
			ATFLTSKDEGLKATTTDVRKNDSIISNVTVTSVTLPNAVSTLQS
			SKPKTETQSSIKTTEIPGSVLQPDASPSKTGTLTSIPVTIPENT
			SQSQVIGTEGGKNASTSATSRSYSSIILPVVIALIVITLSVFVL
		l .	VGLYRMCWKADPGTPENGNDQPQSDKESVKLLTVKTISHESGEH
			SAQGKTKN
5624	159	898	PGVAAAAGALPQYHGPAPALVSCRRELSLSAGSLQLERKRRDFT
			SSGSRKLYFDTHALVCLLEDNGFATQQAEIIVSALVKILEANMD
1		İ	IVYKDMVTKMQQEITFQQVMSQIANVKKDMIILEKSEFSALRAE
1	1	1	NEKIKLELHQLKQQVMDEVIKVRTDTKLDFNLEKSRVKELYSLN
1	1	Į.	
[EKKLLELRTEIVALHAQQDRALTQTDRKIETEVAGLKTMLESHK LDNIKYLAGSIFTCLTVALGFYRLWI
5625	1	1180	
3023	1 ^	1100	TIPSSAAAQRAGPPAGALEALSPGGARAHAERRGEMRATPLAAP
l			AGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLPLSPP
l			TAPDRATAVATASRLGPYVLLEPEEGGRAYQALHCPTGTEYTCR
1			VYPVQEALAVLEPYARLPPHKHVARPTEVLAGTQLLYAFFTRTH
1			GDMHSLVRSRHRIPEPEAAVLFRQMATALAHCHQHGLVLRDLKL
1	1		CRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPE
			ILSSRASYSGKAADVWSLGVALFIMLAGHYPFQDSEPVLLFGKI
			RRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRQ
			DPMPLAPTRSHLWEAAQVVPDGLGLDEAREEEGDREVVLYG
5626	3123	2011	PPRALGSVAMENQVLTPHVYWAQRHRBLYLRVELSDVQNPAISI
			TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN
1	•		ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK
			EEERLNKLRLESEGSPETLTNLRKGYLFMYNLVQFLGFSWIFVN
1			LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT
	ļ		SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAVVFFVFYLWSAIE
			IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ
1			SIPIFNETGRFSFTLPYPVKIKVRFSPFLQIYLIMIFLGLYINF
L	<u> </u>	•	RHLYKQRRRRYGQKKKKIH
5627	3123	2011	PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVQNPAISI
			TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN
ĺ			ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK
i			EEERLNKLRLESEGSPETLTNLRKGYLFMYNLVQFLGFSWIFVN
			LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT
			SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAVVFFVFYLWSAIE
1			IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ
1			SIPIFNETGRESETLPYPVKIKVRESEFLQIYLIMIFLGLYINE
]		RHLYKQRRRRYGQKKKKIH
5628	75	1455	VAGAMASKCLKAGFSSGSLKSPGGASGGSTRVSAMYSSSPCKLP
			SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG
			GGWFGEGILTGNEKETMQSLNDRLAGYLEKVRQLEQENASLESR
			IREWCEQQVPYMCPDYQSYFRTIEELQKKTLCSKAENARLVVEI
			DNAKLAADDFRTKYETEVSLRQLVESDINGLRRILDDLTLCKSD
			LEACUEST KEET TOTAK MINEREMINED BOOT OBST TRIBLET COMES TO THE COMES T
			LEAQVESLKEELLCLKKNHEEEVNSLRCQLGDRLNVEVDAAPPV
			DLNRVLEEMRCQYETLVENNRRDAEDWLDTQSEELNQQVVSSSE
			QLQSCQABIIELRRTVNALEIELQAQHSMRDALESTLAETEARY
1			SSQLAQMQCMITNVBAQLAEIRADLERQNQEYQVLLDVRARLEC
	į į		EINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA
5670	2765	07.0	ARTNCSARPICVPCPGGRF
5629	2287	938	GRPRSSSDNRNFLRERAGLSSAAVQTRIGNSAASRRSPAARPPV
			PAPPALPRGRPGTEGSTSLSAPAVLVVAVAVVVVVVSAVAWAMA
1 i			NYIHVPPGSPEVPKLNVTVQDQEEHRCREGALSLLQHLRPHWDP
			QEVTLQLFTDGITNKLIGCYVGNTMEDVVLVRIYGNKTELLVDR
			DEEVKSFRVLQAHGCAPQLYCTFNNGLCYEFIQGEALDPKHVCN
			PAIFRLIARQLAKIHAIHAHNGWIPKSNLWLKMGKYFSLIPTGF

Deginning	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Mo:	1 -			/A-Alanina C-Custoine D Paramis is in
Corresponding Cofirest Cofi	NO:			Glutamic Acid E-Phonel-1-
Corresponding	1		1	United dies T. Tanlaurianine, G=Glycine,
To first amino acid residue of amino acid amino acid amino acid amino acid amino acid asquence sequenc			1	henistidine, leisoleucine, KeLysine,
amino acid residue of amino acid anino acid sequence where the control of amino acid sequence where the control of amino acid sequence where the control of				D=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence al sequence seque			ľ	P=Proline, Q=Glutamine, R=Arginine,
anino acid sequence Sequence				S=Serine, T=Threonine, V=Valine,
Sequence Codon, /-possible nucleotide deletion,		. –		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
APDINKRYLSUPSCIJUZGENTMUKRISISLOSPVVLCKNDL	1	1	sequence	Codon, /=possible nucleotide deletion.
ADEOL NARP. LSD INSOLICABENT MAKELISSINAL SPVILCHNOL LCKNI LYMENGROUP DIVENSORYMLAD ICHNIPE PROVISOV DYSLYPDRELOGOLLAN LEXINATION CONTRETE PROVISOV DYSLYPDRELOGOLLAN LEXINATE PROFICE PROVISOR OF NATAOTCAHELPES PRILEPES		sequence		\=possible nucleotide insertion)
LCKNI IYMEKGGPUCF IDVESSGYMILADIGNIFMERAGUSDU DISLYPDERLOGGNIRATHLENYER KENGGTEVETEKSVELIFIGV NOFALASHIFMGIMALIQAKYSTI EPDFLGYAIVRINGYKMKE ETTALKYPE GRATAGYCAHHLPROSPELUPAS PWELPEMSSEGYRTLIVALTY ETTALCEGSBEKKVEWHYREKLAVER KOSLSEWGSTITLOVALTY TILCEGSBEKVEWHYREKLAVER KOSLSEWGSTITLOVALTY GLESSLÖKILLDEQAGWKSTILVSNI SHDTVLQCHFTCSGYQESM NENSYVOPPROVILLTOJTLIVAKUKSI TSLEDVEPUDDSLT LELERGISTLENKILLDEQAGWKSTILVSNI SHDTVLQCHFTCSGYQESM NENSYVOPPROVILLTOJTLIVAKUKSI TSLEDVEPUDDSLT LELERGISTLENKILLDEGAGWKSTILVADTE LELERGISTLENKILLDEGAGWKSTILVADTE LELERGISTLENKILLDEGAGWKSTILVADTE LELERGISTLENKILLDEGAGWKSTILDTONGTONG SEVDDFVPREPESSERSE PROSPERSTERGER PREVADENTILVY OVA. LSLEVTSULLCETEGGLEGORMGTYGYBAAMRALPAPER ACKGGYTYDGA QGLIRDTEBHLSKYGFLEKKI EGGLIFAKKIG TENKABALQALKKKKY KEG ING ING INSTERICRALBENANTN TEVLAMMOZAAGAMKAALIDMOD IDVODELIMGATISGGETVOP ACKGGYTYDGA QGLIRDTEBHLSKYGFLEKKI EGGLIFAKKIG TENKABALQALKKKKY KEG ING ING INSTERICRALBENANTN TEVLAMMOZAAGAMKAALIDMOD IDVODELIMGALESIS SALVENGEBWKSTERGERERER TAISKYPOGEDEDAGALEBLEBLDILLDKINTYKI KCUMMPSIGG VAN AKKGGLIVANGPOGELIPREVOGSKREOPOPOPPAYATOTHOG FITYSSADABDLISGS IASPOVKINIGGDFIKESTATTFIRAGKY VAN KAKGGLIVANGPOGULIPREVOGSKREOPOPOPPAYATOTHOG FITYSSADABDLISGS IASPOVKINIGGDFIKESTATTFIRAGKY VAN TILKARUGUNOVACOPULIPRIVOSKREOPOPOPPAYATOTHOG FITYSSADABDLISGS IASPOVKINIGGGFIKVSHITINI ITI ITI ITI ITI ITI ITI ITI ITI IT				ADEDINKRELSDIPSSOILOEEMTWMKEILSNIGSDVVI.CHNDT.
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SSVDDFVRPESSARESRSGRREPARRARTMSVEGKLFGAGGGGV AGKGGPTPGDEALORLANGTHMISKOGELFGAGGGV TKNKRAALQALKRKKYEKQLLQIDGTLSTIEFQREALENANTM TEVLKNMGYAAKAMKAAHDMUDIDKVDELMGDIADGGHASEIS TRAISKEVGFGEEFDEDEMAELEELQGELAKMLEISGPETVB LENVPSIALPSKPAKKKEEDDDMKELENMAGSM VVLGMSPFERLMMGSIGAAADPAFVSGLARSLHVSTRRPHRRA SVEVARGRIGWRAPGPLLPRPVSSRREMOPPGPPAVAPTINGG FIFVSSADABDLGSGTASPDVKLNLGGGFLARSLHVSTRRPHRRA SVEVARGRIGWRAPGPLLPRPVSSRREMOPPGPPAVAPTINGG GWLLEVEDDDPEDMKPLLEELDIDLKDIYYKIRCVLMMMPSLGF INFGVSADABDLGSGTASPDVKLNLGGFTEVSTATPLRGRGY GWLLEVEDDDPEDMKPLLEELDIDLKDIYYKIRCVLMMMPSLGF INFGVSADABASSASSLAVGEFFTKKEPLLIYPTFLLYIY FLSLYTGV VVSTLIKLFGVFWAAYSAASLLVGEFFTKKEPLLIYPTFLLYIY FLSLYTGV VVSTLIKLFGVFWAAYSAASLLVGEFFTKKEPLLIYPTFLLYIY FLSLYTGV CLERNSVSKIMMLCMPFFWSIFFSLSTKKEPLLIYPTFLLYIY FLSLYTGV GGCSKTMSVGGPFYRSSEFMEOLLSSHLHOVPFFCCFTVCLCM CLERNSVSKIMMLCMPFFWSIFFSLSTKKEPLLIYPTFLLYIY FLSLYTGV GGCSKTMSVGGPFYRSSEFMEOLLSSHLHOVPFFCCFTVCLCM CLERNSVSKIMMLCMPFFWSIFFSLSFTKKFPLLIYLHGLSYGSL LLLLLGGHRPGSSMV PRATGRIRSTANJSEPFRAGAGASGAEFRSGRERSLSGRRAPAM ARNILSSFRRVDIDEFDENKFVDEGGEBAAAAAFGGDPSEVD GLLRGODMLRAFHAALRNSPVNTKNQAVKERAGGVVLKVLTNRK SSEIEQAVGSLBRNGVDLIMYTYKFFKENSSAVLLQMHEK ALAVGGLSITRVLTARKTV RSLEPFPTYTSGAPRAVLVGSSMPARMVAPAVKVARGMSGLAL GVRRAVLQLGGLIRVYLTARKTV RSLEPFPTYTSGAPRAVLVGSSMPARMVAPAVKVARGMSGLAL GVRRAVLQLGGLIRVYLKSKTSVEDDFVISKFTNMMIGGNKV LARSIMIGTLEAVKRKOFEKYHAAGAEEQATIERNPYTIFHOAL KNGCFMIGHVEILKGGRYVYPVPUDERFRAKMKMITECDD KNGCFMIGHVEILKGGRYVYPVPUDERFRAKMKMITECDD KNGCFMIGHVEILKGGRYVYPVPUDERFRAKMKMITECDD KNGCFMIGHVEILKGGRYVYPVPUDERFRAKMINGSGFD ALLHEIGG IRETORALEESFETIKENYCHYSILMOTLOGESFR CERLEGOLNDLTELHQMEILNILKGLASMEEXIAVGSYERARDI GEALBACTISKSMELOQOQOVVQLEGLENATROKKHDHINGSGFD ALLHEIGG IRETORALEESFETIKENYCHYSILMOTLOGESFR CERLEGOLNDLTELHQMEILNILKGGLASMEEXIAVGSYERARDI GCEALBACTISKSMELOQOQOQVVQLEGLENATROKHHOHSHIP OQOLDLIFPDR PIGYGARGVWSVTDPROKKVAKHHOHSHIP OQOLDLIFPDR PIGYGARGVWSVTDPROKKVAKHHOHSHIP OQOLDLIFPDR PIGYGARGVWSVTDPROKKVAKHHOHSHIP OQOLDLIFPDR PIGYGARGVAKGTFAELGRICHLFGAAGSPIOOLDL VSCKVYFRELKKLOCTFAELLGRICHLFGAAGSPIOOLDL VSCKVYFRELKKLOCTFAELDRICHT				LSLFVTSVLLCFIFGOHLROORMGTVGVPAAWPRIPOARPR
AGKGGPTPOEATOGLROTTEMLSKKOEFSTLEKKIEGGLTAAKKHE TINNRAALOGLAKIKKKYPEGLAGITOGTLATAKHE TEVLKIMGYAAKAKAHDINMIDIDKVDELMQDIADQGLLAEEIS TAISKPYGFGBEFDEDELMAELEELEGEELDKINLISTGETUP LENVPSIALPSKRAKKEEEDDDMKELEMAGSM 5632 3 952 VVLOWSPERRIMMGSLGAAGRPAVPVSGLAKSLHVETTRPHERA SVRVARGRIGWAGPGPLIPRPUSSREMPGDFPEAVARTPHRORGY GWLLEVEDDDPEDMKPLLEEDLDILKDITYKITRPHERA NRQVVRDNPDFWGPLAVVLFSMISLYGGFRVVSMIJTTHYFOS LTIFILARVLGGEVAYGQVLGVIGYSLUPLTVJAPVLLVVGSFP VVSTLIKLEGFVFMASYSAASLUVGEBFKFULHYPIFLLYVIY FLSLYTGV 6GCSKTMSVGRPFYRSSEPMEDLLSSHLHGVPFPCCFFVVCLCN CLFENSVSKLYMLCFNFPFMSIFFYSLSITKLNLIYLMGLSYQSL LLLLLSGHRPWGSSMW 771 460 6S55 PRATGRIRSRAAJSRPRAGGASGAEFKSGRERSRLSGRRAPAM ARNILSSRPRRVDIDEFDENKFVDEGBEAAAAAAFGFGDPSEVD GLLRGODMLARFHAALRNSVPWKNGAVKEGVVLKVLTNEK SSEIEGAVOSLDRNGVDLLMKYTYKGFKKPTENSSAVLLOWHEK ALAVGGLGSITRVLTARKTV LARSHIFTVTTSGAPRAVUSSWPARVAPAVKVARKWSGLAL GVRRAVLGLOGLTOVMSNRYSPEFNDLDGVKKNSVQISGEKRRFRL RSLFHFFVTTSGAPRAVLUGSSWPARVAPAVKVARKWSGLAL GVRRAVLGLOGLTOVMSNRYSPEFNDLDFUSKYRKPVELITEE EKYVRELKKTOLIKAAPAGKTSSVFEDEVISKFTINMMIGGNTV LARSIMIOTLEAVKKRGPEKYHAASAEEQATIERNPYTIFHOAL KNCEPMIGLVPILKAGRFYQVFVPLPDFRRRFLAKKMMITECDD KRAGKTLMPEKLSHLLEARFINGGVVIKKULHEMBAARALA HYRBW LEFTIGGRPPBEKLYLLTARKTV LARSIMIOTLEAVKKRGPEFTILSTHYGNYSLIMOTLGGERYR GSEDCSSATSGSVGANSTTGGIAVGASSSKITHLOMOSSGFD ALHEIGSIBETQAALEESFETLKBYTCGTYSLIMOTLGGERYR GCRLEEGOLNDLTELHQMEILINLKOGLASMERKIAVGSYBRADI OEALEACOTI SKRMELOQOGQOVUCLEGERNATARNLIGKLINI LLAVAVALLUFYSTVANCVPILMKTRNTFSTLPLVVFIAFLKK HWDALFSVYERPPSS PR ALHEIGSIBETQARLEESFETLKSTYCRYSLIMOTLGGERYR CCRLEEGOLNDLTELHQMEILINLKOGLASMERKIAVGSYBRADI OCALEACOTI SKRMELOQOGQOVUCLEGENATARNLIGKLINI LLAVAVALLUFYSTVANCVPILMKTRNTFSTLPLVVFIAFLKK HWDALFSVYERPPSS PR ASLERNSKAADAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	5631	1053	290	SRVDDFVRPEPSPAFDSPSCDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
TENKRAALQALERKENYERQLAQIDGTLESTIEFOREALENANTH TEVLKMINGSVARAMKAAHNADHINVDIDLADQGELAESIS TAISKPVGFGEEFDBEIMASLEPLEQEELDONLEISGPETVP LENNYSIAJPSKPAKKEEEDDDMKELENMAGUM LENNYSIAJPSKPAKKEEEDDDMKELENMAGUM SVRVARGELGWAQPGPLPPRVSSRREMQPPGPPRAVAPTINGD FTFVSSADABELGSSTASSPVKINLGGGFESTATFLRGRGY GWLLEVEDDDPEDNKPLLEELDIDLKDIYYKIRCVLMMPBLGF NRGVVRDNPDFENGLAVULFFSMISLYGGPVAPTVGGE LTIFLLARVLGGEVAYGQVLGVIGYSLPLIVIAPVLLVVGSFE VVSTLIKLFQUFWAAYSAASLLVGEBFKTKKFLLIYPIFLLYIY FLSLYTGV 460 QGCSKTMSVGRPFYRSSEFMEQLLSSHLHOVPFFCFTVCLCN CLEENSVSKLWHLCFNFFMSIFFYSLSTKKHLIYLHGLSYQSL LLLLLSGHRPWGSSMV 5634 1446 855 PRAGGIRFAASSPPAGAGASGAEPRGRERSRLGGRRAPAM ARNILSGRFRAVDIDEFDENKFVDEQBEAAAAAAFGFDPDFSEVD GLLRGODMLARFIAALRSSPVINTKNQAVKERAGGVVLKUTINK SSEIRGAVGSLENMGVDLLMKYTYKGFEKYFENSSAVLLGWHEK ALAVGGLGSIIRVLTARKTV RSFHPFPVTRSGAPPAULUGSSHPAKWAPAAVKVARGHSGLAL GVRRAVLLD-GATTOVRSKYSPFEKDEDLINKYVEELTEE EKYVRELKKTQLIKAARKSVEEDPVISKFTEMMMIGGNEV LARSIMIQTLEAVKRKQFEKYHAASAEDQATIERNFYTIFHOAL KNGEPMIGLVEILGGRGVYDVPUPDERRALMKMITECAD KNGCEPMIGLVEILGGRGVYDVPUPDERRALMKMITECAD KNGCEPMIGLVEILGGRGVYDVPUPDERRALMKMITECAD KNGCEPMIGLVEILGGRGVYDVPUPDERRALMKMITECAD KNGCEPMIGLVEILGGRGVYDVPUPDERRALMKMITECAD KNGCEPMIGLVEILGGRGVYDVPUPDERRALMKMITECAD KNGCEPMIGLVEILGGRGVYDVPUPDERRALMKMITECAD KNGCEPMIGLVEILGGRGVYDVPUPDERRALMKMITECAD KNGCEPMIGLVEILGGRGVYDVPUPDERRALMKMITECAD KNGCEPMIGLVEILGGRGVYDVPUPDERRALMKMITECAD KNGCEPMIGLVEILGGRGVYDVPUPDERRALMKMITECAD KNGCEPMIGLVEILGGRGVYDVPUPDERRALMKMITECAD KNGCEPMIGLVEILGGRGVORALGVISNFOSSPK YGSEBCGSATSGSVGANSTTGGIAVGASSSKTINTLMOSSGFD ALLHELGE IERTQALEESFETLKENYGVTSLIMOTLOEERYR CFELEGOLNDLIELHOMEILINLKGGLANMEKIAYGSYERADIO GELBEACTSI KSMELOGOGOOOVVLEGLEGLENATARNILLGKLINI LLAVMAVLLVFVSTVANCVVPIMKTRNRTFSTLFLVVFIAFLKW MDDLJFSVERFSSPR MSFCGARNAMAMANGATGGTSAAAAGHHHHHHHHLPHLPPPHLH HHHHOHILLHPGSAAAVHPVOOHTSSAAAAAAAAAAAAAAAMANMENGE OOOPYFSPAPAGAGAGAAAAAROPAOVAAAAATACHHHOHSHHD OOGLDIEPDR PIGYGARGVVSTVED PROKEVALKKWPNVFONL VSCKVPRELKKLCPFKHDNVISALDILGPRIDPFETIVVTE LMGSDLKKITVSPGLSEDHVKVFIYOTLEGKKLMISAGILHRD INGRILLVNSNALDINSGCOTPAALGRUDERLEDGSSTMTGEVVT		-		AGKGGPTPOPA TOPL DOTTERM OVVORED BY TOTAL
TEVLKNNGYAARAMKAAHDMIDIDKYDELMGITADQGELAEEIS TAISKYPGFGEFFDEDEIMAELEEIGELDKILLEISGPETVP LPNYPSIALPSKPAKKKEBEDDDMKELENMAGGM VVLGMSPPRLWMGSLGAAGRPAVFVSGLARSHHYERRPHRRA SVRVARGRIGWAQQPLLDPREVGSKREMQPPOPPAYAPTNGG FTFYSSADAEDLSGSIASPDVKINLGGDFIKBSTATTFLRGRGY GWLLEVEDDPPDMKPLLEELDILLAVYKIRCVLMMPBLGF NRQVVRDNDPMGPLAVVLFFSMISLYGQFRVVSWIITTWIFGS LTIFLLARVLGGEVAYCOVLGVIGYSLLPLIVVARCVLLVUGSSI VVSTLIKLPGVFWAAYSAASLLVGEBFKTKKPLLIYPIFLLYIY FLSLYTGV OGCSKTMSVGRPFYRSSEFMEQLLSSHLHQVPFFCCFTVVCLCN CLFENSVSKIMLCFNFFMSIFFYSLSITKLNLIYLWGLSYQSL LLLLLSGHPWGSSMV GGSKTMSVGRPFYRSSEFMEQULSSHLHQVPFFCCFTVVCLCN CLFENSVSKIMLCFNFFMSIFFYSLSITKLNLIYLWGLSYQSL LLLLLSGHPWGSSMV GGLRQCDMMRAFHAARNSPVNTKNQAKRAQGVVLKVLTNFK SSSIEQAVQSLDRRGVDLLMKYIYKGFEKPTENSAVLLQWHEK ALAVGGLSITRVLTARKTV SSSIEQAVQSLDRRGVDLLMKYIYKGFEKPTENSAVLLQWHEK ALAVGGLSITRVLTARKTV SSPHFFFVTRSAQPAVLVGSSWPAKMAAPAVKVARGMSGLAL CVRRAVLQLPGLTQVTNSKYSPBFFKDLBKYYKKPVELITEE EKYVRELKKTQLIKAAPAGKTSSVFEDPVISKFTNMMIGGNRV LARSIMIOTLEAVKRRGFKKYANSTSPFEKDATENPYTIFHOAL NCCEPMIGLVPILKGGRFYQVPVPLPDRRRFFLAMKWMITECRD KKHQRTLMPEKLSHKKLLEAFFNQGPVIKKMLEYMERVELITEE EKYVRELKKTQLIKAAPAGKTSSVFEDPVISKFTNMMIGGNRV LARSIMIOTLEAVKRRGFKKYANSTSPFEKDATENPTYTIFHOAL NCCEPMIGLVPILKGGRFYQVPVPLPDRRRRFLAMKWMITECRD KKHQRTLMPEKLSHKLLEAFFNQGPVIKRKMLENGANGALA LEDTICGPPABKKULYHRKLREVERNGIPRLPKDVFHDTHQG LTDVRAKVTGFSECVVDSVKGGFSSFSQATHSAAGAVKRPRSI ASLINNKFGSADMIPNLOSLEBEGOVDDAGKALGVISNFQSSFX YGSEEDCSASTSGVADNSTTGGIAVGASSKTNTDMGSSGFD ALHBIGPSIRFTQAALEESFFTLKEHYQNSFRAGAVVKSPRBI ASLINNKFGSADMIPNLOSLEBEGOVDDAGKALGVISNFQSSFX YGSEEDCSATSGVADNSTTGGIAVGASSKTNTDMGSSGFD ALHHELGEIRFTQAALEESFFTLKEHYQNSFLOGERYR CCELEEQUNDLTELHQNISTUANCVVPLMKTRNRTFSTLFLVVFIAFLMK HWDALFSVYREPFSSPR GEALBEACHTOR GERERALDVARAMAAAAAAAAAAAAAAAAAAAAAAAAMNINGG OOOPYFFSPAPGQACFSAAAAAAQAAAAAAAAAAAAAAAAANAMNINGG OOOPYFFSPAPGQACFSAAAAAAQAAAAAAAAAAAAAAAAAAAAAAAAAAAA	(I			TENEDAT TOTAL TRANSPORT TOTAL
TAISKPVGFGEEFFDELMABLEELEGGELDKHLLEISGPETVP LPNNPSIALPSKPAKKREEDDDMKELMAGSM 5632 3 952 VVLGWSPPRLWWGSLGAAGRPAVFVSGLARSLHVETRRPHRRA SVRVARGRIGWAGPGPLIPREVGSKREMGPEPGPPAVAPTNGD FTFVSSADAELLSGSIASPDVKINLIGGFIKESTATTELRGRGY GWLLEVEDDDPEDHKPLIEELDIDLKGIYYKIRCVLMFMPBLGF NRGVVRDNDFPHGPLAVUFFSMELVGPTVSKENGTPEPGPRVSWHITIWIFGS LTIFLLARVLGGEVAYGQVLGVIGYSLLPLIVIAPVLLVVGSFE VVSTLIKLFGVWAAVSAASLLVGEBFKTKKPLLIYPIFLLYIY FLSLYTGV 5633 771 460 GGCSKTMSVGRPFYRSSEPMEGLLSSHLHQVPFFCCFTVVCLCX CLFENSVSKLIMLGFNFMSIFPTSISFMEGLLSSHLHQVPFFCCFTVVCLCX CLFENSVSKLIMLGFNFMSIFPTSISFRGRERSRLSGRRAPAM ARNILSSRFRRVDIDEPDENKFVDEGREAAAAAAPEPGPDFSEVD GLLRQGDMRAFHAALRNSPVSTKNQAVKRAGGVULKVLINFK SSELEGAVGSLLANGVSLLMKYIYYKGPFKPTENSSAVLLQWHEK ALAVGGLGSIIRVLTARKTV 5635 3 943 DRGFRSTATDTGRREVSFMFFLDFGVKNSNVOISGEKREFFTL RSLFHFPFVTRSGAPARVLVGSSMPAKMVAPAVKVARGWSGLAL GVRRAVLCLPGLTQVRNSRYSBEFKDDLDKSYYKRPVEELTEE EKYVBLKKTQLIKAAPAGKTSSVFEDFVISHTMMMIGGNV LARSLMIQTLEAVKRQFFKYHAASAECATTERNPYTIFHOAL KNCEPMIGLVFILKGGRFYQVVVPLPDRRRRFLAMKMMITECRD KRAQRTLMPERLSSKLLEAFFNQGPVIKRKHDLHKMAEANRALA HYRW 5636 2253 1143 LEDTICOHPPAEKKLYLYHRLREVERNGI FRLPKDVFMDTHQG LTDVRAKVTGFSBGVVDSVKGGFSSFSQATHBAAGAVVSRPRBI ASLINNKFGSADNI FNLXOSLEBGQVDDAGKALGVI SNPOSSPK YGGEBCCSSATGSSVANNSTTOGLIVAGSSKTNTLDMOSSPK AGSEBCGSSATGSSVANNSTTOGLIVAGGEBNATARNLLGKLINI LLAWAVLLUFVSTVARPSTVARPSTVARPS FRARDI GEALEACQTRISKMELQOOQQQVVCLEGLBNATARNLLGKLINI LLAWAVLLUFVSTVARPSVERFFSSP CERLEBOLINDLTELHQNEILINLKGELASMEKIANSY FRARDI GEALEACQTRISKMELQOOQQQVVCLEGLBNATARNLLGKLINI LLAWAVLLUFVSTVARPSVERFPSSP OQOPLYFFSPAPGACPGFAAAAAAAAAAAAAAMNINGG OQOPLYFFSPAPGACPGFAAAAAAAAAAAAAAAMNINGG OQOPLYFFSPAPGACPGFAAAAAAAAAAAAAAAMNINGG OQOPLYFSPAPGACPGFAAAAAAAAAAAAAAAAMNINGG OQOPLYFSPAPGACPGFAAAAAAAAAAAAAAAANNINGG OQOPLYFSPAPGACPGFAAAAAAAAAAAAAAAAMNINGG OQOPLYFSPAPGACPGFAAAAAAAAAAAAAAAAMNINGG OQOPLYFSPAPGACPGFAAAAAAAAAAAAAAAAAMNINGG OQOPLYFSPAPGACPGFAAAAAAAAAAAAAAAAMNINGG OQOPLYFSPAPGACPGFAAAAAAAAAAAAAAAAMNINGG OQOPLYFSPAPGACPGFAAAAAAAAAAAAAAAMNINGG OQOPLYFSPAPGACPGFAAAAAAAAAAAAAAAMNINGG OQOPLYFSPAPGACPGFAAAAAAAAAAAAAAAAA				TEM VENCYA TANKA TEKQLAQIDGTLSTIRFQREALENANTN
S632 3 952 VVLGUSPPRILMGSLGARORPAVEVGLARSIHMUTRIPHERA SURVARGRIGUWAQPQPLLPRPVGSRREMQPPGPPAVAPTNGD FTFVSSADAEDLSGSIASPDVIGLNIGGGFIKESTATTFLRGRGY GWLLEVEDDDPEDMKPLLEELDILKYKIRCVLMMPSLGF NRQVVRDNDDFWGPLAVVLFFSMISLYGQFRVVSWIITITHIFGS LTIFILLARVIGGGFIKASTATTFLRGRGY VVSTLIKLBYGVEWAAYSAASLLVGEEFKTKKPLLIYPIFLLYIY FLSLYTGV GCSKTMSVGRPFYRSEFMEQLLSSHLHOVPFFCCFTVVCLCN CLFENSVSKLYMLCFNFFMSI FYSLSITKINLIYLWGLSYQSL LLLLLSGHFPWGSSMV CLFENSVSKLYMLCFNFFMSI FYSLSITKINLIYLWGLSYQSL LLLLLSGHFPWGSSMV GCSKTMSVGRPFYRSSEFMEQLLSSHLHOVPFFCCFTVVCLCN CLFENSVSKLYMLCFNFFMSI FYSLSITKINLIYLWGLSYQSL LLLLLSGHFPWGSSMV GCSKTMSVGRPFYRSSEFMEQLLSSHLHOVPFFCCFTVVCLCN CLFENSVSKLYMLCFNFFMSI FYSLSITKINLIYLWGLSYQSL LLLLLSGHFPWGSSMV GCSKTMSVGRPFYRSSEFMEQLSGRAPAM ARNTLSSRFRRVDIDEFDENKFVDGGRAAAAARAAFGPDFDSEVD GLLRQGDMLRAFHAALRNSPVMTKNQAKRAGGVULKUTINKK SSEIEQAVQSLDRRGVDLLMKY1YKGFEKFTENSAVLLQWHEK ALAVGGLGSITRVLTARKTV GSENGAMMAAYAGGSIRVLTNFKK SSEIEQAVQSLDRRGVDLLMKY1YKGFEKFTENSAVLLQWHEK ALAVGGLGSITRVLTARKTV GVRAVLQLDGLGTRAFVLAGSSMPAKMVAAYAGMSGGLAL GVRAVLQLDGLGTVANSRYSPBFKOPLIDKSYYRKVPEELTEE EKVYRELKKTQLIKAAFAAAKTSSVFEDPVISKYTINMMIGGNKV LARSIMIOTLEAVKRRGFKYNAVSPSERDPVISKYTINMMIGGNKV LARSIMIOTLEAVKRRGFKYNAVSPFRENDPLIDKSYYRKVPEELTEE EKVYRELKKTQLIKAAFAAGKTSSVFEDPVISKYTINMMIGGNKV LARSIMIOTLEAVKRRGFKYNAVSPRENDPLIDKSYYRKVPEELTEE EKVRELKKTQLIKAAFANGKTSSVFEDPVISKTTHMMIGGNKV LARSIMIOTLEAVKRRGFKYNAVSVFRENDPLIDKSVYRKVPEELTEE EKVRELKKTQLIKGGRFYQVPVDLPGRRRFLAMKWMITECDA KNCCPMIGLIVEILKGGRFYQVPVDLPGRRRFLAMKWMITECDA KNCCPMIGLIVEILKGGRFYQVPVDLPGRRRFLAMKWMITECDA KNCCPMIGLIVEILKGGRFYQVPVDLPGRRRFLAMKWMITECDA KNCCPMIGLIVEILKGGRFYQVPVDLPGRRRFLAMKWMITECDA KNCCPMIGLIVEILKGGRFYQVPVDLPGRRRFLAMKMITECDA KNCCPMIGLIVEILKGGRFYQVPVDLPGRGRFSGATHSAAGAVSKPRBI ASLINNKFGSADMIPNLOSIGGFSFSGATHSAAGAVSKPRBI ASLINNKFGSADMIPNLOSIGGFSFSGATHSAAGAVSKPRBI ASLINNKFGSADMIPNLOSIGGFSFTTIKEHLYGYSFRADDI GCALERCATGRITISMMELOQOQQQVVUGGGRAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1 1			TEVEKNMGYAAKAMKAAHDNMDIDKVDELMQDIADQQELAEEIS
952 VVLGWSPPRLWWGSLGRADRPAVPVSGLARSLHVETERPERRA SVEVARGRIGVWADPOPLLPRPVGSRREMQPPGPPARAPTINGD FTFVSSADAEDLSGSIASPDVKLNLGGDFIKESTATTFLRQRGY GWLLEVEDDDPEDNRPLLEELDIDLKDIYYKRCVLMPMPSLGF NRQVVERNDPFWGPLAVVLFFSWISLYGGFRVSWITTINFGGS LTTFLLARVLGGEVAYGQVLGVIGYSLLPLLIVIAPVLLVVGSPE VVSTLIKLPGVFWAAYSAASLLVGEBFKTKKPLIYPFILTIY FLSLYTGV 5633 771 460 GGCSKTMSVGRFFYRSSEFMEQLLSSHLHOVFFFCCFTVVCLCN CLFENSYSKLYMLCENFFMSIFFYSLSITKINLIYLMGLSYGSL LLLLLSGHRPWGSMV 5634 1446 855 PRATGRIESRAAJASRFRAGAGASGAEFRSGRERSGRERAPAM ARNTLSSRFRRVDLDEFDENKFVDEGBEAAAAAEFOPDPSEVD GLLRQGDMRAPHAALRNSPVNTKNQAVERRAGGVVLKVLTNRK SSEIEQAVQSLDRNSVDLLMKYIYKGFEKPTENSSAVLLQWHEK ALAVGGLGSITRVLTARKTV 5635 3 943 DRGPRSTATDTGRARVSFWFFDLDFVKNSNVQISGEKRRFRTL RSLFHFFVTRSGAPRAVLVGSSWPAKWVAPAVKVARGWSGLAL GVRRAVLQLPGLTQVRNSRYSPFKDPLUBEVYRKPVEELITE EKYWRELKKTQLIKAPAGKTSSVFDPVISKFTNMMIGGNKV LARSLMIQTLEAVKRQFEKYHAASAEEQATIERNPYTIFHQAL KNCGFMIGLVPILKGGFTQVPVPLDFDRRRFLAMKWMITECRD KNCGFMIGLVPILKGGFTQVPVPLDFDRRRFLAMKWMITECRD KNCGFMIGLVPILKGGFTQVPVPLDFDRRRFLAMKWMITECRD KNCGFMIGLVPILKGGFTQVPVPLDFDRRRFLAMKWMITECRD KNCGFMIGLVPILKGGFTQVPVPLDFDRRRFLAMKWMITECRD KNCGFMIGLVPILKGGFSFSGATHSAAGAVVSKPRBI ASLINNKFGSADNIPHLXDSLEEGGVDDAGKALGVISNTGSSFK YGSEBCSSATSGSVGANSTTGGIAKGSSKYNTLDMGSSGFD ALLHBLQGIRBTDARLEESFETLKRHYGRDYSLIMGTLQGENYR CFELEGOLNDLTBLHQNEILMKGLASSKYNTLDMGSSGFD ALLHBLQGIRBTDARLEESFETLKRHYGRDYSLIMGTLGGENYR CFELEGOLNDLTBLHQNEILMKGLASSKYNTLDMGSSGFD ALLHBLQGIRBTYVEFFSSR 5637 948 2532 MSFCGRRRAMMAAYNGGTSAAAAGHHHHHHHLPHLPHPPHLH HHHHPCHHLHPGSAAAVHAVOCHTSSAAAAAAAAAAAAAMMANNPG OQODFFFSPAGGAFGVWSVTDPRGGRVALKMMNNVFCNL VSCKWFRELKMLCPGPAAAAFAGVAAAAAAAAAAAAMMANNPG OQODFFFSPAGGAFGVWSVTDPRGGRVALKMMNNVFCNL VSCKWFRELKMLCPGFKHDNILSALDLLQPHIDYFBEIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILGGKYLLKSAGILHRD IKPGRLUNNSNCVLKCDFGLARVEELDESRIMTGEVVTQYYRA PSILMGSSHYSNALDIWSWGCTFAELGREILPGEGPGOLDL VSCKRYFELKMLCTPFKHDNUSALDELDESRIMTGEVVTQYYRA PSILMGSSHYSNALDIWSWGCTFAELGREILPGLEGDEGDIOLDL VSCKRYFELKMLCTPFKHDNUSAGLTPBLGGRVPLKDSGLIHRD IKPGRLUNNSNCVLKCDFGLARVEELDESRIMTGEVVTQYYRA				TAISKPVGFGBEFDEDELMAELEELEQEELDKNLLEISGPETVP
SVEWARGRIGVMAQPQPLIPEPPVGSRREMQPPGPPPAYDTINGG FTFYSSADABDLSGSIASPDVKLNLGGDFIKESTATTELRQRGY GWLLEVEDDDPEDNEPLBELDIDLYPKTRCVLMPMPSLGF NRQVVRDNPDFMGPLAVVLFFSMISLYQGFRVVSWITTINIFGS LTIFILARVIGGVAYGQVLGVIGYSLLELIVJAPVLLVVGSFE VVSTLIKLRGVBWAAYSAASLLVGEBFKKKPLLIYPIFLLYIY FLSLYTGV 5633 771 460 QGCKKTMSVGRPFYRSSEFMEQLLSSHLHQVFFFCCFTVVCLCN CLFENSVSKLYMLCFNFFMSIFFYSLSITKLNLIYJLMGLSYQSL LLLLLSGHRPMGSSMV GLLRQGDMLRAFHAALRNSPVNTKNQAVKERAGQVVLKVLTINK SSEIEQAVQSLDRNGVDLLMKYIYKFFEKPTENSSAVLLQWHEK ALAVGGLGSIIRVLTARKTV SEIGAVQSLDRNGVDLLMKYIYKFFEKPTENSSAVLLQWHEK ALAVGGLGSIIRVLTARKTV DRIPGSTATDTGARAVSFWMFPLDFQVKNSNVQISGEKRFFRTL RSLFHPFPVTRSGAPRAVLVGSSWPAKWVAPAVKVARGMSGLAL GVRRAVLQLPGITQVRNSRVSPEFDDFQVKNSNVQISGEKRFFRTL RSLFHPFPVTRSGAPRAVLVGSSWPAKWVAPAVKVARGMSGLAL GVRRAVLQLPGITQVRNSRVSPEFDDFQVKNSNVQISGEKRFRTL RSLFHPFPVTRSGAPRAVLVGSSWPAKWAPAVKVARGMSGLAL GVRRAVLQLPGITQVRNSRVSPEPDDFGVKNSNVQISGEKRFRTL RSLFHPFPVTRSGAPRAVLVGSSWPAKWAPAVKVARGMSGLAL GVRRAVLQLPGITQVRNSRVSPEPDDFGVKNSNVGISGEKRFRTL RSLFHPFPVTRSGAPRAVLVGSSWPAKWAPAVKVARGMSGLAL GVRRAVLGLPGITQVRNSRVSPEPDDFGVKNSNVGISGEKRFRTL RSLFHPFPVTRSGAPRAVLVGSSWPAKWAPAVKVARGMSGLAL GVRRAVLGLPGITQVRNSRVSPEPDDFGVKNSNVGISGEKRFRTL RSLFHPFPVTRSGAPRAVLVGSSWPAKWAPAVKVARGMSGLAL GVRRAVLGLPGITQVRNSRVSPEPDDFGVKNSNVGISGEKRFRTL RSLFHPFVTRSGAPRAVLVGSSWPAKWAPAVKVARGMSGLAL GVRRAVLGLESVFRUDGFFTLKRDHTMMGGMKV LARSLMIQTLEAVKRQFESVFRDPVISKTMMGGMKV LARSLMIQTLEAVKRQFESVFRDPVISKTMMGGMKV LARSLMIQTLEAVKRQFESVFRDPVISKTMMGGMKV AKCHTLMPEKLSKKLLEAFHNQGFVIRKMDHKMAEANRALA HYRMW LEPTICQHPPAEKKLVJLYHRKLREVERNGIFRLDKOVFDTTQG LTDVRAKVTGFSEGVVDSVKGGFSSPQATHSAAGAVVSKPREI ASLIRNKFGSADAINIPHLKDGLBEGQVDDAGARAVSINTQGSSPR YGSEEDCSSATSGSVQANSTTGGIAVGASSKINTLDMGSGCP ALLHEIQGIRETQARLEESFFTLKEHYQRDYSLIMOTLQEERYR CERLESOLNDLTELHONG LINLKQELAMBEKIAVGSVERREDI QEALEACOTRISKMELQQQQQVVQLEGLENATARHLGKLINI LLAVMAVLLVVSTVANCVVPLMTTRNRTFSTLFLVVFIAFLWK HHHPQHILHPGSAAAVHPVOQHTSSAAAAAAAAAAAAAANAMNPG QQQDFFSPAPGGAGPGAAAAAAQQAAAAATVKAHHQHGSHHP QQQLDIEPDRPIGGAFGVWSVTDPRGGRVALKKMMNVFCONL VSKKWFRELLMLCFFKHNONLSALLUPPHLDYFEITVVTE LMQSDLHKIIVSQQFJECLLQPHLDYFEITVV	F (7.7)			LPNVPSIALPSKPAKKKEEEDDDMKELENWAGSM
FTFYSSADABLSGSIASPDVKNLGGDFIKESTATTFLRQRGY GWLLEVEDDDPEDNEPLLEBLDILLKIPTYKIR CVLMPMPSLGF NRQVVRDNPDFWGPLAVVLFFSMISLYGGFRVVSWITTINIFGS LTTIFLLARVLGGEVAYGQVLGVIGYSLLPLIVJAPVLLVVGSFE VVSTLIKLFGVWAAYSAASLLVGEBFKKKPLLIYPIFLLYIY FLSLYTGV 5633 771 460 QGCKKRINSVGRPFYRSSEFMEQLLSSHLHQVFFFCCFTVVCLCN CLFENSVSKLYMLCFNFFMSIFFYSLSITKKINLIYLMGLSYQSL LLLLLSGHRPWGSSMV 5634 1446 855 PRATGIR SRANASEPRAGAGAGAEPESGRERSELSGRRAPAM ARNTLSSRPRRVDIDEPDENKFVDEQBEAAAAAAEPGPDPSEVD GLLRQDMLRAPHAALINSPYNTKNQAVKERAGQVVLKVLTINK SSEIEQAVQSLDRNGVDLLMKYIYKFFEKPTENSSAVLLQWHEK ALAWGGLGSIIRVLTARKTV DRGPBSTATDTGRARVSFWMFPLDFGVKNSNVQISGEKRFFTL RSLFHPFPVTRSGAPRAVLVGSSWPAKWVAPAVKVARGWSGLAL GVRRAVLQLPGLTQVRNSRVSPFKDPLIDKEYYRKEVEELITEE EKYVRSLKKTQLIKAPAGKTSSYEPTISHTYTIFHQAL KNCEPHIGLVPILKGGRFYQVPVPLPBTRRRFLAMKWMITECRD KNCRTLMPEKLSKKLLEAFHNGGPVIRRKHDLHKWAEANRALA HYRWW LARSLMIQTLEAVKRKOFEKYHAASAESGATIERNPYTIFHQAL KNCEPHIGLVPILKGGRFYQVPVPLPBTRRRFLAMKWMITECRD KNCRTLMPEKLSKKLLEAFHNGGPVIRRKHDLHKWAEANRALA HYRWW LEFTICOHPPAEKKLVJLYHRKLREVERNGIPRLPKDVFMDTTGG LTDVRAKVTGFSEGVVDSVKGGFSSPQATHSAAGAVVSKPREI ASLIRNKFGSADNIPHLKOGRFYQVDVLPKGRAGAVISNTOGSSPK YGSEEDCSSATSGSVGANSTTGGIAVGASSKINTLDMGSSGFD ALLHEIQEIRETQARLEESFETLKEHYGNDYSLIMOTLGEERYR CERLEGOLNDLTELHONELLIKKQELASMEEKIAYGSYERARDI QEALEACOTRISKMELQQOOQVVQLEGLENATARHLIGKLINI LLAVMAVLLVVSTVANCVVPLMTTRNRTFSTLFLVVFIAFLWK HHDALHSTYVEFFESSPR GEGGRANAMMAAVNGGTSAAAAGHHHHHHHHLPHLPFPPHLH HHHHPQHILHPGSAAAVHPVOCHTSSAAAAAAAAAAAAAAANMLNPG QOQDFFFSPAPGGAGPGPAAAAEAGVQAAAAATVKAHHQHSHHP QOQLDIEDDRPIGGAGFGVWSVTDPRIGGRVALKMMNNVGONL VSCKRYFELKMLCFPKHONLSALULGPHDYFEBIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILEGKKYLKSAGILHRG IKPGRILVNSNCVLKCDFGLARVEELDESRIMTGGEVTYTYTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILEGKKYLKSAGILHRG IKPGRILVNSNCVLKCDFGLARVEELDESRIMTGGEVTYTYTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILEGKRYLKSAGILHRG IKPGRILVNSNCVLKCDFGLARVEELDEERRIMTGEVUTQYTYRA PEILMGSSHYSNLDIDWSGCTFFELLGGRRIFTGPQSVTQTYRA	3632	3	952	VVLGWSPPRRLWWGSLGAAQRPAVPVSGLARSLHVETRRPHRRA
FTFYSSADABLSGSIASPDVKNLGGDFIKESTATTFLRQRGY GWLLEVEDDDPEDNEPLLEBLDILLKIPTYKIR CVLMPMPSLGF NRQVVRDNPDFWGPLAVVLFFSMISLYGGFRVVSWITTINIFGS LTTIFLLARVLGGEVAYGQVLGVIGYSLLPLIVJAPVLLVVGSFE VVSTLIKLFGVWAAYSAASLLVGEBFKKKPLLIYPIFLLYIY FLSLYTGV 5633 771 460 QGCKKRINSVGRPFYRSSEFMEQLLSSHLHQVFFFCCFTVVCLCN CLFENSVSKLYMLCFNFFMSIFFYSLSITKKINLIYLMGLSYQSL LLLLLSGHRPWGSSMV 5634 1446 855 PRATGIR SRANASEPRAGAGAGAEPESGRERSELSGRRAPAM ARNTLSSRPRRVDIDEPDENKFVDEQBEAAAAAAEPGPDPSEVD GLLRQDMLRAPHAALINSPYNTKNQAVKERAGQVVLKVLTINK SSEIEQAVQSLDRNGVDLLMKYIYKFFEKPTENSSAVLLQWHEK ALAWGGLGSIIRVLTARKTV DRGPBSTATDTGRARVSFWMFPLDFGVKNSNVQISGEKRFFTL RSLFHPFPVTRSGAPRAVLVGSSWPAKWVAPAVKVARGWSGLAL GVRRAVLQLPGLTQVRNSRVSPFKDPLIDKEYYRKEVEELITEE EKYVRSLKKTQLIKAPAGKTSSYEPTISHTYTIFHQAL KNCEPHIGLVPILKGGRFYQVPVPLPBTRRRFLAMKWMITECRD KNCRTLMPEKLSKKLLEAFHNGGPVIRRKHDLHKWAEANRALA HYRWW LARSLMIQTLEAVKRKOFEKYHAASAESGATIERNPYTIFHQAL KNCEPHIGLVPILKGGRFYQVPVPLPBTRRRFLAMKWMITECRD KNCRTLMPEKLSKKLLEAFHNGGPVIRRKHDLHKWAEANRALA HYRWW LEFTICOHPPAEKKLVJLYHRKLREVERNGIPRLPKDVFMDTTGG LTDVRAKVTGFSEGVVDSVKGGFSSPQATHSAAGAVVSKPREI ASLIRNKFGSADNIPHLKOGRFYQVDVLPKGRAGAVISNTOGSSPK YGSEEDCSSATSGSVGANSTTGGIAVGASSKINTLDMGSSGFD ALLHEIQEIRETQARLEESFETLKEHYGNDYSLIMOTLGEERYR CERLEGOLNDLTELHONELLIKKQELASMEEKIAYGSYERARDI QEALEACOTRISKMELQQOOQVVQLEGLENATARHLIGKLINI LLAVMAVLLVVSTVANCVVPLMTTRNRTFSTLFLVVFIAFLWK HHDALHSTYVEFFESSPR GEGGRANAMMAAVNGGTSAAAAGHHHHHHHHLPHLPFPPHLH HHHHPQHILHPGSAAAVHPVOCHTSSAAAAAAAAAAAAAAANMLNPG QOQDFFFSPAPGGAGPGPAAAAEAGVQAAAAATVKAHHQHSHHP QOQLDIEDDRPIGGAGFGVWSVTDPRIGGRVALKMMNNVGONL VSCKRYFELKMLCFPKHONLSALULGPHDYFEBIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILEGKKYLKSAGILHRG IKPGRILVNSNCVLKCDFGLARVEELDESRIMTGGEVTYTYTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILEGKKYLKSAGILHRG IKPGRILVNSNCVLKCDFGLARVEELDESRIMTGGEVTYTYTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILEGKRYLKSAGILHRG IKPGRILVNSNCVLKCDFGLARVEELDEERRIMTGEVUTQYTYRA PEILMGSSHYSNLDIDWSGCTFFELLGGRRIFTGPQSVTQTYRA	1			SVRVARGRLGVWAQPQPLLPRPVGSRREMQPPGPPPAYAPTNGD
GWLLEVEDDPEDNKPLLEELDIDLKDITYKIRCULMPMPSLGF NRQVVRDNDPFMOPLAVULFSMISLYGGFRVVSWIITIWIFGS LTIFLLARVLGGEVAYGQVLGVIGYSLLPLLVLAPVLLVVGSFE VVSTLIKLFGVFWAAYSAASLLVGEEFKTKKPLLIYPIFLLYIY FLSLYTGV 5633 771 460 GGCSKTMSVGRPFYRSSEFMEQLLSSHLHQVPFFCCFTVVCLCN CLFENSVSKLYMLCFNFFMSIFFYSLSTKINLIYLWGISYGSL LLLLLSGHRPWGSSMV 5634 1446 855 PRATGRIRSBAAASFRRAGAGAGGAEPRSGRERSRLSGRRAPAM ARNTLSSRPRRVDIDEFDENKFVDEQBEAAAAABFORPDFSEVD GLLRQGDMRAPHAALRNSPVNTKNQAVKERAGGVVLKVLTNFK SSELEQAVOSLDRNGVDLLMKYIYKGFEKFTENSSAVLLQWHEK ALAVGGLGSIIRVLTARKTV RSPHFFFPVTRGGAPRAVLVGSSWPARWAPAVKVARGRSGLAL GVRRAVIQLDGLTGVWSRYSPBFKDLDIKEYTRYPVELTEE EKYVRELKKTQLIKAAPAGKTSSVFEDPVISKFTNMMIGGNKV LARSLMIQTLEAVKRKQFEKYHAASAGATISRNFYTIFHOAL KNCEPMIGLVPILKGGRFYQVPVPLPDRRRFLAMKWMITECRD KNCQRTLMPEKLSHKLLEAFHNQGPVIKRKHDLHKMAEANRALA HYRW 5636 2253 1143 LEDTICQHPPAEKKLYLYHRKLREVERNGIPRLPKDVFMDTHQG LTDVRAKVTGFSEGVVDSVKGGFSSFSQATHSAAGAVSKFREI ASLIRNKFGSADNIPNLMSDLEEGQVDDAGKALGYISNFOSSPK YGSEBCCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD ALLHEIGPIRRTQARLEESFETLKEHYGRYSLIMOTLGERYR CERLEBOLNDLTEHLQMEILINKGELASMERKIAVGSVERREDI OEALEACOTRISKMELQOQOQQVVQLEGLBNTARNLLGKLINI LLAVWAVLLVFVSTVANCVVPLMKTRNRFSTLFLVVFIAFLMK HHDALFSVVERFPSSPR 5637 948 2532 MSFCGARNANMAMANYNGGTSAAAAAHHHHHHHHPHLPPHLPPHLH HHHPOHLLHPGSAAAVHPVQOHTSSAAAAAAAAAAAAAAAAANANANALNPG OQOPYFPSPAPGGAPGPAAAAFAQVQAAAAATVKAHHHQHSHHP OQOQLDIETDRIGGAFGVVWSVTDPROKKRVALKKWPNVFONL VSCKRVFRELKMLCFFFHDDWILSALDDILQPPHIDYFERIYVVTE LMGSDLHXIVSPQPLSSDHVKVFLYQILRGLKYLLHSAGILHRD IVPGMLLVNSNCVLKILOFGLARVEELDESRRMTQEVTGYYRA	ł l			FTFVSSADAEDLSGSIASPDVKLNLGGDFIKESTATTFLRORGY
NRQVYRDNPDFMOPLAVULFFSMISLYGOFRVUSMILTHIPIGS LTIFLLARVLGGEVAYGQVLGVIGYSLLPLIVIAPVLLVVGSFE VVSTLIKLPGVWAAYSAASLLVGEEFKTKKPLLIYPIFLLYIY FLSLYTGV 5633 771 460 GGCSKTMSVGRPPYRSSEFMEQLLSSHLHQVPPFCCFTVVCLCN CLFENSVSKLYMLCFNFFMSIFFYSLSITKINLIYLWGLSYQSL LLLLLSGHRPWGSSMV FRANGEIRSGRANARSPRAGAGASGAEPRSGRERSRLSGRRAPAM ARNTLSSRPRVDIDEFDENKFVDEQBEAAAAAEPGPDPSEVD GLLRQGDMURAPHAALRNSPVNTKNQAVKERQGVVLKVLTNFK SSEIEQAVQSLDRNGVDLLMYLYYKGFFKPTENSSAVLLQWHEK ALAVGGLGSIIRVLTARKTV 5635 3 943 DRGPRSTATDTGRARVSFWRFPLDFGVKNSNVQISGEKRRFRTL RSLFHPFPTRSGAPRAVLVGSSMPAKMVAPAVKVARGMSGLAL GVRRAVLGLGCLTQVRNSRYSPEFKDPLIDKEYYRKPVEELTEE EKYVRELKKTQLIKAAPAGKTSSVFEDPVISKFTNNMMIGGMKV LARSLMIQTLEAVKRQFEKYHAASASEQATIERNYFIFHQAL KNCEPMIGLVPILKGGRYQVPVPLDPRRRFLAMKWMITECRD KKHQRTLMPFKLSHKLLEAFHNQGPVIKRKHDLHKMAEANRALA HYRWW 5636 2253 1143 LEDTTCQHPAEKKLYLYHRKLREVERNGIPRLPKDVFMDTHQG LTDVRAKVTGFSEGVVDSVKGGFSSPSQATHSAAGAVVSKPRBI ASLIRNKFGSADNIPNLXDSLEBGQVDDAGKALGVISNFQSSPK YGSEBDCSSATSGSVGANSTITGJIAVSASSKTNTLDMQSSGPD ALLHEICGIERTGAALESFFTLKEHVQRDYSLIMOTLQEERYR CERLEEOLNDLTELHQNEILNLKQELASMERKIAVGSYERREDI QEALEACOTRISKMELQQQQQVVQLEGLENATARNLIGKLINI LLAWAVLLVFYSTVANCVVPLMKTRNTFSTLFILVVFIAFLWK HWDALFSYVERFPSSPR 948 2532 MSFCGRRANAMMAAYNGGTSAAAAAHAAAAAANLNPG CQOPYFPSPAPGAPGAPGAAAAPAAAAAAAAAANLNPG CQOPYFPSPAPGAPGAPGVWSVTDPROKKRVALKKMYBNVPQNL VSCKRVFRELKMLCFFKHDNULSALDILLQPBILDYFEIYVTTE LMGSDLHKI VISPQPLSSDHVKVFLYQILRGLKYLLKRMPNVPQNL VSCKRVFRELKMLCFFKHDDVLSALDILLQPBILDYFEIYVTTE LMGSDLHKI VISPQPLSSDHVKVFLYQILRGLKYLLKRGLHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRRMTQEVVTOYYRA	1 1			GWLLEVEDDDPEDNKPLLEELDIDLKDIVYKIRCVI.MPMPGI.GE
LTIPILARVIGGEVAYGQVLGVIGYSLIPLIVIAPVILLVUGSFE VVSTLI KLFQVFWAAYSAASLLVGEEFKTKKKPLLIYPIFILYIY FLSLYTGV GGCSKTMSVGRPFYRSSEFMEQLLSSHLHQVPFPCCFTVVCLCN CLFENSVSKLYMLCFNFFMSIFFYSLSITKLNLIYLWGLSYGSL LLLLLSGHRPWGSSMV 5634 1446 855 PRATGRIRSRAAASFPRAGAGASGAEPRSGRERSRLSGRRAPAM ARNTLSSRPRRVDIDEFDENKFVDEQBEAAAAAAFRGPDPDSEVD GLIRQGDMLRAPHAALRNSPVNTKNQAVKERQGVVLKVLTNFK SSEIEQAVQSLDRNGVDLLMKYIYKGFEKPTENSSAVLLQWHEK ALAWGGLGSIIRVLTARKTV 85635 3 943 DRGPRSTATDTGRARVSFWRFPLDPGVKNSNVQISGEKRRFRTL RSLPHPFPVTRSGAPRAVLVGSSMPAMVAPAVKVARGWSGLAL GVRRAVLQLPGLTQVRWSKYSPEFKDPLIDKEYYRKPVELITEE EKVVRELKKTQLIKAAPAGKTSSVFEDPVISKFTNMMIGGNKV LARSLMIQTLEAVRKQFEKYHAASABEQATIERNPYTIFHOAL KNCEPMIGLVPILKGGRFYQVVPVPDPRRRFLAMKMMITECRD KKHQRTLMPEKLSHKLLEAFINOGPVIKRRHDLHKMAEANRALA HYRRW 5636 2253 1143 LEDTICQHPPAEKKLYLYHRKLREVERNGIPRLPKDVFMDTHQG LTDVVRAKVTGFSEGVVDSVKGGFSSFSQATHSRAGAVVSKPREI ASLIRNKFGSADNIPNLXDSLEEGQVDDAGKALGVISNFQSSPK YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLUNGSSGFD ALHELGEIRETQARLEESFETLKEHYORDYSLIMGTLQEERYR CERLEBOLNDLTELHQNE ILNLKQELASMERIAVQSVERRRDI QEALEACOTRISKMELQQQQQVVULGELENATARNLIGKLINI LLAVMAVLLVFVSTVANCVVPIAKTRNRTFSTLFLVVFIAFLWK HMDALFSYVERFFSSPR MSPCGARANAKMAAAYNGGTSAAAAGHHHHHHHHLPHLPFPHLH HHHHPCHILHIGSAAAVHPVQOITSSAAAAAAAAAAAAAMMINPG QQQPFFSSPAGQAPGPAAAPAQVQAAAAATVKAHHQHSHHP QQQLDIEPDRP IGYGAFGVVWSVTDROKKVALKKWPNVFQNL VSCKRVFRELKMLCFFKHDNVLSALDILQPHIDYFEIYVVTE LMGSDLHKIVSPQPLSSDHVKVFLVQLLRGLKVLHSAGILHRD IKPGNLLVNSNCVLKICDPGLAVFEEIGHTQPT	1 1			NROVVRDNPDFWGPLAVVLFFSMISLVGOFPWGWIITTTWIFGG
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GLLRGGMLRAPHAALRNSPUNTKNQAVLERAQGVVLKVLTNFK SSEIEQAVQSLDRNGVDLLMKYIYKGPEKPTENSSAVLLQWHEK ALAVGGLGSIIRVLTARKTV DRGPRSTATDTGRARVSFWRFPLDPGVKNSNVOISGEKRRFRTL RSLFHPFPVTRSGAPRAVLVGSSWPAKMVAPAVKVARGWSGLAL GVRRAVLQLPGLTQVRWSRYSPEKDPLDIKSYYRKPVEELITEE EKYVRELKKTQLIKAAPAGKTSSVFEDPVISKFTNMMIGGNKV LARSLMIQTLEAVKRKQFEKYHAASAEEQATIERNPYTIFHQAL KNCEPMIGIVPILKGGRFYQVPVPLPDRRRRFLAMKWMITECRD KKHQRTLMPEKLSHKLLEAFHNQGPVIKRKHDLHKMAEANRALA HYRRW LEDTICQHPPAEKKLYLYHRKLREVERNGIPRLPKDVFMDTHQG LTDVRAKVTGFSEGVVDSVKGGFSSFSQATHSAAGAVVSKPREI ASLIRNKFGSADNIPNLXDSLEEGQVDDAGKALGVISNFQSSPK YGGEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGPD ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMOTLQEERYR CERLEEQLINDLTELHQNEILNLKQELASMEEKIAYQSYERARDI QEALEACQTRISKMELQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFILVVFIAFLMK HWDALFSYVERFPSSPR 5637 948 2532 MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHHHLPHLPPPPHLH HHHHPCHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAAMLNFG QQQPYFFSPAPGQAFGPAAAPQQVQAAAAATVKAHHQHSHHP QQQLDIEPDRPIGGGAFGVVMSVTDPRDGKRVALKKMPNVFQNL VSCKRVFRELKMLCFFKHDNVLSALDILQPPHIDYFEBIYVVTE LMQSDLHKIIVSPQFLSSDHVVFIYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNALDIUSVGCIFAELLGRRILFQAQSSIQQUDL				ARNTLSSRFRRVDIDEFDENKFVDEQBEAAAAAAEPGPDPSEVD
SSEIEQAVQSLDRNGVDLLMKYIYKGFEKPTENSSAVLLQWHEK ALAVGGGSIIRVLTARKTV DRGPRSTATDTGRARVSFWRFPLDFGVKNSNVQISGEKRRFRTL RSLFHPFPVTRSGAPRAVLVGSSWPAKMVAPAVKVARGWSGLAL GVRRAVLQLPGLTQVRNSRYSPEFKDDLIDKEYYRKPVEELTEE EKYVRELKKTQLIKAAPAGKTSSVFEDPVISKFTIMMMIGGNKV LARSLMIQTLEAVKRKQFEKYHAASAEQATIERNPYTIFHQAL KNCEPMIGLVPILKGGRFYQVPVPLPDRRRRFLAMKWMITECRD KKHQRTLMPEKLSHKLLEAFHNQGPVIKRKHDLHKMAEANRALA HYRWW 5636 2253 1143 LEDTICQHPPAEKKLYLYHRKLREVERNGIPRLPKDVFMDTHQG LTDVRAKVTGFSEGVVDSVKGGFSSFSQATHSAAGAVVSKPREI ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFQSSPK YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMOTLQEERYR CERLEEQLNDLTELHQNEILNLKQELASMEEKIAYQSYERARDI QEALEACQTRISKMELQQQQQVVQLEGLENATARNLIGKLINI LLAVWAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR 5637 948 2532 MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHHLPHLPPPHLH HHHHPQHHLHBGSAAAVHPVQOHTSSAAAAAAAAAAAAAAAAAAAAAAAAAMLNFG QQQLDIEPDRPIGYGAFGVVWSVTDPRCGKRVALKKWPNVFQNL VSCKRVFRELKMLCFFKHDNVLSALDILQPPHIDYFEEIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNALDIWSVGCIFAELLGRRILFQAQSPIQOLDL				GLLROGDMLRAFHAALRNSPVNTKNOAVKERAOGVVLKVLTNEK
5635 3 943 DRGPRSTATDTGRARVSFWRFPLDPGVKNSNVQISGEKRRFRTL RSLFHPFPTTRSGAPRAVLVGSSWPAKMVAPAVKVARGWSGLAL GVRRAVLQLPGLTQVRWSRYSPBFKDPLIDKEYYRKPVEELTEE EKYVRELKKTQLIKAAPAGKTSSVFEDPVISKFTNMMIGGNKV LARSLMIQTLEAVKRKQFEKYHAASAEEQATIERNPYTIFHQAL KNCEPMIGLVPILKGGRFYQVPVPLPDRRRRFLAMKWMITECRD KKHQRTLMPEKLSHKLLEAFHNQGPVIKRKHDLHKMAEANRALA HYRWW 5636 2253 1143 LEDTICQHPPAEKKLYLYHRKLREVERNGIPRLPKDVFMDTHQG LTDVRAKVTGFSEGVVDVKGGFSSFSQATHSAAGAVVSKPREI ASLIRNKFGSADNIPNLXDSLEEGQVDDAGKALGVISNFQSSPK YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMQTLQEERYR CERLEEQLINDLTELHQNEILNLKQELASMEEKIAYQSYERARDI QEALEACQTRISKMELQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR 5637 948 2532 MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHHHPLPPPPHLH HHHPQHHLHPGSAAAVPPVQOHTSSAAAAAAAAAAAMNPG QQQYFFSPAPGQAPGPAAAAPAQVQAAAAATVKAHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKVALKKMYPNVFQNL VSCKRVFRELKMLCFFKHDNVLSALDILQPPHIDYFEBIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGGIFAELLGRRILFQAQSPIQQDDL	1 1			SSEIEQAVOSLDRNGVDLLMKYIYKGFEKPTENSSAVIJOWHEN
DRGPRSTATDTGRARVSFWRFPLDPGVKNSNVQISGEKRRFRTL RSLFHPFFVTRSGAPRAVLVGSSWPAKMVAPAVKVARGWSGLAL GVRRAVLQLPGLTQVRWSRYSPBFKOPLIDKEYYRKPVEELTEE EKYVRELKKTQLIKAAPAGKTSSVFEDPVISKFTIMMMIGGNKV LARSLMIQTLEAVKRKQFEKYHAASAEEQATIERNPYTIFHQAL KNCEPMIGLVPILKGGRFYQVPVPLPDRRRFLAMKMMITECRD KKHQRTLMPEKLSHKLLEAFHNQGPVIKRKHDLHKMAEANRALA HYRWW LEDTICQHPPAEKKLYLYHRKLREVERNGIPRLPKDVFMDTHQG LTDVRAKVTGFSEGVVDSVKGGFSSFSQATHSAAGAVVSKPREI ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFQSSPK YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD ALLHEIQEIRETQARLEESFETLKEHYGRDYSLIMOTLQEERYR CERLEEQLINDLTELHQNEILNLKQELASMEEKIAYQSYERARDI QEALEACQTRISKMELQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVFVSTVANCVVPLMKTRNTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR 5637 948 2532 MSFCGARAAKMMAAYNGGTSAAAAGHHHHHHHHLPHLPPPHLH HHHPQHHLHPGSAAAVHPVQOHTSSAAAAAAAAAAAAAANLPG QQQYFFSPAPAGQAPGPAAAAPAQVQAAAATVKAHHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKWPNVFQNL VSCKRVFRELKMLCFFKHDNVLSALDILQPPHIDYFEBIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQQDDL				ALAVGGLGSIIRVLTARKTV
RSLFHPFVTRSGAPRAVLVGSSWPAKMVAPAVKVARGWSGLAL GVRRAVLQLPGLTOVMSKYSPEFKDPLIDKEYYRKPVEELTEE EKYVRELKKTQLIKAAPAGKTSSVFEDPVISKFTMMMIGGNKV LARSLMIQTLEAVKRKQFEKYHAASABEQATIERNPYTIFHQAL KNCEPMIGLVPILKGGRFYQVPVPLPDRRRFLAMKWMITECRD KKHQRTLMPEKLSHKLLEAFHNQGPVIKRKHDLHKMAEANRALA HYRWW 5636 2253 1143 LEDTICQHPPAEKKLYLYHRKLREVERNGIPRLPKDVFMDTHQG LTDVRAKVTGFSECVVDSVKGGFSSFSQATHSAAGAVVSKPRBI ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFQSSPK YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMGTLQEERYR CERLEEQLINDLTELHQNEILNLKQBLASMEEKIAYQSYERARDI QEALEACOTRISKMELQQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR 5637 948 2532 MSFCGARANAKMAAAYNGGTSAAAAGHHHHHHHHHPHLPPPHLH HHHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAAANLNPG QQQPYFPSPAPGQAPGPAAAAPAQVQAAAAATVKAHHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKMPNVFQNL VSCKRVFRELKMLCFFKHDNVLSALDILQPPHIDYFEBIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDJWSVGCTFAELLGRRILFQAQSPIQOLDL	5635	3	. 943	
GVRRAVLQLPGLTQVRWSRYSPEFKDPLIDKEYYRKPVEELTEE EKYVRELKKTQLIKAAPAGKTSSVFEDPVISKFTIMMMIGGNKV LARSLMIQTLEAVKRKQFEKYHAASAEQATIERNPYTIFHQAL KNCEPMIGLVPILKGGRFYQVPVPLPDRRRFLAMKWMITECRD KKHQRTLMPEKLSHKLLEAFHNQGPVIKRKHDLHKMAEANRALA HYRWW 5636 2253 1143 LEDTICQHPPAEKKLYLYHRKLREVERNGIPRLPKDVFMDTHQG LTDVRAKVTGFSEGVVDSVKGGFSSFSQATHSAAGAVVSKPRBI ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFQSSPK YGGSEDCSSATGGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMQTLQEERYR CERLEEQLNDLTBLHQNEILNLKQELASMEEKIAYQSYERARDI QEALEACOTRISKMELQQQQQQVVQLEGLBNATARNLLGKLINI LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFPSSPR 5637 948 2532 MSFCGARANAKMAAYNGGTSAAAAGHHHHHHHHHPLPPHPHLH HHHHPQHHLHPGSAAAVHPVQOHTSSAAAAAAAAAAAAAAMLNPG QQQPYFPSPAPGQAPGPAAAAPQVQAAAAATVKAHHHQHSHHP QQQLDIEFDRPIGYGAFGVVWSVTDPRDGKRVALKKMPNVFQNL VSCKRVFRELKMLCFFKHDNVLSALDILQPPHLDYFEBIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRIMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL				PSI-FUPED/TDSCADDAIT MCCOUDAMAIS DAMES DAMES
EKYVRELKKTQLIKAAPAGKTSSVFEDPVISKFTNMMIGGNKV LARSLMIQTLEAVKRKQFEKYHAASAEEQATIERNPYTIFHOAL KNCEPMIGLVPILKGGRFYQVPVPLPDRRRFLAMKWMITECRD KKHQRTLMPEKLSHKLLEAFHNQGPVIKRKHDLHKMAEANRALA HYRWW LEDTICQHPPAEKKLYLYHRKLREVERNGIPRLPKDVFMDTHQG LTDVRAKVTGFSEGVVDSVKGGFSSFSQATHSAAGAVVSKPREI ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFGSSPK YGSEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMOTLQEERYR CERLEEQLNDLTELHQNEILNLKQELASMEEKIAYQSYERARDI OEALEACQTRISKMELQQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR 948 2532 MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHHHPLPPPPHLH HHHPQHHLHPGSAAAVHPVQOHTSSAAAAAAAAAAAAAMLNPG QQQPYFPSPAPGQAPGPAAAAPAQVQAAAAATVKAHHHQHSHPP QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKMPNVFQNL VSCKRVFRELKMLCPFKHDNVLSALDILQPPHIDYFEEIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL	I I			CURRAUI OF DOL TOURNERS A PRESENT TRUE TOURS OF THE STATE
LARSLMIQTLEAVKRKQFEKYHAASAEEQATIERNPYTIFHQAL KNCEPMIGLVPILKGGRFYQVPVPLPDRRRRFLAMKWMITECRD KKHQRTLMPEKLSHKLLEAFHNQGPVIKRKHDLHKMAEANRALA HYRWW LETTICQHPPAEKKLYLYHRKLREVERNGIPRLPKDVFMDTHQG LTDVRAKVTGFSEGVVDSVKGGFSSFSQATHSAAGAVVSKPRBI ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFQSSPK YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMQTLQEERYR CERLEEQLNDLITELHQNEILNLKQELASMEEKIAYQSYBRARDI QEALEACQTRISKMELQQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFPSSPR 5637 948 2532 MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHHHPPPPHLH HHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAAMLNPG QQQYFFSFAPGQAFGPAAAAPAQVQAAAAATVKAHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPROGKRVALKKWPNVFQNL VSCKRVFRELKMLCFFKHDNVLSALDILQPPHIDYFEBIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL				EVARAVLODEGLIQVRWSRYSPEFKDPLIDKEYYRKPVEELTEE
KNCEPMIGLVPILKGGRFYQVPVPLPDRRRRFLAMKWMITECRD KKHQRTLMPEKLSHKLLEAFHNQGPVIKRKHDLHKMAEANRALA HYRWW LEDTICQHPPAEKKLYLYHRKLREVERNGIPRLPKDVFMDTHQG LTDVRAKVTGFSEGVVDSVKGGFSSFSQATHSAAGAVVSKPREI ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFQSSPK YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMGSSGFD ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMQTLQEERYR CERLEEQLNDLTELHQNEILNLKQELASMEEKIAYQSYERARDI QEALEACQTRISKMELQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR 5637 948 2532 MSFCGARANAKMAAYNGGTSAAAAGHHHHHHHHHPHPPPHLH HHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAAAMINPG QQQYFFSFAPGQAPGPAAAAPAQVQAAAAATVKAHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPRGKRVALKKWPNVFQNL VSCKRVFRELKMLCFPKHDNVLSALDILQPPHIDYFEEIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLJVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL	1			EKIVRBLKKTQLIKAAPAGKTSSVFEDPVISKFTNMMMIGGNKV
KKHQRTLMPEKLSHKLLEAFHNQGPVIKRKHDLHKMAEANRALA HYRWW LEDTICQHPPAEKKLYLYHRKLREVERNGIPRLPKDVFMDTHQG LTDVRAKVTGFSEGVVDSVKGGFSSFSQATHSAAGAVVSKPREI ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFQSSPK YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMQTLQEERYR CERLEEQLNDLTELHONEILNLKQELASMEEKIAYQSYERARDI QEALEACQTRISKMELQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR 5637 948 2532 MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHHHHPHPPPHLH HHHPQHHLHPGSAAAVHPVQOHTSSAAAAAAAAAAAAAAAMINPG QQQPYFPSPAPGQAPGPAAAPAQVQAAAAATVKAHHHQHSHPP QQQLDIEPDRPIGYGAFGVVWSVTDPRGKRVALKKMPNVFQNL VSCKRVFRELKMLCFFKHDNVLSALDILQPPHIDYFEEIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL	1			TAKSLMIQTLEAVKRKQFEKYHAASAEEQATIERNPYTIFHQAL
KKHQRTLMPEKLSHKLLEAFHNQGPVIKRKHDLHKMAEANRALA HYRWW LEDTICQHPPAEKKLYLYHRKLREVERNGIPRLPKDVFMDTHQG LTDVRAKVTGFSEGVVDSVKGGFSSFSQATHSAAGAVVSKPREI ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFQSSPK YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMQTLQEERYR CERLEEQLNDLTELHONEILNLKQELASMEEKIAYQSYERARDI QEALEACQTRISKMELQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR 5637 948 2532 MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHHHHPHPPPHLH HHHPQHHLHPGSAAAVHPVQOHTSSAAAAAAAAAAAAAAAMINPG QQQPYFPSPAPGQAPGPAAAPAQVQAAAAATVKAHHHQHSHPP QQQLDIEPDRPIGYGAFGVVWSVTDPRGKRVALKKMPNVFQNL VSCKRVFRELKMLCFFKHDNVLSALDILQPPHIDYFEEIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL				KNCEPMIGLVPILKGGRFYQVPVPLPDRRRRFLAMKWMITECRD
1143 LEDTICQHPPAEKKLYLYHRKLREVERNGIPRLPKDVFMDTHQG LTDVRAKVTGFSEGVVDSVKGGFSSFSQATHSAAGAVVSKPREI ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFQSSPK YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMOTLQEERYR CERLEEQLINDLTELHQNEILNLKQELASMEEKIAYQSYERARDI QEALEACOTRISKMELQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR 5637 948 2532 MSPCGARANAKMMAAYNGGTSAAAAGHHHHHHHHHPLPPPPHLH HHHPQHHLHPGSAAAVHPVQOHTSSAAAAAAAAAAAAAAAMINPG QQQPYFPSPAPGQAPGPAAAAPAQVQAAAAATVKAHHHQHSHPP QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKMPNVFQNL VSCKRVFRELKMLCPFKHDNVLSALDILQPPHIDYFEEIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILEGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL	1 1			KKHQRTLMPEKLSHKLLEAFHNQGPVIKRKHDLHKMAEANRALA
LTDVRAKVTGFSEGVVDSVKGGFSSFQATHSAAGAVVSKPREI ASLIRNKFGSADNI PRLKDSLEEGQVDDAGKALGVI SNFQSSPK YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMQTLQEERYR CERLEEQLNDLTELHONE ILNLKQELASMEEKI AYQSYERARDI QEALEACQTRISKMELQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR 5637 948 2532 MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHHHPHPPPHLH HHHPQHHLHPGSAAAVHPVQOHTSSAAAAAAAAAAAAAAMINPG QQQPYFPSPAPGQAPGPAAAAPAQVQAAAAATVKAHHHQHSHPP QQQLDIEPDRPIGYGAFGVVWSVTDPROGKRVALKKMPNVFQNL VSCKRVFRELKMLCFPKHDNULSALDILQPPHIDYFEEIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL				HYRWW
LTDVRAKVTGFSEGVVDSVKGGFSSFSQATHSAAGAVVSKPREI ASLIRNKFGSADNI PNLKDSLEEGQVDDAGKALGVISNFQSSPK YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMOTLQEERYR CERLEEQLNDLTELHQNEILNLKQELASMEEKIAYQSYERARDI QEALEACQTRISKMELQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR 5637 948 2532 MSFCGARANAKMAAYNGGTSAAAAGHHHHHHHHHPHLPPPHLH HHHPQHHLHPGSAAAVHPVQOHTSSAAAAAAAAAAAAMLNPG QQQYFFSPAPGQARGPAAAAPAQVQAAAAATVKAHHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKWPNVFQNL VSCKRVFRELKMLCFFKHDNVLSALDILQPPHIDYFEBIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL	5636	2253	1143	LEDTICQHPPAEKKLYLYHRKLREVERNGIPRLPKDVFMDTHOG
ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFQSSPK YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMOTLQEERYR CERLEEQLNDLTELHQNEILNLKQELASMEEKIAYQSYERARDI QEALEACOTRISKMELQQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFPSSPR 5637 948 2532 MSFCGARANAKMAAYNGGTSAAAAGHHHHHHHHLPHLPPPHLH HHHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAMLNPG QQQYFFSPAPGQAFGPAAAPAQVQAAAAATVKAHHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPROGKRVALKKWPNVFQNL VSCKRVFRELKMLCFPKHDNVLSALDILQPPHIDYFEBIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL			i	LTDVRAKVTGFSEGVVDSVKGGFSSFSOATHSAAGAVVSKDDBT
YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMQTLQEERYR CERLEEQLNDLITELHQNEILNLKQELASMEEKIAYQSYBRARDI QEALEACOTRISKMELQQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFPSSPR 5637 948 2532 MSFCGARANAKMAAYNGGTSAAAAGHHHHHHHHHPHPPPHLH HHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAMLNPG QQQYFFSFAPGQAFGPAAAPAQVQAAAAATVKAHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPROGKRVALKKWPNVFQNL VSCKRVFRELKMLCFFKHDNVLSALDILQPPHIDYFEEIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL]	ì		ASLIRNKFGSADNIPNLKDSLEEGOVDDAGKALGUTSNEGGG
ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMQTLQEERYR CERLEEQLMDLTELHQNEILNLKQELASMEEKIAYQSYERARDI QEALEACQTRISKMELQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR 5637 948 2532 MSFCGARANAKMAAYNGGTSAAAAGHHHHHHHHHPHPPPHLH HHHPQHHLHPGSAAAVHPVQOHTSSAAAAAAAAAAAAMINPG QQQPYFPSPAPGQAPGPAAAPAQVQAAAAATVKAHHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPROGKRVALKKMPNVFQNL VSCKRVFRELKMLCPFKHDNVLSALDILQPPHIDYFEEIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL	1			YGSEEDCSSATSGSVGANSTTCGTAVCAGGGGTTNTT DMCCCCT
CERLEEQLMDLTELHQNEILNLKQELASMEEKIAYQSYERARDI QEALEACOTRISKMELQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR 5637 948 2532 MSFCGARANAKMAAYNGGTSAAAAGHHHHHHHHHHPLPPPPHLH HHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAAAMINPG QQQPYFPSPAPGQAPGPAAAAPAQVQAAAAATVKAHHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPROGKRVALKKMPNVFQNL VSCKRVFRELKMLCPFKHDNVLSALDILQPPHIDYFEEIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL	1	I		ALLHETOETRETOARLEESERTLEBUVORDVOLTHOMY
QEALEACOTRISKMELQQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR 5637 948 2532 MSPCGARANAKMMAAYNGGTSAAAAGHHHHHHHHHLPHLPPPHLH HHHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAAMINPG QQQPYFPSPAPGQAPGPAAAAPAQVQAAAATVKAHHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKMPNVFQNL VSCKRVFRELKMLCFPKHDNVLSALDILQPPHIDYFEBIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL	1			CERTEROLUDITEL HONELL MI MORE ACCURATE AND A
LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR 5637 948 2532 MSPCGARANAKMMAAYNGGTSAAAAGHHHHHHHHLPHLPPPHLH HHHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAMLNPG QQQPYFPSPAPGQAPGPAAAAPAQVQAAAATVKAHHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKMPNVFQNL VSCKRVFRELKMLCFPKHDNVLSALDILQPPHIDYFEBIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL		İ		OF A PACCETA COMPTON OF THE PACCETA
HWDALFSYVERFFSSPR 5637 948 2532 MSPCGARANAKMAAYNGGTSAAAAGHHHHHHHHLPHLPPPHLH HHHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAMLNPG QQQPYFPSPAPGQAPGPAAAAPAQVQAAAAATVKAHHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKYPNVFQNL VSCKRVFRELKMLCFPKHDNVLSALDILQPPHIDYFEBIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESSHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL] [ļ		VEALEACUTRISKMELQQQQQQVVQLEGLENATARNLLGKLINI
948 2532 MSFCGARANAKMAAYNGGTSAAAAGHHHHHHHHHHHHPPPPHLH HHHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAMLNPG QQQPYFFSFAPGQAFGPAAAPAQVQAAAAATVKAHHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPROGKRVALKKWPNVFQNL VSCKRVFRELKMLCFFKHDNVLSALDILQPPHIDYFEBIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL	1	ļ		LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK
HHHHPQHHLHPGSAAAAGHHHHHHHHLPHDPPHILH HHHHPQHHLHPGSAAAAHAAAAAAAAAAAAAMINPG QQQPYFPSPAPGQAPGPAAAAPAQVQAAAAATVKAHHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKMPNVFQNL VSCKRVFRELKMLCFFKHDNVLSALDILQPPHIDYFEBIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL	F 5637			
HHHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAAMLNPG QQQPYFFSPAPGQAFGPAAAPAQVQAAAAATVKAHHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKWPNVFQNL VSCKRVFRELKMLCFPKHDNVLSALDILQPPHIDYFEBIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL	363/	948	2532	MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHHLPHLPPPHLH
QQQPYFPSPAPGQAPGPAAAPAQVQAAAAATVKAHHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKMPNVFQNL VSCKRVFRELKMLCPFKHDNVLSALDILQPPHIDYFEEIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL				HHHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAAAAAAMI.MDG
QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKMPNVFQNL VSCKRVFRELKMLCFFKHDNVLSALDILQPPHIDYFEBIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL			1	QQQPYFPSPAPGOAPGPAAAAPAOVOAAAATVKAHUUOUGUUD
VSCKRVFRELKMLCFFKHDNVLSALDILQPPHIDYFEBIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL				OOOLDIEPDRPIGYGAFGVVWGVTDDDIYGEVAT VOULINGASHIP
LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL		İ		VSCKRVERELKMLCERKHINGIG CALINII ODDUTAVERET TOTAL
IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL	1 1	}	1	TWOCDPHKI INCOUNT COMMUNICATION AND A SOCIAL
PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQOLDL			1	TABOMI I MENON AT OBSESS STATEMENT AND SELECTION OF SELEC
PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQQLDL				TAPGNEDANSNCVEKICDFGLARVEELDESRHMTQEVVTQYYRA
	1			PELLMGSKHISNAIDIWSVGCIFAELLGRRILFQAQSPIQQLDL
ITDLLGTPSLEAMRTACEGAKAHILRGPHKQPSLPVLYTLSSQA				

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	ļ	\=possible nucleotide insertion)
			THEAVHLLCRMLVFDPYKRISAKDALAHPYLDEGRLRYHTCMCK
			CCFSTSTGRVYTSDFBPVTNPKFDDTFEKNLSSVRQVKEIHQF
5638	125	1155	ILEQQKGNRVPLCINPQSAAFKSFISSTVAQPSEMPPSPLVWE DRKMSELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVG
3636	125	.1133	RIQMRTRRTLRGHLAKIYAMHWGTDSRLLVSASQDGKLIIWDSY
			TTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTR
ļ			EGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET
l		,	GQQTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM
			CROTFTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADOEL
	1		MTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRA
			GVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN
5639	125.	1155	DRKMSELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVG
		1	RIQMRTRRTLRGHLAKIYAMHWGTDSRLLVSASQDGKLIIWDSY
			TTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTR
			EGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET
	Į		GQQTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM
	1		CRQTFTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADQEL
			MTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRA
5640	280	1092	GVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN
5640	280	1092	QQGNKKTMLSHNTMMKQRKQQATAIMKEVHGNDVDGMDLGKKVS IPRDIMLEELSHLSNRGARLFKMRQRRSDKYTFENFQYQSRAQI
			NHSIAMQNGKVDGSNLEGGSQQAPLTPPNTPDPRSPPNPDNIAP
ļ			GYSGPLKEIPPEKFNTTAVPKYYQSPWEQAISNDPELLBALYPK
İ		1	LFKPEGKAELPDYRSFNRVATPFGGFEKASRMVKFKVPDFELLL
1		ĺ	LTDPRFMSFVNPLSGRRSFNRTPKGWISENIPIVITTEPTDDTT
			VPESEDL
5641	27	332	CRHNCNGDVKLLSNOMDKLFAFHLFTFHGLLHFLDGSIOKLIOA
i	}		EIILSDNSSILVLENNFLFKVKSKQFIHLIAKKFYISITIVSAS
			NGESFVLSMIVTG
5642	199	1247	ITPCRMDFLVLFLFYLASVLMGLVLICVCSKTHSLKGLARGGAQ
			IFSCIIPECLQRAMHGLLHYLFHTRNHTFIVLHLVLQGMVYTEY
			TWEVFGYCQELELSLHYLLLPYLLLGVNLFFFTLTCGTNPGIIT
1			KANELLFLHVYEFDEVMFPKNVRCSTCDLRKPARSKHCSVCNWC
1	1		VHRFDHHCVWVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTTF
		1	LVHLVVMSDLYQETYIDDLGHLHVMDTVFLIQYLFLTFPRIVFM
	1		LGFVVVLSFLLGGYLLFVLYLAATNQTTNEWYRGDWAWCQRCPL VAWPPSAEPQVHRNIHSHGLRSNLQBIFLPAFPCHERKKQB
5643	1	847	PSGGVRDVETRGPGSRAARGPRVVMHRRGVGAGAIAKKKLAEAK
	_		YKERGTVLAEDQLAQMSKQLDMFKTNLEEFASKHKQEIRKNPEF
			RVQFQDMCATIGVDPLASGKGFWSEMLGVGDFYYELGVQIIEVC
			LALKHRNGGLITLEELHQQVLKGRGKFAQDVSQDDLIRAIKKLK
1			ALGTGFGIIPVGGTYLIQSVPAELNMDHTVVLQLAEKNGYVTVS
			FIKASLKWETERARQVLEHLLKEGLAWLDLQAPGEAHYWLPALF
			TDLYSQEITABEAREALP
5644	83	1138	PRRMGSWVQLITSVGVQQNHPGWTVAGQFQEKKRFTEEVIEYFQ
	1		KKVSPVHLKILLTSDEAWKRFVRVAELPREEADALYEALKNLTP
			YVAIEDKDMQQKEQQFREWFLKEFPQIRWKIQESIERLRVIANE
	1		IEKVHRGCVIANVVSGSTGILSVIGVMLAPFTAGLSLSITAAGV
	1	1	GLGIASATAGIASSIVENTYTRSAELTASRLTATSTDQLEALRD
1	İ		ILHDITPNVLSFALDFDEATKMIANDVHTLRRSKATVGRPLIAW
			RYVPINVVETLRTRGAPTRIVRKVARNLGKATSGVLVVLDVVNL
5645	537	799	VQDSLDLHKGEKSESAELLRQWAQELEENLNELTHIHQSLKAG
2043	137	133	VQSVRDLKRLSPTDPPGDSGNRDVTREDPVTGPLNSASSQVPTL YLCLQNSLLGHSSVEDARATMELYQISQRIRARRGLPRLAVSD
5646	3745	3328	AEQYGTSPHLLPTMLLSSCLPPANVTTKAATPPPLVLSLTTADP
] 3070	","	3328	AGKPAPCRVTLTLLRASIPATKRASFLSSFIKMFFEELEYILGF
			LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL
			RAEGGAQ
5647	288	800	GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCSLH
			EEDTQRHETYHQQGQCQVLVQRSPWLMMRMGILGRGLQEYQLPY
	·		

SEO	Predicted	Predicted end	Amino acid coment
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid)	P=Proline, Q=Glutamine, R=Arginine,
ì	residue of	residue of	S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
ļ	sequence		\=possible nucleotide insertion)
ı			QRVLPLPIFTPAKMGATKEEREDTPIOLOELLALETALGGOCVD
L			RQEVAEITKQLPPVVPVSKPGALRRSLSRSMSOEAORG
5648	7	1518	VLSELCGRHEALREVGAEWPPPTCSPNICSGLQQAGNTDWSLTM
1			APQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPEK
1]	SSTKETERKETKAEEELDAEVLEVFHPTHEWQALQPGQAVPAGS
			HVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTNTYTSQDLKS
			ALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVV
			IETDMQIMVRLINKFNSSSSLEEKIAALFDLEYYVHQMDNAQD
			LLSFGGLQVVINGLNSTEPLVKEYAAFVLGAAFSSNPKVQVEAI
İ	}		BGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLK
1			I.GOLOVI.DTI.VOEKCTEVI AUDITUM : 1751-1771 AUDITUM
1			LGGLQVLRTLVQEKGTEVLAVRVVTLLYDLVTEKMFAEEEAELT
			QEMSPEKLQQYRQVHLLPGLWEQGWCEITVHLLALPEHDAREKV
			LQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLASLELQDGE
5649	1172	3006	DEGYFQELLGSVNSLLKELR
	14,2	3006	MLQEQLDAINEEIRMIQEEKESTELRAEEIETRVTSGSMEALNL
]	İ		KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAQDLDR
			MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPPSSPR
			TLRLEKLGHPALSQEEGKSALEDQGSNPSSSNSSQDSLHKGAKR
[]			KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM
1	i		VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL
			ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR
			LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK
1 1			TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPOYRSYPMECLV
			DARMLDHLTKKDLRVHLKMVDSFHRTSLOYGIMCLKRLNYDRKE
			LEKRREESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV
			HGALLALDENFDHNTLALILQIPTONTOAROVMEREFNNILLALG
			TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASARTI.PA
1-555			GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD
5650	1172	3006	MLQEQLDAINEBIRMIQEEKESTELRAEEIETRVTSGSMFAINL
1 1			KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAODLDP
			MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPDSSDD
		j	TLRLEKLGHPALSQEEGKSALEDOGSNPSSSNSSODSLHKGAKP
1 1			KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM
			VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL
l i			ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR
			LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK
! !			TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV
1			DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGIMCLKRLNYDRKE
			LEKRREESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV
1			HGALLALDENFDHNTLALILQIPTQNTQARQVMEREFNNLLALG
l í			TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASAETLPA
			GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD
5651	646	1869	ARQGOROPWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL
			AWGEGAGIR*ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP
1 [ı		WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAAALSPASPAGP
1 1		1	ADP*LPGHSSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASQ
1 1			QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS
1 1			PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA
1			PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSSDYCGGLGA
1 1			GWPAGISDRII CAACI CDAWARCHORDON CONTRACTOR C
[[1	1	GWRAGISPELLGAAGLSDNWARCPGPGPAB*GGQPGCRTIPASA
	1		CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL
5652	735		LGPRGRTGRPSSPS
			HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI
! !	1		CEFCARSFRTSSNLVIHRRIHTGEKPLQCEICGFTCRQKASLNW
5653	66	740	HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA
5055	00	1401	RGRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL
		1	CFPQPCQPGTRRGRRRSLKEATEPQLAMAEEFVTLKDVGMDFTL
		1	GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED
! !		1	LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSOEI/SRDVIO
L			GWLLELQFRRSLYRGHLVR+FARRSRKSSEV+YCHQRGKSHGMQ

CEO	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ	1	I .	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
		aequence	· -
	sequence		\=possible nucleotide insertion)
			ES*IKERTQSCVHRFHGRRFHG\DNVSEKTLTPAKSKEYRGEFF
			SYSDHSQQDSVQEGEKPYQCSECGKSFSGSYRLTQHWITHTREK
	ì	1	PTVHQECEQGFDRKASHSGYPKTHTGYKFYVCNEYGTPFSQSTY
			LWHQKTHAGEKPCKSQDSDHPPSHDTQSGEHQKTHTDSKSYNCN
	Į.		ECGKAFTRIFHLTRHQKIHTRKRYECSKCQATFNLRKHLIOHOK
			THAANV .
5654	3	598	TLPLFPGRRFRGWRRCGAVAARKNSTGGNVSINQRRDSVRMSAL
	· -		NWKPFVYGGLASITAECGTFPIDLTKTRFQ1QGQTNDAKFKEII
	1		YRGMLHALVRIGREEGLKALYSG*VGLHAFLCHCSLFHMGIDFR
	1	}	
			PRLHRSQVKSLRCV*KEQIA**/MFSLLISTLISKYIYYAADVL
			EKLFYYIQVQTDNNKKICLFKNI
5655	2	867	RPPGIRAPRQLHPAAGRRPDASARPRFRPTVLLHDPFQLSFPPP
	1		PLSYPSVFPAVARVLPQRSGDYRAAGMPQLSGGGGGGGGDPELC
1	Ī		ATDEMIPFKDEGDPQ\REKIFAEIVNPEEEGDLADIKSSLVNES
1		1	EIIPASNGHEVARQAQTSQEPYHDKAREHPDDGKHPDGGLYNKG
			PSYSSYSGYIMMPNMNNDPYMSNGSLSPPIPRTSNKVPVVQPSH
	1	1	AVHPLTPLITYSDEHFSPGSHPSHIPSDVNSKQGMSRHPPAPDI
	1		PTFYPLSPGGGGOITPPLGWOGOP
5656	228	1066	PRRVPPLPEFASGPGAAFFHSGRLQRSLTKDSAGCFSQCRSRAM
1 3030		1	LVLRSGLTKALASRTLAPOVCSSFATGPROYDGTFYEFRTYYLK
1			PSNMNAFMENLKKNIHLRTSYSELVGFWSVEFGGRTNKVFHIWK
1			YDNFPHRAEVRKALANCKEWQEQSIIPNLARIDKQETEITYLIP
I	1	<u> </u>	WSKLQKPPKEGVYELAVFQMKPGGPALWGDAFERAINAHVNLGY
ľ			TKVVGVFHTEYGELNRVHVLWWNESADSRAAVRHKSHEDPISWG
			GVRESVNYL\VSQQNM
5657	105	1052	GQRLQSPRVQMPVQPPSKDTEEMEAEGDSAAEMNGEEEESEEER
			SGSQTESEEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEKL
			FRERLSQLRLRLEEVGAERAPEYTEPLGGLQRSLKIRIQVAGIY
			KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQERIQR
1	1		LEEDROSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG
	İ	1	PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ
1		1	GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL
		1	ALVWTPPL
5658	2346	3541	
3636	2346	3341	TERRVYNPWPEPDPD\CIQEDPWNLPNSIKTLVDNIQRYVEDGK
			NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY
1		1	RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE
1]	1	RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA
1	[1	LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS
1			PGSQAAEDLQQDINAQSLEKVQQYYRKLRAFYLERSNLPTDAST
	1	1	TAVKIDQLIRPINALDELCRLMKSFVHPKPGAAGSVGAGLIPIS
	1 .	1	SELCYRLGACOMVMCGTGMQRSTLSVSLEQAAILARSHGLLPKC
			IMQATDIMRKQGPRVEILAKNLRVKDOMPQGAPRLYRLCOPKMN
1			GDL
5659	2	696	WKRSGEVSPKGELGAWRGNSGRPKIIGRAAEAENEDRTLGRLLP
	1	1	GNERSQPRSPLRLLAPQLKAEAAADKGLAPVPPPFSSGHSGPC\
			EREGEGQRGRGRSRRGAHLELKPSPGLRAGAPTDRGRGGPAEVA
1	1		,
1	1		AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG
	1		EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPWVMEQRKEL
5660		 	FRRLQKWELNTYL
5660	229	853	PVTMWAFSELPMPLLINLIVSLLGFVATVTLIPAFRGHFIAARL
	i		CGQDLNKTSRQQIPESQGVISGAVFLIILFCFIPFPFLNCFVKE
	1		QRKAFPHHEFVALIGALLAICCMIFLGFADDVLNLRWRHKLLLP
	1	1	TAASLPLLMVYFTNFGNTTIVVPKPFRPILGLHLDLGR*SYHCC
	L	1	PYGTYFREPFLVLHILLQVFLFCLCVFPDPFW
5661	2	473	LNLYPSPCGGIPKLPGLPREAAAALGASFLAEAPLPVTVRGSGL
	1		AGMAVTCDPKAFLSICFVTLVFLQLPLASICQN*GTDSCASRGK
1	1		ADFDVTGPHAPILAMAGGHVELQCQLFPNISAEDMELRWYRCQP
	1		SLAVHMHERGMDMDGEQKWQYRGRT
5662	2	1318	LRKEGRCRRGSNRGVWAAPAEGLGGRGMLGVRCLLRSVRFCSSA
1	· -		PFPKHKPSAKLSVRDALGAQNASGERIKIQGWIRSVRSQKEVLF
	i	ı	I TITIES AND A LONG OF THE PROPERTY OF A LONG AND A LON

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion\
1			LHVNDGSSLESLQVVADSGLDSRELTFGSSVEVOCOLTKEDGKD
			UNVELKAEKIKVIGNCDAKDFPIKYKERHPI.EVI.POVDUEDCDT
			NVLGSILRIRSEATAAIHSFFKDSGFVHTHTDITTSNDSEGACE
			LFQLEPSGKLKVPEENPFNVPAFLTVSGOLHLEVMSGA FTOURT
1	}		FGPTFRAENSQSRRHLAEFYMIRAETSFVDSLODIMOVIDETEV
İ			ATTMMVLSKCPEDVELCHKFIAPGOKDRI.*HMI.KNNRI.TTCVTR
			AVEILKQASQNFTFTPEWGADLRTEHEKYLVKHCGNIDVEVINV
5663	119		PLTLKPFYMRDNEDGPQELEGSVA+HSIGIMILISTAUTGOR
3003	119	698	PADIGRSTAKTPGPPRSLEMDDPRYGMCPLKGASGCPGAERSLL
			VQSYFEKGPLTFRDVAIEFSLEEWQCLDSAQQGLYRKVMLENYR
1	İ		NLVFLGIALTKPDLITCLEOGKEPWNIKRHEMVAKDDVICCURD
			QDLWAEQDIKDSFQEAILKKYGKYGHANFQLQKGCKSVDECKVH
5664	118	572	KEHDNKLNQCLIPKKKK
		372	SLSMESNHKSGDGLSGTQKEAALRALVQRTGYSLVQENGQRKYG
	-	İ	GPPPGWDAAPPERGCEIFIGKLPRDLFEDELIPLCEKIGKIYEM
1			RMMMDFNGNNRGYAFVTFSNKVEAKNAIKQLNNYEIRNGRLLGV CASVDNCRLFVGGIPKTKK
5665	347	702	VVQHLIILLHCERTSPAMITSELPVLQDSTNETTAHSDAGSELE
1			ETEVKGKRKRGRPGRPPSTNKKPRKSPGEKSRIEAGIRGAGRGR
			ANGHPQQNGEGEPVTLFEVVKLGKSAMQRC
5666	213	540	VSCLPTSCKMITLNNQDQPVPFNSSHPDEYKIAALVFYSCIFII
			GLFVNITALWVFSCITKKRTTVTIYMMNVALVDLIFIMTLPFRM
			FYYAKDEWPFGEYFCQILGA
5667	1	695	HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP
			SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLABSKGFP
ļ.			VLDACSSEATHVVMEETSAEEAVSWOERRMAAAPPGCTDDALLD
ĺ			ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMDAVACOP
			PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL
5668	691		PSPVTTLSQLQ
2000	937	894	CSFLFCIPDLFLQFLLGRKEEEAVLVGGEWSPSLDGLDPQADPQ
5669	407	1	VLVRTAIRCAQAQTGIDLSGCTKW
		4	DSGAPEGLSPLMSTQEGLSMHAHPQAYTPFIYLHARKRRGEIGD
ļ			ADSRFNDRYAHKSAQLYFLYFVCWIFQDVYYFTIKEKNHFFFPK
			ARGAPTKYSGSPIGSPTTTPPTRPPSFNLHPAPHLLASMQLQKL
5670	3	373	SSECLTMAWIPLLPLLILCTVSVASYELAQPSSVSVSPGQTAK
			ITCSGDVLAKKYARWFQQKPGQAPVLVIYKDTERPSGIPERFSG
			STSGTTVTLTISGAQVEDRADYFCYSATDNFLWVF
5671	280	524	KFPPKKTPPHLGMESAITLWQFLLQLLLDQKHEHLICWTSNDGE
			FKLLKAKKVAKLWGLRKNKTNMNYDKLSRALRLLFMT
5672	2	557	FVPATPDPGVWLPPSRDPAMAKRSSLYTRTVEGKNT.PAKDTTCC
			SDPYCIVKVDNEPIIRTATVWKTLCPFWGEEVOVHI.DDTGUANA
{			FYVMDEDALSRDDVIGKVCLTRDTIASHPKGKFSLPSHTGLDSD
			WPPSHSETSPLGSVWSPAQGKPFLLSPEAGATFCTPGLCSAACS
5672			QAWLLLPLP
5673	327	696	ITVADQISHWSAGRIKNRTRIPECIHSSAATTLAGPHTMEGESV
			KLSSQTLIQAGDDEKNQRTITVNPAHMGKAFKVMNELRSKOLLC
5674	17		DVMIVAEDVEIEAHRVVLAACSPYFCAMFTGDMS
30,4	11	984	GGGSMEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLGEVKGE
			AKNSITDSQMDDVEVVYTIDIOKYIPCYOLFSFVNSSGFVNFOA
			LKKILSNVKKNVVGWYKFRRHSDOIMTFRERIJHKNIJOEHBENO
			DLVFLLLTPSIITESCSTHRLEHSLYKPOKGLFHRVPLVVANLG
			MSEQLGYKTVSGSCMSTGFSRAVOTHSSKFFEEDGSLKEVHKIN
			EMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRDGA
			QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKID
5675	80	753	MFLKVAVTTTTISM EGSERCETELARI GARAGE
	= =	, , , ,	EGSRRGPTRLARLSARAGRLHFPPGFSSRLIHFRGVSECRRPPG
	1	J	KSGVPVSAPGSDGKWWEERPGMFSLMASCCGWFKRWREPVRKVT
	1	ļ	LLMVGLDNAGKTATAKGIQGEYPEDVAPTVGFSKINLRQGKFEV TIFDLGGGIRIRGIWKNYYAESYGVIFVVDSSDEERMEETKEAM
			

	-	F 37 3	Table - Id College - Idea - Id
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
140:	1		H=Histidine, I=Isoleucine, K=Lysine,
1	location	corresponding	
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ĺ	i e		
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	sequence		
l		ł	SEMLRHPRISGKPILVLANKQDKEGALGEADVIECLSLEKLVNE
Į.		1	HKCL
5676	2	930	FVSSPPPRPVOPARPGGFGLSGRRSLLCOVASTPAHVGVMRSPV
3676	1] 330	
			RDLARNDGEESTDRTPLLPGAPRAEAAPVCCSARYNLAILAFFG
		l .	FFIVYALRVNLSVALVDMVDSNTTLEDNRTSKACPEHSAPIKVH
	1		HNOTGKKYOWDAETOGWILGSFFYGYIITQIPGGYVASKIGGKM
1			
ł			LLGFGILGTAVLTLFTPIAADLGVGPLIVLRALEGLGEGVTFPA
i	Į.	l .	MHAMWSSWAPPLERSKLLSISYAGAQLGTVISLPLSGIICYYMN
	i		WTYVFYFFGTIGIFWFLLWIWLVSDTPQKHKRISHYEKEYILSS
			L
L		ļ	
5677	1	1028	PPRDGFLELRRLSVPLCSGPCPLTSLSRQGERSGGHLVAAARAA
I		1	VTAETHPLPLLAPLAVCQSVKSPAACQVRPRPRAVALPAALGGP
1		1	GRSLPGLTAATMSSFSESALEKKLSELSNSOOSVOTLSLWLIHH
ì	1	1	
1	1	1	RKHAGPIVSVWHRELRKAKSNRKLTFLYLANDVIQNSKRKGPEF
Į.	1		TREFESVLVDAFSHVAREADEGCKKPLERLLNIWQERSVYGGEF
	i	1	IOOLKLSMEDSKSPPPKATEEKKSLKRTFQOIQEEEDDDYPGSY.
1	1	1	SPODPSAGPLLTEELIKALODLENAASGDATVROKIASLPOEVO
1	1	1	
1)		DVSLLEKITDKEAAERLSKTVDEACLRNRGPGTS
5678	3	593	SSSPSSTPSLPLPFYLLLGQLRLQLLWGTAHLSGAGEAAPCPG
1 30.0	1	1	GSGRTAAPRTRADPAAQSLMIMNKMKNFKRRFSLSVPRTETIER
l	1		_
ļ		1	SLAEFTEQFNQLHNRRNENLQLGPLGRDPPQECSTFSPTDSGEB
		1	PGQLSPGVQFQRRQNQRRFSMEVRASGALPRQVAGCTHKGVHRR
1		i	AAALQPDFDVSKRLSLPMDI
	ļ		
5679	2	623	LNSRVDDFVAVPGAIMDEDYYGSAAEWGDEADGGQQEDDSGEGE
ł			DDAEVQQECLHKFSTRDYIMEPSIFNTLKRYFQAGGSPENVIQL
{	1	1	LSENYTAVAQTVNLLAEWLIQTGVEPVQVQETVENHLKSLLIKH
		i	
	i	1	FDPRKADSIFTEEGETPAWLEQMIAHTTWRDLFYKLABAHPDCL
		1	MLNFTVKVGRVLELRRKVFMNVYFWLLVCFL
5680	258	592	RRLTSTSEKLONRNSHTPLESLIHPQPSYKGFGIMFGKKKKKIE
1 2000		1	ISGPSNFEHRVHTGFDPQEQKFTGLPQQWHSLLADTANRPKPMV
l .	1	1	
1		l	DPSCITPIQLAPMKTIVRGNKPC
5681	45	869	LLCAKTLGVRTKESQAEGYNRSGINNHQAEDPRFCPSFCWMRSA
	1		ROTRPORLRKEAARPPTPGSCPGGTGMDGKKCSVWMFLPLVFTL
	i	i	FTSAGLWIVYFIAVEDDKILPLNSAERKPGVKHAPYISIAGDDP
1	1	1	
	1	1.	PASCVFSQVMNMAAFLALVVAVLRFIQLKPKVLNPWLNISGLVA
1	1	4	LCLASFGMTLLGNFQLTNDEEIHNVGTSLTFGFGTLTCWIQAAL
1		1	TLKVNIKNEGRRVGIPRVILSASITLCVGPLLHPHGPKHPHVCS
1	1	1	II i
1_		<u> </u>	QGPVGPGHVL
5682	39	622	PSRSCLGTMRKWRHREVNLPEVTQQDAVCPAPIPSPGLSAQTGL
	1	1	OKIWGTIHCOVCPGAPAWPGSPWHEEMGLLLLVPLLLLPGSYGL
1	1	1	PFYNGFYYSNSANDONLGNGHGKDLLNGVKLVVETPEETLFTYO
	1	1	
		1	GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIG
	.		LRHRSFGDYQGRVHLRQD
5683	89	778	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMORA
3003	0,	/ "	
	1		HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEEESKGS
		1	ATYCTVCSKKFASFNAYBNHLKSRRHVELEKKAVQAVNRKVEMM
1		1	NEKNLEKGLGVDSVDKDAMNAAIQQAIKAQPSMSPKKAPPAPAK
	1	1	EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEQQAKKLAKHSEDD
1	1		SEDEEHDLC
5684	195	677	TWCFRGYLGPRVIMKALDEPPYLTVGTDVSAKYRGAFCEAKIKT
	1	1	AKRLVKVKVTFRHDSSTVEVQDDHIKGPLKVGAIVEVKNLDGAY
1			17
1		1	QEAVINKLTDASWYTVVFDDGDEKTLRRSSLCLKGERHFAESET
1	1	1	LDQLPLTNPEHFGTPVIGKKTNRGRRYE
5685	779	1262	LLLOOPVVHCFLLFPPFRFSHHMIPGPPGPHTTGIPHPAIVTPQ
3003	1 113	1202	
1		1	VKQEHPHTDSDLMHVKPQHEQRKEQEPKRPHIKKPLNAFMLYMK
1		1	EMRANVVAECTLKESAAINQILGRRWHALSREEQAKYYELARKE
Ī		1	ROLHMOLYPGWSARDNYVSPSSIPVALHS
F202	 	1100	
5686	128	1181	CTWWQVNITLLDINDNHPTWKDAPYYINLVEMTPPDSDVTTVVA
j			VDPDLGENGTLVYSIQPPNKFYSLNSTTGKIRTTHAMLDRENPD
	ı	1	PHEAELMRKIVVSVTDCGRPPLKATSSATVFVNLLDLNDNDPTF
Į			

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	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
		amino acid	
	residue of		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	t	\=possible nucleotide insertion)
	<u> </u>		QNLPFVAEVLEGIPAGVSIYQVVAIDLDEGLNGLVSYRMPVGMP
1	į.		RMDFLINSSSGVVVTTTELDRERIAEYOLRVVASDAGTPTKSST
	1	1	STLTIHVLDVNDETPTFFPAVYNVSVSEDVPR\GSGWSG*AARN
		1	•
			NDVGLNAELSYFITGGNVDGKFSVGYRDAVVRTVVGLDRETTAA
L	l		YMLILEAIDNGPVGKRHTGTATVFVTVLDVNDKRPIILQSSYV
5687	17	917	AAPPAPPDG/PPP/PPPAPPT/PGPAA/APASSCQPRLSAGRAA
ł			QGDGGAAAVGHVLVVPAVGPVRVNPGLQTPVPRPELLPGP\SSS
			LHSDSSYPPDAGLSDDEEPPDASLPPDPPPLTVP/ADA/PMPVT
		1	SGCRMPSTSASE/AAGGQGACTHAKGSETPPPASPOTSEPAPSP
	1		
			LPPHLTGGPGMYSSEAKLPNSFSCLGLAGTGAGI*GTASAHGTG
			PPVLPHVCTPSLANPQP\AVGPBASSLPLGVSGIGMSA/SAPIS
1	1	ł	SSPFVAIGSCWLRGIPPPGSGFLCPGRAPGPVPITTHGQEGQGP
1			VLDI
5688	<u> </u>	420	LTKWDLFGNCYRLLKTGIEHGAMPEOVGVYWYS/CLYDSRKLFF
3000	1	1 320	*SHMIIRSLL*KVIDDSLGQLPLLRELLL**LNVIDRCIILAYV
i		1	
1		ł	LRVEKTFAITYLKNFTVKVDFSLLGEIPLISMAAILKLWIMKID
			DGYIPAVF
5689	1504	3	HELSGKHISMVSGNTCNWHPGGHSPGGGGGGEITSKDRGEIPAL
Ŧ		i	IWA/RKPIGTWTATKPTHRAG*GGAEEYQPPPQPCEGPRSTSRG
1	1	ļ	GEG*GHAVGPGREIGKEGSLPFLGPKALGF*SASCORAFEGGAH
1		j	GSTARKPAPATPGTRHPRTMETREVAQGWPAGPRSQFWDQHPHS
		1	
			PGEHRPSG\SPLPACPPRAWPKAGAVASATGTG\PQLPGSRGKQ
			KLPRTREPPLLQAGWAVRKPPWSEAKEGLGQAGRPSGMDSSAS\
1			PQTPGGRGSLEWGLPLYLGPHHDVK*RSDRLG*PP*GGQGGGGH
	1		GAPSTPGPGGEAW*LPQQTSRPKPGPQAY*GE\GSPGLOCPCSK
1			EL*RVPPGSLGPSTQCMYEPTDKHS\GGADAQLEVSTAGSRSTF
			GQELKGPLDAGRLWPGAPSASSSHR*GG*ERARAGAGHRGST*A
	1		
			SSKIEQGRPRPGPTSDALADVEGGAES/GPHPWPLPGTLPNR/P
			GSPPPA*ASAGRKGTVSTLGGGLL
5690	1424	58	PSPFAGVCAAPAPLPLLALARRDRRPCSPGAEAAPWQTGGPAID
1	!		GAWRTSVSALRRGATG/APCSPGAEAAPWQTGGPAIDG\DGELP
1			*VRSEEAPRGCGAEGGGPGSGPVRRPGAGRGAHAGQGRQQDPEP
1		ĺ	DGLRHRQHGAASHARHRLQRLRPGHHONRHVRRDPOAPPGGPAP
			GHAAALPERTRGVAEPPAWAHAGSDAWRAGR*SQRT*ERARPRH
ļ		,	
ł			PTFQGRAGS\GQPGYQPPNPHPGPSSPPAAP\GPRGA+GNPQLE
1			KAPRSDRNPSOGLRTRIRRPETPDCGPPSPAGSSASASTFRCTS
	,		SLSLLGP/PGAHNLDTAPQDR+HGP+GDKRGAPGVAGEDPRPP+
1			GNFVR*LLLMP/GVA*RHGTSPFLGPSLGENGGQWDSGNLFGTP
1			KG*SHPAFTKST*SMEAEKSYWNHPHR\DRGRQGVRINCLRVGE
Į.		Ī	SEMWGPYSAPRPGTVFLSSFLSPASEEH\PEGSSSFNTPFPPAG
1			PEGDPGLNSPGLLP
5691	107	550	ISNDPSPGYNIEQMAKRGKKLVELPYTVKGMDVSFSGILSFIED
1			VAHRMLATGECTPEDLCFSLQVMQ*KTGTESWG*RFYIVEQN*S
1			GDAPLIFSPYLSLTGNCGFAMLVEITERAMAH\CGSPGGPSLWG
[GVGVYVLLESVPLSYS
5692 ·	1193	548	TQAWTRAEKDRKGSVRALRLHLERGPPT*RGSHPL\QSVPCIOK
50,52 '	****	0 40	
1		1	PSIFSSYPI/GLPQSGGEPGPVGEQQPVRRPEQPSCGPASRMPL
			TSRSVPPGRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQ
			RLNLPVMGATRSNLQPPRKVAVPGPTR*RDQDSKQDFSSKPLQS
ļ			VPGLASTQQTLTPADSGPGTGGRDATRAGLPGVETMGNGVD
5693	1258	1330	ALTVVPVRKGTTWWAQPHGCSNLVSRARLDLSSRPSQNTEPQAP
			*QAGPPSSLRPP\SRRR*APEWPKRATGSRCRGLSAPPWPWPAA
1			
	1		RGE/PGSAPSHAP/PNSPRPSGTRHP/PGPSSRVLYSPSLPRNS
<u></u>	1	L	PEAIVWRSSRFPLWFPLRCCFWVSGFKDPNPVLRFF
5694	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
			QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
1			SLAESGLSWFSESEBKAPKKLEYDSGSLKMEPGTSKWRRERPES
!	!		
1	1		CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL
1	1		KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
			LARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV
			· · · · · · · · · · · · · · · · · · ·

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	
1			W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
1			VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
}		}	VIGGROUPE VSSSIDPSDLSIRQGGLTPSRLKEPTKVASGRTT
ĺ			PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
			PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
	1	1	DTTQCI
5695	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
1	_		OBCI / MM CCEREM COOL MC DCCOM COMMON TO STAGALIG - KOLHO * WT
1			QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
1			SLAESGLSWFSESBEKAPKKLEYDSGSLKMEPGTSKWRRERPES
1	!	•	CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL
			KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
1	1	ł	IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV
	1		VENDODUMOL DUGUES PROFILE TO THE STATE OF TH
1	1		KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
1	1		VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
1		[PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
1	1	ļ	PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
		i	DTTOCI
5696	3	1338	-
5555		"330	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
í	(ĺ	QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
i .		· ·	SLAESGLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPES
i	· ·		CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL
	ĺ		KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
1			IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV
1	l		KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
			VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
1			PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
1	ì	1	PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
			DITOCI
5697	1147	4.7	
3037	114/	4 /	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA
			QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS
			DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL
1			SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT
}			RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP
İ		•	TODIA ON CHARRED TO THE TODIA OF THE TODIA O
Ì.			EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE
			DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK
ì			EGKTPSKENKKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR
}			RRQQRPPRSRBRTAA
5698	2	666	GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT
[550	OFFICOI DEPOSITION DATE OF THE CONTROL OF THE CONTR
:			QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ
ļ			GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI
1			ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF
			NASSBYISSDGRYARMKADECSGCGKSLLHIKLEKTHPGDQAYE
			FNQ
5699	2	1440	
	-	1448	RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD
			EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA
			RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS
			DSQRSSSKGSGWETPVPWS*AQPGWVSGLLLLGDPSGPGSL*RS
) 1			TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS*HLDPNT
(i	j		WTOWWTCE / CDA DODECA VA DA DOCOMA CHICAGON TO THE CONTROL OF THE
j i	İ		WTQKWTGE/SPAPGEEG\VAPAPRGPTAEHGHCELTTESQYSNN
ı İ			VPILFQNPSGALRSRRTEPAGWVPPTRHE*DDG*TAAPASGGAP
			VSTPTWAGTP/LNASLGPTDPQGKPGCRPPCALPKPAGPERSA*
, ,			GGSLGCR/SMLPASSGPPPAPGPRRLAAGAHTSASARCPPAAAA
}]		GWQPRRPGFAGRAALPGPPHPPSS*RELGGLPGPGW*TLDPLPA
) l			ADVADDOCY DDMOY I COMPANDE OF BEING THE TOTAL AT THE TOTA
]			HPAHPPGSAPPWGALGGWAAARASLPWSPSLCLSFPAVTPVAGL
احييكا			PPPGRG
5700	923	597	NGHKGVWEINIY*RRSNIHKNSKSESHLNQDHSFPPPTPNSARS
		f	KLHSTGTAKNTGLPLSGAPRQRAVFSGRTICQEFSSCLQCAYLD
			E*CSIASSLIKAILRVSVLSE
5701	59	410	
5,04	33	410	IFEKICSDTQEFISPEINPQICSWLIFDKGAK/NHATGKDSLFN
			KWSWKNWLSTCR*MRPGPYFTPYTKINSK*IK/DANIRCETVKL
1			LEENTGENLHDTGLGNVFLDMTPKTQPTKQK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
5702	3	1517	ETFVDPSQCGGIPSDSPHPVITPSRASESSASSDGPHPVITPSR
			ASESSASSDGPHPVITPSRASESSASSDGLHPVITPSRASESSA
ĺ			SSDGPHPVITPSRASESSASSDGPHPVITPSRASESSASSDGLH
			PVITPSRASESSASSDGPHPVITPSWSPGSDVTLLARALVTVTN
			IEVINCSITEIETTTSSIPGASDTDLIPTEGVKASSTSDPPALP
		,	DSTEAKPHITEVTASAETLSTAGTTESAAPHATVGTPLPTNSAT
			EREVTAPGATTLSGALVTVSRNPLEETSALSVETPSYVKVSGAA
			PVSIEAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETLIMDI
1			TTKGPFPTSRDPLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKP
İ			PTATPTTARTRPTT\A*VQVKMEVSSSCG*VWLPRKTSLTPEWQ
			KG*CSSSTGNSTPTRLTSRSPYCVSGEANG/PSAAARHVPYAKR
			GCCP*PGPPPTDCSCVTVLRGTQKVPMKGSMSKPLTPDVATGPS
1			LTSTGVYVWGGASPVPRGVLGLTLAHVLCFSKEKT
5703	14	1117	HHKDSRSQGLPRTQECARPELRPLLCPRALWPVTRLSYRCPWQA
			PKAGIGTKAKPSESHLKLHPGWPSLDRQGEPATLGTGTGHCSDS
1			RILRWHP*HTAAR*PRWRRLPSSHRWTRHLGVLRVQDKS**VSL
			DPSCRPRFLRTC**YGMRSVASSSNPPPGWSGPGASVFPARPVS
			ALPTGPRCW*APRGRTRQPCGWPRLSSPHATADWGPGCPLSPSR
			GSWETAPGS*WCPWL*AARWIGWRTASGASAGLGRAADRPSAWA
			RRVAGLLPGQGLTVRR*H*TAGAPASVRSSQGATRSPAPGGDQC
			ACGRGPGSC*HPPPWPVSPSSPVPCPSGR*HLRGPLLSAARPRA
	h		AGWPRHSPHDTQTPEP
5704	23	562	GDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWI
	-		SGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPE
1			QSSTAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAARAA
			KSDNVAPRRP*LPPQPQMEVPPQPLMAVSPQPPMEASLQPLMGE
			SPQP
5705	23	562	GDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWI
1	•		SGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPE
1			QSSTAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAARAA
			KSDNVAPRRP*LPPQPQMEVPPQPLMAVSPQPPMEASLQPLMGE
			SPQP
5706	1161	610	QLGRFXAQDTVAIRKVKEVFGTGAMRHVVILFTHKED*GGQALD
			DYVANTDNCSLKDLVRECERRYCAFNNWGSVBEQRQQQAELLAV
			IERLGREREGSFHSNDLFLDAQLLQRTGAGACQEDYRQYQAKVE
			WQVEKHKQELRENESNWAYKALLRVKHLMLLHYEIFVFLLLCSI
			LFFIIFLF
5707	28	609	GSPAPTPGPRRRPGRGTPSPGTRHHQGRAEPEPDAPERAPLRR*
			MFAIQPGLAEGGQFLGDPPPGLCQPELQPDSNSNFMASAKDANE
		•	NWHGMPGRVEPILRRSSSESPSDNQAFQAPGSPEEGVRSPPEGA
			EIPGAEPEKMGGAGTVCSPLEDNGYASSSLSIDSRSSSPEPACG
			TPRGPGPPDPLLPSVAQA
5708	44	1925	SFSWEETISPCFPKMPAEPWWLSPVSLGAAGWPGQPRPYLDLPA
			QASVSRPHDRA+GEAVSLSLSSGDVCGHTDGGGAGSDPQAKPKP
			PRCPFTAMPSPRTKQKVRNKVCLLIAIRYSDIPSDVSKAP\GPA
			GNPHDRSSTAA*LHRRAGAGSLCLSASLLPPSFSLGAPGAPSPL
	l		RVSPASGGPRKEGRQGSGG+AGGGGP\ARTHADLPCVGFVCSPP
			LLK*SDSPVKQLPA\SGQGSGAGMPPVGSSDILRPRPTSVSGTG
			RAAG*CSWQPAACCTPRSQ*WAVARSPSRCSRW*RQSGR*RG*S
			SRRRRGP*AAGRSTPAVP*PCS*GGAGRRAYACRTGWGYAPSR*
			LEPSGPTSGSAL*TWASHSTGA**SRLCGTAGTGPLCSQSSRS*
			AG*RCCCTAASPCGGSGPSHPGSPSAHCLSWSGGRTQPRAPSAH
	ļ		GRGRAMGSRCVCTCTGLPCPGIPLSGASPGGSGETGAGRSHTLK
			AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPPSAGHLLVGG*NS
			QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPPP
			PPRPPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GEAPA
			PPPRPEPPPPARRP
5709	2	2031	ITLCPLPQTEKCLNVVTEAATPLGIYLKARVEAGGLKELEISWG
			LHQIVVRWGAVVMRAGMGGCRCWGVMAPFAPR/NALSFLVNDCS
لــــــا			LIHNNVCMAAVFVDRAGEWKLGGLDYMYSAQGNGGGPPRKGIPE

C-050	1 5 12 -6 - 3	Predicted end	
SEQ	Predicted		Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
		 	LEQYDPPELADSSGRVVREKRSADMWRLGCLIWEVFNGPLPRAA
ì		ŀ	ALRNPGKIPKTLVPHYCELVGANPKVRPNPARFLONCRAPGGFM
ľ			SNRFVETNLFLEEIQIKEPAEKQKFFQELSKSLDAFPEDFCRHK
			VLPQLLTAFEFGNAGAVVLTPLFKVGKFLSAEEYQQKIIPVVVK
			MFSSTDRAMRIRLLOOMEOFIOYLDEPTVNTOIFPHVVHGFLDT
	i .		NPAIREQTVKSMLLLAPKLNEANLNVELMKHFARLOAKDEOGPI
1		i	RCNTTVCLGKIGSYLSASTRHRVLTSAFSRATRDPFAPSRVAGV
i	1		
			LGFAATHNLYSMNDCAQKILPVLCGLTVDPBKSVRDQAFKAIRS
1			FLSKLESVSEDPTQLEEVEKDVHAASSPGMGGAAASWAGWAVTG
			VSSLTSKLIRSHPTTAPTETNIPQRPTPEGVPAPAPTPVPATPT
1	1		TSGHWETQEEDKDTAEDSSTADRWDDEDWGSLEQEAESVLAQQD
1]	DWSTGGQVSRASQVS\TPTTNPPNPQSPTGAAGK\RGLLGTGLA
L			GAKLPGATS*RYTAGQRV
5710	1	562	IPGSTISCEVELMARMAKTIDSFTQNQTRLVVIIDGLDACEQDK
			VLQMLDTVRVLFSKGPFIAIFASDPHIIIKAINQNLNSVPSGFK
			\LNGHDYMRNIVHLPVFLNSRGL/RQ/LQENFS*LQQQMETFHA
1		1	QILQGYRKMLTEEFHRTALGR*QNLVARQPSIDG*DAIGFELYV
			CIAIQFNTNKDDAT
5711	1526	1130	RRHPFQWTTVTQEAFSHHDVAFTSTPVLFYPDSAQPFIVKSESS
			SQIAKAVLSQQRPSLFHECAFHFFS*SLORHTINLDOGIF*LLM
			LSEBROHLFESS/IWTTPHNLK*/FEIHEHLGSHEGHWTLFFLL
]			OIL
5712	 	1391	
3/12	3	1391	GRKLFQSLDISERLKFLLTLDCVDDTLIVLAEEHGCLDIIKELP
į			ETVIDLLNKCLTFHPSKRPTPDELMKDKVFSEVSPLYTPFTKPA
1			SLFSSSLRCADLTLPEDISQLCKDINNDYLAERSIEEVYYLWCL
		1	AGGDLEKELVNKEIIRSKPPICTLPNFLFEDGESFGQGRDRSS/
		ĺ	TFR*YHWDIVVMPAKK*IERCWGRSILPITLKMTSLILPYSNSN
			NELSAAATLPLIIREKDTEYQLNRIILFDRLLKAYPYKKNQIWK
			EARVDIPPLMRGLTWAALLGVEGAIHAKYDAIDKDTPIPTDRQI
ļ		1	EVDIPRCHQYDBLLSSPEGHAKFRRVLKAWVVSHPDLVYWQGLD
1			SLCAPFLYLNFNNEALVYACMSAFIPKYLYNFFLKDNSHVIQEY
i		i	LTVFSQMIAFHDPELSNHLNEIGFIPDLYAIPWFLTMFTHVFPL
			HKIFHLW\DTLLLGEFLFPILYWE
5713	634	284	PVCAVPVDRWPVLPREDQEGQQL*AKLPRDFRR*FQILGPMEGH
1			TACRCSRRGAOVOHLPREDIRAAE*DPHLREVWPGLPTSSATSP
}		1	*RAVLTSPCSHLGSADAASSHWLCGVSFH
5714	212	613	WGLGLGPTMSSLGGGSODAGGSSSSSTNGSGGSGSSGPKAGAAD
3/14	414	613	
			KSAVVAAAAPASVADDTPPPERRNKSGIISEPLNKSLRRSRPLS
1		I	HYSSFGSSGGSGGSMMGGESADKATAAAAASLLANGHDLAAA
		1	MA
5715	131	1979	ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE
			QTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\
1			GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVBNN
			DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS
1	1		PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS
			QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR
			TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL
1			YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG
			L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT
	Ì		PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP
1	1		VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE
			EGPLRLPGQDRGAQPCSHCPGRAAGQPRPGAGAPCRE/GG*DPT
1			1
			GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E
1			RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL
			TDLTEAQTSQH
5716	1711	1370	RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD
			*LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC*
l			RCPLVL*SGFFTIIVGGYSCCMPLKT
5717	44	1489	LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD
1			EGPGALVLESDLLLGQDLEFEEEEEEEGDGNSDQLMGFERDSE
		A.,	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	Amino acto segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:			Giutamic Acid, F=Phenylaianine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
,	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
	100410.00		GDSLGARPGLPYGLSDDESGGGRALSAKSEVEEPARGPGEARGE
	i		
			RPGPACQLCGGPTGEGPCCGAGGPGGGPLLPPRLLYSCRLCTFV
			SHYSSHLKRHMQTHSGEKPFRCGRCPYASAQLVNLTRHTRTHTG
			EKPYRCPHCPFACSSLGNLRRHQRTHAGPPTPPCPTCGFRCCTP
			RPARPPSPTEQEGAVPRRPEDALLLPDLSLHVPPGGASFLPDCG
	· J		Q\CGVKGRASAGLDQNHCQS/SLFPWTCRGCGQELEEGEGSRLG
	1		AAMCGRCMRGEAGGGASGGPQGPSDKGFACSLCPFATHYPNHLA
	l		RHMKTHSGEKPFRCARCPYASAHLDNLKRHQRVHTGEKPYKCPL
i			CPYACGNLANLKRHGRIHSGDKPFRCSLCNYSCNQSMNLIRHM
5718	120	204	
3/10	120	284	VAHALSLPAESYGNDVSMTHPQLPPTQLAWDLCRTCLPLSYNFT
			S**STADPLHL
5719	48	428	ELNNGPFQMPLCNGGNLAVTGSWADRSPLHEAASQGRLLALRTL
	1		LSQGYNVNAVTLDHVTPLHEACLGDHVACARTLLEAGANVNAIT
1			IDGVTPLFNACSQGSPSCAELLLEYGAKAQP\ESCLPSP
5720	ī	1051	LQAFRNASEVPMVLVGTQDAISAA\NPRVYRRTSRARKLSTDLK
		1	\RCT\YYE\TCGGTYGLQMWSVSFQDVAQKVVAL\RKKQQ\LAI
1	1	1	GPCK/SLPN/SPSH/SAVSAASIPARAPINQGHE/SGGGSAFSD
1			V\ CCCUPCTECT COPET B TETTA COMPETATION CONTEST
			Y\SSSVPSTPSISQRELRIETIAASSTPTPIRKQSKRRSNIFTS
į	!		RKGADP\DREKKAAGCKVDSIGSGRAIPIKQGILLKRSGKSLNK
1	j		EWKKKYVTLCDNGLLTYHPSLHDYMQNIHGKEIDLLRTTVKVPG
		1	KRLPRATPATAPGTSPRANGLSVERSNTQLGGGTGAPHSASSAS
		ľ	LHSERPLSSSAWAGPRPEGLHQRSCSVSSADQWSEATTSLPPGM
			QHPASG
5721	97	492	RHSSPCCSLRRTERSSNAAVST/TTVQQFKRFIENYRRHIGCVA
			VFYAIAGGLFLERAYYYAFAAHHTGITDTTRVGIILSRGTAASI
1			
5722	88	1045	SFMFSYILLTMCRNLITFLRETFLNRYVPFDAAVDFHRLIASTA
5/22	88	1043	VALDVLAGSSPGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP
			GSLGVSHAAAPPARPQGAAQSPHRGRRHGGGGAGLPPPRSPRFP
	J]	QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRRPGAGVGAPRR
1			GRARGQAGLLGRQGQGGRGAERERAALQARRGRRPGPEPDQSCG
}			GRPRRAAAAPGRAPADPQPPAPRPAPAPDVRPPADAPAPAPA
	i		PPPPPHLGALTAGSGEERQSQPRAETLRLGRGAPLP\PRAERGG
	1	1	RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT
		ĺ	KSSTREIPEMI
5723	88	1043	VALDVLAGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP
			GSLGVSHAAAPPARPQGAAQSPHRGRRHGGGGAGLPPPRSPRFP
1		!	QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRRPGAGVGAPRR
1			GRARGQAGLLGRQGQGGRGAERERAALQARRGRRPGPEPDQSCG
1			GRPRRAAAAPGRAPADPQPPAPRPAPAPDVRPPADAPAPAPA
Ţ	1	}	PPPPPHLGALTAGSGEERQSQPRAETLRLGRGAPLP\PRAERGG
1			RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT
			KSSTREIPEMI
5724	3	1841	FTNEAPPAPLPDASASPLSPHRRAKSLDRRSTEPSVTPDLLNFK
1			KGWLTKQYEDGQWKKHWFALADQSLRYYRDSVABEAADLDGBID
1	1		LSACYDVTEYPVQRNYGFQIHTKEGEFTLSAMTSGIRRNWIOTI
l			MKHVHPTTAPDVTSSLPEEKNKSSCSFETCPRPTEKQEAELGEP
1			DPEQKRSRARE\RREGRSKTFDWAEFRPIQQALAQERVGGVGP
1			ADTH\DPWRPEAEHGELERERARRREERRKRFGMLDATDGPGTE
1	1	1	DAALRMEVDRSPGLPMSDLKTHNVHVEIEQRWHQVETTPLREEK
1			QVPIAPVHLSSEDGGDRLSTHELTSLLEKELEQSQKEASDLLEQ
			NRLLQDQLRVALGREQSAREGYVLQATCERGFAAMEETHQKKIE
1			DLQRQHQRELEKLREEKDRLLAEETAATISAIEAMKNAHREEME
}			RELEKSQRSQISSVNSDVEALRRQYLEBLQSVQRELEVLSEQYS
1		1	QKCLENAHLAQALEAERQALRQCQRENQELNAHNQELNNRLAAE
1			ITRLRTLLTGDGGGEATGSPLAQGKDAYELEVPSGARPCLTQLC
	 		TQEPQGSAAWPLSYRVVGGTDLRQQESQGPGRSKSPEGGEEQ
5725	3	1049	VNGHSEETSQSPNRTEPHDSDCSVDLGISKSTEDLSPQKSGPVG
1	1		SVVKSHSITNMEIGGLKIYDILSDN\DLSSHLQPLK/FTSAVDG
1			KNIVRSKAATLLYDQPLQVFTGSSSSSDLISGTKAIFKFDSNHN
1			PE/GAKYNKRPHKWAHNLHLKYMVLHSIISNTVAV\RSQRHFVA
	•		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine.
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			LQTKSPNRPCQFSSSAPS/VDQRAQ/INQSYAKHSANMNFSNHN
			NVRANTAYHLHQRLGPARHGEMWAISPNDRLIPAVTRSTIQRQS
			SVSSTASVNLGDPGSTRRAQIPEGDYLSYREFHSAGRTPPMMPG
		}	SQRPLSARTYSIDGPNASRPQSARPSINEIPERTMSVSDFNYSR
1			TSP
5726	2	486	SRSLSMWWNSGLPASSHSSKLPVTVGFSGCVKRLRLHGRPLGAP
			TRMAGVTPCILGPLEAGLFFPGSGGVITL/ESVGAGIPGPSRAG
ŀ			QGSPGGSGEGPPLSSPSQPLPADLPGATLPDVGLELEVRPLAVT
] .			GLIFHLGQARTPPYLQLQVTEKQVLLRADDG
5727	21	221	RPILILKETRRLPWATGYAEVINAGKSTHNEDQASCEVLTVKKK
			AGAVTSTPNRNSSKRRSSLPNGE
5728	2	877	GTRNGQFEPRRGRAWEGSAGGLRAPGAAAGGPGVQPRGSG/LPG
1 1			NAIRAGVNPGRGPASPFWDLSLPWDLWPPPTDHAPGAPDFPAVE
			GR\PWAGGRPPWPVSGVLGSRVCGPLYSTSPAGPG/SGGLSPSQ
]	GGPAGAGGDAG/LPGRCPSAPWRAGSRPAASCPDWIPGPQGLWL
			HRNPTS/GPPSQIGEGAEQGDEGVADAPQIQCKN/GAEDPPAED
J i			EPPQVPEAGEEDAVPABEGPGGTPETQADQVRERPEAHLAEGGA
]			KGSPRRLADPQDLPAGQMSLAPPFPPVAAVIRSNK
5729	1	1525	AGGAREVLTLQLGHFAGFVGAHWWNQQDAALGRATDSKBPPGEL
1 1			CPDVLYRTGRTLHGQETYTPRLILMDLKGSLSSLKEEGGLYRDK
			QLDAAIAWQGKLTTHKEELYPKNPYLQDFLSAEGVLSSDGVWRV
			KSIPNGKGSSPLPTATTPKPLIPTEASIRVWSDFLRVHLHPRSI
			CMIQKYNHDGEAGRLEAFGQGESVLKEPKYQEELEDRLHFYVEE
			CDYLQGFQILCDLHDGFSGVGAKAAELLQDEYSGRGIITWGLLP
			GPYHRGEAQRNIYRLLNTAFGLVHLTAHSSLVCPLSLGGSLGLR
			PEPPVSFPYLHYDATLPFHCSAILATALDTVTCS\YRLCSSPVS
			MVHL\ADMLSFCGKKVVTAGAIIPFPLAPGQSLPDSLMQFGGAT
1 1			PWTPLSACGEPSGTRCFAQSVVLRGIDRACHTSQLTPGTPPPSA
1 1			LHACTTGEEILAQYLQQQQPGVMSSSHLLLTPCRVAPPYPHLFS
			SCSPPGMVLDGSPKGAAVESVPVFG
5730	1258	1713	KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK
			LSLGTYASLHGRIYCKPHFNQLFKSKGNYDEGFGHRPHKDLWAT
			KIETEGFWERPRNFENQGRPLKSPGGEDCPSC*GGCPGSNY*AQ
			GSSSREKGGQASWNPKLRVA
5731	122	443	RSHRGELIPKDSCYMRKPPRRPKKRRQG/CALPQGCLTFKDVAI
			EFSLEEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK
			KPGRGRGKQRRQEWFFLRVY
5732	226	772	PPSRSCQSPRRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF
			PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N
			LLGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA
			QVSTNLLDFEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK
			ALLDAA
5733	1	460	PALQEVNANALAWGKQYENDARTLFEPTSGVNDTESPIIYRDES
			MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM
			AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS
			FDEI\VP\EFIGKMDEVLSRDPM
5734	3	968	RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFIVFTVI
			GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS
1 1	İ		SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY
[[GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG
			HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC
			VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS
			TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP
			SMKPMAVVASTVLGL
5735	2	540	FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL
1			ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNO
			YPVFPWVLTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE
			RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY
			LKILT
			
5736	1	382	GTRPSTKKSGYSPQQVAVIHCKGHQKENTAVAHSNQKADSAAQV

Predicted and predicted and nucleotide corresponding corresponding corresponding corresponding anio acid amino acid residue of amino acid amino acid sequence Provide amino acid amino acid sequence Provide amino acid amino acid sequence Provide amino acid a		15-11-11	1 5 12 -4 - 3 3	Table Till Timent containing signal beautiful
No:	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
corresponding to first amino acid amino ac	ID		nucleotide	
to first maino acid residue of amino acid residue of amino acid residue of amino acid sequence sequenc	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
to first maino acid residue of amino acid residue of amino acid residue of amino acid sequence sequenc		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
to first residue of amino acid amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid amino acid sequence sequence sequence (2000,)-possible nucleotide deletion, \(\) -possible nucleotide deletion, \(\) -possible nucleotide deletion, \(\) -possible nucleotide deletion, \(\) -possible nucleotide deletion, \(\) -possible nucleotide deletion, \(\) -possible nucleotide deletion, \(\) -possible nucleotide deletion, \(\) -possible nucleotide deletion, \(\) -possible nucleotide deletion, \(\) -possible nucleotide intertion TARLSYPPRILIPYSE/POSPODED/BNPVSTTTELLASDLRANKN OES**ILDDSGTPPTTTSLLQSTTHLRARACIPOLLER REPORT REALIZED AMINOR REPORT REALIZED AMINOR REPORT REALIZED AMINOR REPORT REALIZED AMINOR REPORT REALIZED AMINOR REPORT REALIZED AMINOR REPORT PLANCE REPORT REALIZED AMINOR	1			
amino acid residue of amino acid sequence sequen	ł			
maino acid sequence amino acid sequence codon, /-possible nucleotide deletion,	l .	to first	amino acid	
amino acid sequence Codon, /=possible nucleotide deletion,	ĺ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
amino acid sequence Codon, /=possible nucleotide deletion,		residue of	amino acid	Walryntophan, Yalvrosine, Xalinknown, *ston
Sequence Sequence	Í			
TARLSYTEPRILIPTVSFTQEDLIPTNEYSTTTEKLASDILARIN QES**ILDBOGIFIP**IT*SYLQSTILLBRAKLPQLIRR 5737 290 1041 KACHALLSSFITSNFIPNILLPSSLYSVERASQRANIGPCRKK RTADGSCGROPGAHIPOFKSSNRASRLIJGGLGSHHLDAYG RDLGGTPAPLOLGI POPGRIPAPITOGAGRINGGGGSP*V ETRPLITORR**PGWPPWITPAHPAGTILPRGAWPESVSACGK APPSTGGCCGGCGCAWARWRIANARTICGG 5738 8 460 DTLSINCTLEFILMTSFFICHTCGGGRSHGGSP*V ATQPARTSGCCGGGGAWFINARATICGSQ 5739 1 1222 SFORRGIEWWYNTHIPPSFVLSFLFFGLARAKSIPTKTYSNEW TATQPARAPLETVSIPPBULGSTYFEMATGRFLFFGSTVEEQLHFI PTLLSERMALCAWFINAMAGTGGGGS*ALLGRARAPALC 5739 1 1222 SFORRGIEWWYNTHIPPSFVLSFLFFGLARAKSIPTKTYSNEW TRILISERMALCAWFUNG SFORRGIEWWYTHIPPSFVLSFLFFGGLARAKSIPTKTYSNEW TRILISERMALCAWFUNG SFORRGIEWWYTHIPPSFVLSFLFFGGLARAKSIPTKTYSNEW TRILISERMALCAWFUNG SFORRGIEWWYTHIPPSFVLSFLFFGGLARAKSIPTKTYSNEW TRILISERMALCAWFUNG SFORRGIEWWYTHIPPSFVLSFLFFGGARAARAPALC SFORRGIEWWYTHIPPSFVLSFLFFGGGGGS*ALLGGRARAPALC SFORRGIEWWYTHIPPSFVLSFLFFGGGGGS*ALLGGRARAPALC SFORRGIEWWYTHIPPSFVLSFLFFGGGGGS*ALLGGRARAPALC LOCOMPYLLGSPHEDCGGRINTVTRQVIGHLCYRLTNGPFAARAFHLK LOCOMPYLLGSPHEDCGGRINTVTRQVIGHLCYRLTNGPPSKABRG HKVRLAVSSLEPPTWERFRERRERGENGLINTSSLLAUMTHNY TORGANGARASHLYKHIPPSFLLRFDUTTGFFT RDPGGHCMATS PROBEGGLINAPVSGGSFFTGANGGFFLGKACKLLGUWFRENDATIN TRILINCDGGFILPFUDRTGDPFRHKGENVALTTVARVPPALDF TRILINCDGGFILPFUDRTGDPFRHKGENVALTTVARVPPALDF TRILINCDGGFILPFUDRTGDPFRHKGENVALTTVARVPPALDF TRILINCDGGFILPFUDRTGDPFRHKGENVALTHVARVPPALDF TORGANIANATURE TRILINCDGGFILPFUDRTGDPFRHKGENVALTHVARVPPALDF TRILINCDGGFILPFUDRTGDPFRHKGENVALTHVARVPPALDF TRILINCDGGFILPFUDRTGDPFRHKGENVALTHVARVPPALDF TRILINCDGGFILPFUDRTGDPFRHKGENVALTHVARVPPALDF TRILINCDGGFILPFUDRTGDPFRHKGENVALTHVARVPPALDF TRILINCDGGFILPFUDRTGDPFRHKGENVALTHVARVPPALDF TRILINCDGGFILPFUDRTGDPFRHKGENVALTHVARVPPALDF TRILINCDGGFILPFUDRTGDPFRHKGENVALTHVARVPPALDF TRILINCDGGFILPFUDRTGDFTGARTENSSLAUMTHNARVPPALDF TRILINCDGGFILPFUDRTGDPFRHKGENTTNARVPDLITGPFRHKGGFILPFTHARF TRILINCDGGFILPFTHARF TRILINCDGGFILPFTHARF TRILINCDGGFILPFTHARF TRILINCDGGFILPFTHARF TRILINCDGGFILPFTHARF TRILINCDGGFILPFTHARF TRILINCDGGFILPFTHARF TRILINCDGGFILPFTHARF		1	sequence	
OES+*ILDBSGTPIP*T-TSYLQSTHILBRANLPQDEREK S737	ļ	sequence		\=possible nucleotide insertion)
S737 290 1041			1	TARLSVTPPNLLPTVSFPOPDLPDNPVYSTTTEKLASDLRANKN
S737 290 1041		1	1	
LQTIMBLAAGFQYSSHKDPSLSAKERHTUTNIMEARGFWIDGYUS RIADSGCROFDAJHIGP RISS SHRASELLJEGIGGSHILDAYUS RDLEGGTPAPLOLBI PPOPRGHPAPLTTTOQAGFRISGRASPI-V ETRELTIDGER* FORDPYBYGT PAPADTIRPRGAGSSHILDAYUS RDLEGGTPAPLOLBI PPOPRGHPAPLTTOQAGFRISGRASPI-V ETRELTIDGER* FORDPYBYGT PAPADTIRPRGAGSSYSCKW APSPTSQCCCGRCDAYPHRAMRTPLCSQ 5738 8 460 DTISLINCTIDEPTLIPPTSFF-LSF-IP-FGLAARGI PPKTYSNEV VILWARPPDILLGETDYSTOLDM*-QOVEWQOPCOKOGGLVTT ATQPARAPLTYUSPLERGVOLTYPEMATGRPLPPGSTVERGULT! FRILGEBANALCAVETHR 5739 1 1222 SFQRRGI RMVNITLHPIPRAVWAGIGRGHGS*-ALLGRARAPALC FPILLEFILSELDED FARLAMGLELMRAAG RPTIPRGISDLLAEV SARVDGEVPOLISS PGUTDTCLY! FTISGTTGLIFRAARISHLKI LQCQFYQLGGVHGRDVITVLGY! FTISGTTGLIFRAARISHLKI LQCQFYQLGGVHGRDVITVLGY! GELGRALLWAPP PSAVAG HKVRLAWGSGLRPUTMERFVERREPLQVULSTTGLIFIGENVATINY TGGRGAVARASHLKHIFPFSLIRIDVITCEPIRROGGIGATV VLISKFSAGGFBEDCQHRVIVYQY! GELGRALLWAPP PSAVAG HKVRLAWGSGLRPUTMERFVERREPLQVULSTTGLIPRAARISHLKI LQCQFYQLGGVHGRDVITVLGY! GELGRALLWAPP PSAVAG HKVRLAWGSGLRPUTMERFVERREPLQVULSTTGLIRGNVATINY TGGRGAVARASHLKHIFPFSLIRIDVITCEPIRROGGICARIA HKVRLAWGSGLRPUTMERFVERREPLQVULSTTGEIRGNVATINY TGGRGAVARASHLKHIFPFSLIRIDVITCEPIRROGGICARIA HKVRLAWGSGLRPHAGLEGSHALQHAPPA LQSELHKLJDBETQGSVFILGAGKLKUNGPFSAGARIAP TYVERVYN*NISRAVHALDQKRIPPAGLSSSMALQLARCHMAN TYVERVYN*NISRAVHALDQKRIPPAGLSSSMALQLARCHMAN TYVERVYN*NISRAVHALDQKRIPPAGLSSSMALQLARCHMAN TYVERVYN*NISRAVHALDQKRIPPAGLSSSMALQLARCHMAN TYVERVYN*NISRAVHALDQKARIPPAGLSSSMALQLARCHMAN ACKEPKK*CTLLAGSAMTLPHIGKRGGTPPPLCGAIPASGL TYARGOVXARRVANDGDGWILAEVGSVSHATTKYEVDDLDE GEKKHILSRRYIPLDGWANAPETDFDBLIFKGRUNLALLYPQT TCYPRALIHAPPQRQDDVSULFEDTSVADGSSPADIKHIEPHIKK 5742 2 362 TQSVKEILKNNNNNLTDBCONTAMIASKGGHTETVOGLUGDON TALTYAVEKKNATAVROLLQCANDFTSICTKOG SKERKK*CSRDSPNDTCOGGSRGACIKHIEPHIKK TALTYAVEKKNATAVROLLQCANDFTSICTKOGG KATCHTURSTANAPACKNATAVROLLQCANDFTSICTKOG TCYPRALIHAPPQRADDSVALARCHMANAPACHICANDGAV VENRESSASSTSAGVYLLAKKERSPONGSRGACHILTEGETSR SPRGATTTGRGSSSKEREVYDDASSTOTTVORGARGERFTCPKM MGDYLETCCUTCRUNSRPTYTHROCGLESTREISSERGHTGSVS SDAMSASSTSAGVALLTARGSGNATAGTROLTSDASSARC TCHATTARAADEEPRAPTGREVTDATTGA				
RTADGSCORPPOANHERERSSNRASELLEGGGSHLHADVER RDLECOTRAPLOLIS PPOPREMENP LYGOLOGENSOFGCASP*V RDLECOTRAPLOLIS PPOPREMENP LYGOLOGENSOFGCASP*V ETRRITORS**ROWERY PAPRAGTLERROGUES VACCEN APSPETOGCCGGGCAVPHENBARTHELCSQ TILLIANT LIBERT PRESTITION OF CONTROL OF CONTROL OF CONTROL OF CONTROL TATORAPLIT VPSILOR OF CONTROL OF CONTROL OF CONTROL TATORAPLIT VPSILOR OF CONTROL OF CONTROL TRILLIANT ACTUAL OF CONTROL TRILLIANT ACTUAL OF CONTROL TRILLIANT ACTUAL OF CONTROL TRILLIANT ACTUAL OF CONTROL TRILLIANT ACTUAL OF CONTROL TO THE CONTROL OF CONTRO	5737	290	1041	
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RDLECOTPAZIOLALIPPOPRGHPAPITPROGAGERNSOPCASPY ETRILITORIP *ROTPPOSTATA PROGAGERNSOPCASCAN APSPTSOCCEGRCDAVPRHAMBETLESQ 5738				RTADGSCGRGPDGAHHPGPKSSSWRASRLIJPGLGGSHHLDAYVG
### STRUITORR* FOUND TANDRAGTIR PREGAVEPS VACCEM APPSTSQCCEGERCADYPHENSH PILCS 5738 8 460 DTLSINCTLDETLDRTDSF*LSFL*FFGLARASE PPKTYSENG TATORAPPILLETUR PTTSF*LSFL*FFGLARASE PPKTYSENG* ATORAPPILLETUR PTTSF*LSFL*FFGLARASE PPKTYSENG* ATORAPPILLETUR PTTSF*LSFL*FFGLARASE PPKTYSENG* TATORAPPILLETUR PTTSF*LSFL*FFGLARASE PPKTYSENG* TATORAPPILLETUR PTTSF*LSFL*FFGLARASE PPKTYSENG* \$	l			
### APSPTSOGCCEGGCDAVPKHRAWRTPLCSO ### ST38 ### ST518CTLPST.PWTSPT-15PL-SPEJARAKSIPTKTYSNEV			I	
S738 B	[ETRPLTDGRR*PGVRPVGWTPAHPAGTLRPRGAVEPSVSACGKW
VTLWYR PPDILLGSTDYSTGIDMM GQVEWNGGPCGKGGGLVTT ATQPARPLIFTVPSDRAUGCIFYEMATGRPLFPGSTVEEQLHFI FRILSEEAMALCAVETHR 5739 1 1222 SFORRGIRWRVHTLHFIFRAVWAGIGRGHGS*ALLGRARARAL FPPLLEFIESLESEDLPALRAMGLHLWAGGFGHAGISDLLAEV SAEVDGPVPGVISSPQSITDTCLYIFTSGTTCLPKARAT,SILKI LQCQGFYQLCGVIGGDVIYLLAPLYHYMGSGLLGIVGCMGIGATY VLKSKFSAGQPWEDCQQHRVTVFQYIGBLGYKLWAPPSKAERG HKWRLAVGSGLRFPWRGFVRAFGPLQULEFTGLFGTGHAVATINY TGQRGAVGRASMLYHHIFPSLIRTDUTTGFFIEDPOGLAMTS PGEFGLLVAPPSQSFFLGYAGGPFLAGXGLLKDVPRPGDVFFN TRDLLVCDDQGFLRFHDRTGDPFRKGENVATINYA DGGRGLAVGRASHWYHHIFPSSLIRTDUTTGFFIEDPOGLAMTS PGEFGLLVAPVSQSFFLGYAGGPFLAGXGLLKDVPRPGDVFFN TRDLLVCDDQGFLRFHDRTGDPFRKGENVATTEVARVPEALDF LQGVNYGVTV AVERRYN*NISAMVHALEGKRHPAGISSSMALGLMPCLGHMAN LQGELHKLYDFETGSWVSGSAGGYF FRITMRGVLMTLLQQSAMTLFLMTGKGFRFPFLCGAILAFGG TYVARFDGVVARAVRAVOGDBOGHLAEVVSYSKATNYEVDDIDE GGKERHTLSRRVIFLDGWKAMFBTDDEALFGKEQULALLYFOT TCYFRALHAPPORPODDYSVLFBGTSYAADSFPINVAQRXVV ACKEPKKK*CRLADSSSPNDTGODSGRAGIKHIPPLKKK 5742 362 TGSVKELIKRNFWVILDTGWGRAMIASKEGHTEIVQDLLDGG TYVNIFDRSGGTVLLGAVGGRVSTURALLGKYADDLIRGGDWK TALYMAVEKGNATMYRDLLQCKPDTEICTKDG TALYMAVEKGNATMYRDLLQCKPDTEICTKDG TALYMAVEKGNATMYRDLLQCKPDTEICTKDG TALYMAVEKGNATMYRDLLQCKPDTEICTKDG TALYMAVEKGNATMYRDLLQCKPDTEICTKDG TALYMAVEKGNATMYRDLLQCKPDTEICTKDG TRRTTTSFTTTSPTTTSPTTTSPTTTSPTTVTTTTPLLTTGTPLLGMTTIN VPTTANTCLSLTSTLPERATGLLTPEPSKEGPILTAESETVLP SDBWSSASSTSADTVLLITSKESKWDLLPSTSHYSMKKTSDVSS PQGASDTAVPGKNTKTKTGHOEGIFMSKMEMBESOVSS PQGASDTAVPGKRUSSRPTKMTFOQLFSTHOMSKRKTDSVSS PQGASDTAVPGKRUSSRPTKMTFOQLFSTHOMSKRKTDSVSS PQGASDTAVPKURSSPTSTTHFOORTTPDALPTTVYTTTPLLTTGTPLLGMTTIN VPTTANTCLSLTSTLPERATGLLTPSFSKEGPILTAESETVLP SDBWSSASSTSADTVLLITSKESKWDLLPSTSHYSMKKTSDVSS PQGASDTAVPKURSSPTSTTHFOQLFTYNSTHTOMSKRKTNPDGG KKSEFNILMKRKSCEBELDLGRYSNGFTKNSKEGGGSRGEELHHISLT STAG SPAGGSTFPCPVCKKFRSRPTTMTFFOQLFTYPRSCRIPTYPRSCNIPOTY VENRLPGMLPAHDSLLLDSLSTQCPTTROTSSEPPVLNTRQGC YCKKFTSTAGRRUSHLKFRGNCLYSKGERRATKKKKCGGGGSRTEEDMLMOGI LGF PSFAGGKTSTSCREWKHTHTFNKGGCGSTSGSGGEELLHHISLT AHGBPERPLAATSAAPPQDPQDQPDPPQPGPPPGPRE EATPTPADAAPEEPPADPEPFCQVCXGSFTQSWFLKGRMKKKAKA SPDHACPV	1			APSPTSQGCCEGRCDAVPKHRAWRTPLCSQ
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FPTLLEFILESLEPIDLPALRAMGLHLWAGQPOTTEPGISDLLAEV SAEVUGPVPGYLSSPQSITDTCLYIFTSGTTGLFAARISHLKI LQCGGFYQLGCVINGBUYTYLALPLYHMGGSLLGYLVNQPPSKAERG HKWRLAVSGGREDTWERFVPKRRFQDQVITGJEGNATINY TGRGAVGRASHLYKHIFPFSLIRIDVTTGEPIRDPOGHCMATS PGEFGLLVAPVSQOSPFILAFWAGGPELAGGKLOAVERVATINY TGRGAVGRASHLYKHIFPFSLIRIDVTTGEPIRDPOGHCMATS PGEFGLLVAPVSQOSPFILAFWAGGPELAGGKLOAVERPGHCWATS PGEFGLLVAPVSQOSPFILAFWAGGPELAGGKLOAVERPGADVERN TRDLLVCDDQGFLRFHDRTGDPFRWKGENVATTEVAEVFEALDP LQEVNVYGVTV 5740 265 231 PAYWLKVETICLESKTDLREKASHVSAQLQGEVRGLAGALMM-A YVYERVYN*NISZRVHÄLEGKRIFAGLSSNÄLQLAPCLGMLMA LQSELHKLYDEETQSKVSGASCAGYP 5741 1 650 PRYMMRGGVLMTLLQSAMTLPLWIGKRGDRPPLCGALPMA LQSELHKLYDEETQSKVSGACGYP EGKERHTLSRRRVIPLPQW KANPBTDPEALFQKEQLUVLALYPQT TCYYRALHAPPQRPCDDYSVLEDETSVADGYSPFLMVAGKYV AKCEPKKK*CALABSSENDTCGDSRGRGKIHIPPLKKK 5742 2 362 TGSVKBILKRNPWNITDRODNTALMIASKGHTEIVQDLUDAG TCYYNALPHASCGTVLLAURGHEVIVALLAVAGYVV AKCEPKKK*CALABSSENDTCGDHSRGGLWIPPLKKK 5743 2 415 GKTPEGIDAIEEIGLDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPRKTPEVIDATEELDKDLEETKREISPEENGPEE VKVVDEMETDLKTTGREGSSREKTERVIDABVIETDLEETERE ISPQE 5744 3 703 TRRTTTSPTTROMTTPAALPTTVTPDLTTGPLQMTTA VFTTANTCLSLTPSTTPEBATGGLTPEPSKEGPILTARSETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS PQGASDTAVPEONKTTKTGQMGGIPMSKNEMPISQLIMIIAP SLGFVLPALVAVLLEGKLMETYCSQKHTVLGDSKNVLNDV QHGREDEDLETL KGSFFVLMKHSKKTYDSFQDELEPTIKMSKENVENDY OHGREDEDLETL KGSFFVLMKHSKKTYDSFDDELEPTIKMSKENVENDY OHGREDELEPT KLNNREKKSKEDVSKKERERTKKKKROGGENTEEEMVPLNPNQGE YIGGSHGVEHKVYKHFSSDNSTSTHQASHKOHONSESS RAGGRFFPCVVCKRFRFNSILALHLRTHOPERFSPARALLLE LEERALLEAALGRARSSGGMQATFATEGLARPARSSAPRCP YCKNGFRFTSARFREHLHILHERPKGGLGSGGREELLHHISLT AHGAPERPLAATSAAPPPQOPQPPPPPEPROPERPOPER PYCKNGFRFTSARFREHLHILHERPKGGLGFGSSGBEELLHHISLT AHGAPERPLAATSAAPPPQOPQPPPPPEPROPERPOPER PYCKNGFRFTSARFREHLHILHERPKGGLGFGSGSGEELLHHSLT AHGAPERPLAATSAAPPPQOPQPPPPPEPROPERPOPER PYCKNGFFTSARFRETHLHILHERPKGGLGFGSGGBEELLHHSLT AHGAPERPLAATSAAPPPQOPQPPPPPEPROPERPOPER PYCKNGFTSARFRETHLHILHERPKGGLGFGGNVENSES PSRGKGVSSNYRRSPERFTGOLKREKKKROPVOTEPQKRYTE	5730	1	1222	
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LQCGGFYQLCGWHQEDUTYLALPLYHMSGSLLGITYCCMGIGATY VLKSKFSAGQPMEDCQQHRTVTQYQTGCRYLVNQPSAGARG HKVRLAVOSGGRPTDERFVRRFGPLQVLETYGLTEGNVATINY TGQRGAVGRASHLYKHIFFFSLIRIDUTTGEFIR IPPQGHCMATT PGEPGGLUAPYSQQSFIEYAGGFELAGGKLLKDVFRRGDVFRN TRDLLVCDDQGFLRFHDRTGDFFRNKGENVATTEVAEVPEALDF LQENVNYGVTV 5740 265 231 PAYWLKVPTLCLESKTDLRSKASHVSAQLQGEVRGLAGALNM*A YVVERVYN*NISRWHALSQKRHPAGISSSALQLIPCLGMLNA- YVVERVYN*NISRWHALSQKRHPAGISSSALQLIPCLGMLNA- YVVERVYN*NISRWHALSQKRHPAGISSSALQLIPCLGMLNA- YVVERVYN*NISRWHALSQKRHPAGISSSALQLIPCLGMLNA- YVRERVYN*NISRWSGAGGGFY 5741 1 650 PRKTMRRGVLMTLLQGSAMTLFLHIGKRGGRPFPLCGAIPASGD VARPGGKVAAVKANDGEOMILAEVYSYSHATNKYBVDDIDE EGKRHTLISRRVIPLDGWKAMPRTDPEALFQKEQLVLALYPOT TCPYRALIHAPPQRPQDDYSVLPEDTSYADGYSPPLNVAQRYVV ACKEPKK*CALADSSFNDTOQDSRGRAGIKHIPPKKK 5742 2 362 TQSVKEILKRNFNNNITDKDGMTALMIASKEGHTEIVQDLDLDAG TYNNIPRSGOTVLIGANKGGHVEIVALGKYADDIDTGGDNK TALYWAVEKGNATNVRDILQCMPDTEICTKDG (KTPEGIDAIESIBILDEFTERETSPENGLEVKPLGEMGTDL KATGREISPREKTPEVIDATEEIDKDLEETGREISPEENGPEE VKVVDEMETDLKTTGREGSSREKTREVIDAASVIETDLEETERES 15744 3 703 TRRTTTSFTTTRGMTTTPAALPTTVVTTFDLTTGTPLQMTTIA VFTTANTCISLTPSTLEPERSGSSREKTREVIDAASVIETDLEETERES 15744 3 703 TRRTTTSFTTTRGMTTTPAALPTTVVTTFDLTTGTPLQMTTIA VFTTANTCISLTPSTLEPERSGTGJERSTVLYSTSHVSWKKTSDSVSS POPGASDTAVPBONKTTKTGGMDGIPMSMKNEMPISQLLMIIAP SLGFVLFFALFVAFLLSRKLMETYCSGVHTALDYIGDESNVLNDV QHGREDEDGLETIL 5744 3 5745 GKSEFVINKHISKKTYDSFODELEDYIKVQKANGLEPKTCFRKM KGDYLFTCGYKGEVNSRPTYRHFDQRLPSSTIQTTPRSCHIPOT VENRLPQWLPAHDSRLRLDSLSYCOFTROFFSKEVPLNFNQG YICGSKGVENNYKHYSSNSTSTHQASHKQIHOKRKHPEEGR EKSEERSKHRKKSCEGEIDLDKHISIQRKKTEVEIETVHVSTE KLKNRKKKSCEUSLKEKSRRVTKKKEGQRSTTEEDHLADGI LGF 5746 3 621 SPAGGRLTFSSPAPDGELDLQRYSNGPAVSAMSLGMGAVSWSES RAGERRFPCPVCKRFFFNSILALHLRTHNOGCGRFTEEDENHOGSI LGF YCKKFFTSABEREHLHILHIHPRWKGGGSSSGSGEELLHISLT AHGAPEPLAATSAAPPPQOPQPPPPEPRSVPQDEPEPQPER EATPTETAPAAPEEPPAPPEFFCOVCGGSFTOSSFCELLHISLT AHGAPEPLAATSAAPPPOPQPPPPEPRSVPGPEPPQPER EATPTETAPAAPEEPPAPPEFFCOVCGGSFTOSWFLKKHMKKA SFDHACPV 5747 2 1328 DRHVETLCIHHILHIHPRWKGGTSSSSGSEELLHISLT AHGAPEPPAPPEPTGOLEERIKKNRGDVDTEFPCKHTE	1			
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QHGREDEGLFTL 5745 1400 599 GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQRKKRHPBEGR EKSEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER EATPTTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE		1	1	
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KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRYYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEERSKHKKKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPPQPER EATPTTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE		1	1	QHGREDEDGLFTL
KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRYYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEERSKHKKKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPPQPER EATPTTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	5745	1400	599	GKSRFVNLMKHSKKTYDSFODELEDYIKVOKARGLEPKTCPRKM
VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPPPQPEPRSVPQPEPPQPER EATPTFAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	3,43	1 1100	1	
YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPPQPER EATPTTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	1		1	1
EKSEEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER EATPTTAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	1		1	VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE
EKSEEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER EATPTTAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	1	1	1	YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR
KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLETHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPPPPQPEPRSVPQPEPPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	1		1	
LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	1			
5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	ł	1	1	-
RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPPPQPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	1		1	LGF
RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPPPQPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	5746	3	821	SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES
LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE		1		
YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQEEELLHHSLT AHGAPERPLAATSAAPPPQPQPPPPPPPPPPPPPPPPPPPPPPPPPPPP	1		1	
AHGAPERPLAATSAAPPPQPQPPPPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	1		1	
EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	1	1	1	YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT
EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	1	1	1	1 -
SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	1	1	1	1
5747 2 1328 DRHVETLCIHFLØPSTØSTAKTØGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE		}		
PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE				SFDHACPV
	5747	2	1328	DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG
	1		1	PSPRGKGYSSNYRRSPERPTGDLRERIKNKRODVDTEPOKRNTE
ESSSPVKAESSKGRAREAEDIATIAERIPESSEERVEWEINKUD				· ·
	L			ESSSEAUVESSKOUUTEVEDIUTI VEKILESEEMARMEIUKDD

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	1	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
l wo:	1	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
	 		SDNGDINYDYVHELSLEMKRQKIQRELMKLEQENMEKREEIIIK
1	İ		KEVSPEVVRSKLSPSPSLRKSSKSPKRKSSPKSSSASKKDRKTS
j	1		
1	1		AVSSPLLDQQRNSKTNQSKKKGPRTPSPPPPIPEDIALGKKYKB
	1		KYKVKDRIEEKTRDGKDRGRDFERQREKRDKPRSTSPAGQHHSP
		1	ISSRHHSSSSQSGSSIQRHSPSPRRKRTPSPSYQRTLTPPLRRS
	1		ASPYPSHSLSSPQRKQSPPRHRSPMREKGRHDHERTSQSHDRRH
		1	ERREDTRGKRDREKDSREEREYEQDQSSSRDHRDDREPRDGRDR
			RE
5748	934	473	SEGPQVFYKGLAPTLIAIFPYAGLQFSCYSSLKHLYKWAIPAEG
			KKNENLONLLCGSGAGVISKTLTYPLDLFKKRLQVGGFEHARAA
1	1	1	FGQVRRYKGLMDCAKQVLQKEGALGFFKGLSPSLLKAALSTGFM
		\$	FFSYEFFCNVFHCMNRTASOR
5749	552	1	
3/43	332	1	GFPVDPRVRGSTLSLAERPKGMIRSGSFRDPTDDVHGSVLSLAS
	1		SASSTYSSAEERMQSEQIRKLRRBLESSQEKVATLTSQLSANAN
	i		LVAAFEQSLVNMTSRLRHLAETAEEKDTELLDLRETIDFLKKKN
	i		SEAQAVIQGALNASETTPKELRIKRQNSSDSISSLNSITSHSSI
	1		GSSKDADA
5750	22	866	IFISICLWNAHLCFLLLPKDCIDQVMKLQNLFVDDSGRYLAIQF
	1		HLEWAYVFLYYYEYRKAKDQLDIAKDISQLQIDLTGALGKRTRF
	1		QENYVAQLILDVRREGDVLSNCEFTPAPTPQBHLTKNLELNDDT
1		ļ	ILNDIKLADCEQFQMPDLCAEEIAIILGICTNFQKNNPVHTLTE
			VELLAFTSCLLSQPKFWAIQTSALILRTKLEKGSTRRVERAMRQ
1	1		TQALADQFEDKTTSVLERLKIFYCCQVPPHWAIQRQLASLLFEL
			GCTSSALQIFEKLEMWE
5751	3	751	=
3/31	3	/51	SCGSALRAWRCGAAALATFPAPALPGLMYRALYAFRSAEPNALA
Į			FAAGETFLVLERSSAHWWLAARARSGETGYVPPAYLRRLQGLEQ
			DVLQAIDRAIEAVHNTAMRDGGKYSLEQRGVLQKLIHHRKETLS
			RRGPSASSVAVMTSSTSDHHLDAAAARQPNGVCRAGFERQHSLP
			SSEHLGADGGLFQIPLPSSQIPPQPRRAAPTTPPPPPVKRRDREA
			LMASGSGGHNTMPSGGNSVSSGSSVSSCI
5752	3	471	GPVCGVGLSVAWAGPWRGPVHSVGGGGRAALHGAELPCLSGAAT
1	1		VEREMELRHKNEMLRVETBARARAKAERENADIIREQIRLKASE
			HRQTVLESIRTAGTLFGEGFRAFVTDRDKVTATVNIFIKQGWQV
	, ,		AERQHVGASWSPRSCPCRLCTAL
5753	34	483	
3,33	3-9	#63	DDSXAIPGGVQAPFGAVRNIYTPRTGHRIRKLDQIQSGGNYVAG
			GQEAFKKLNYLDIGEIKKRPMEVVNTEVKPVIHSRINVSARFRK
1	1		PLQEPCTIFLIANGDLINPASRLLIPRKTLNQWDHVLQMVTEKI
		<u> </u>	TLRSGAVHRLYTLEGRLV
5754	14	331	TLVHVVEFAGEHAEAIASREQEVLQGWKELLSACEDARLHVSST
l	1		ADALRFHSQVRDLLSWMDGIASQIGAADKPRCPSSLLGLPASPW
<u></u>	<u> </u>		WPTPATPSPLTAPFSME
5755	3	888	LGDQFYKEAIEHCRSYNSRLCAERSVRLPFLDSQTGVAQNNCYI
1			WMEKRHRGPGLAPGQLYTYPARCWRKKRRLHPPEDPKLRLLEIK
			PEVELPLKKDGFTSESTTLEALLRGEGVEKKVDAREEESIQEIQ
1			RVLENDENVEEGNEEEDLEEDIPKRKNRTRGRARGSAGGRRRHD
l			
1	J l		AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDBAQ
1	}		DQETRSPPNHRNENHRPQKGPDGTVIPNNYCDFCLGGSNMNKKS
	<u> </u>		GRPEELVSCADCGRSAHLGGBGRKEKEAAA
5756	3	621	SSKLQALFAHPLYNVPEEPPLLGAEDSLLASQEALRYYRRKVAR
!			WNRRHKMYREQMNLTSLDPPLQLRLEASWVQFHLGINRHGLYSR
1			SSPVVSKLLQDMRHFPTISADYSQDEKALLGACDCTQIVKPSGV
1	į l		HLKLVLRFSDFGKAMFKPMRQQRDEETPVDFFYFIDFQRHNAEI
1	1		AAFHLDRILDFRRVPPTVGRIVNVTKEIL
5757	3	473	YKDALLLPDNHRQVVFENGTLKLTDVQKGMDEGEYLCSVLIQPQ
1	1		
1			LSISQSVHVAVKVPPLIQPFEFPPASIGQLLYIPCVVSSGDMPI
			RITWRKDGQVIISGSGVTIESKEFMSSLQISSVSLKHNGNYTCI
	<u> </u>		ASNAAATVSRERQLIVRVPPRFVV
5758	1	474	FRRGAGAERGEHREGERGAAGMGEFKVHRVRFFNYVPSGIRCVA
			YNNQSNRLAVSRTDGTVEIYNLSANYFQEKFFPGHESRATEALC
L			WAEGQRLFSAGLNGBIMEYDLQALNIKYAMDAFGGPIWSMAASP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of.	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ			
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\-possible nucleotide insertion)
			SGSQLLVGCEDGSVKLFQITPDKIPV
5759	2	1240	GNAAFAGQGVVYETFHMSDLPSYTTNGTVHVVVNNQIGFTTDPR
		ĺ	MARSSPYPTDVARVVNAPIFHVNADDPBAVIYVCSVAAEWRNTF
			NKDVGADLVCYRRRGHNEMDBPMFTQPLMYKQIHRQVPVLKKYA
1		ļ	DKLIAEGTVTLQEPEEEIAKYDRICEEAYGRSKDKKILHIKHWL
	ł		DSPWPGPFNVDGEPKSMTCPATGIPEDMLTHIGSVASSVPLEDF
ł			KIHTGLSRILRGRADMTKNRTVDWALAEYMAFGSLLKEGIHVRL
			NGODVERGTFSHRHHVLHDQEVDRRTCVPMNHLWPDQAPYTVCN
ł			SSLSEYGVLGFELGYAMASPNALVLWEAOFGDFHNTAOCIIDOF
ļ	1	ì	ISTGOAKWVRHNGIVLLLPHGMEGMGPEHSSARPERFLOMSNDD
	1]	SDAYPAFTKDFEVSQL
	<u> </u>		
5760	1	1221	VRDITSDSLSLSWTVPEGQFDHFLVQFKNGDGQPKAVRVPGHED
		1	GVTISGLEPDHKYKMNLYGFHGGQRVGPVSAVGLTAPGKDEEMA
]	1	PASTEPPTPEPPIKPRLEELTVTDATPDSLSLSWTVPEGQFDHF
		1	LVQYKNGDGQPKATRVPGHEDRVTISGLEPDNKYKMNLYGFHGG
1			QRVGPVSAIGVTAAEEETPTPTEPSMEAPEPPEEPLLGELTVTG
			SSPDSLSLSWTVPQGRFDSFTVQYKDRDGRPQVVRVGGEESEVT
1			VGGLEPGRKYKMHLYGLHEGRRVGPVSTVGVTAPQEDVDETPSP
ļ.			TEPGTEAPEPPEEPLLGELTVTGSSPDSLSLSWTVPQGRFDSFT
			VQYKDRDGRPQAVRVGGQESKVTVRGLEPGRKYKMHLYGLHEGR
1			RLGPVSAIGVT
5761	3	1275	SCDMAEAAALVWIRGPGFGCKAVRCASGRCTVRDFIHRHCQDQN
3.52]	1	VPVENFFVKCNGALINTSDTVQHGAVYSLEPRLCGGKGGFGSML
l .			RALGAQIEKTTNREACRDLSGRRLRDVNHEKAMAEWVKQQAERE
Ì			AEKEOKRLERLORKLVEPKHCFTSPDYQQQCHEMAERLEDSVLK
k			GMQAASSKMVSAEISENRKRQWPTKSQTDRGASAGKRRCFWLGM
1	1		EGLETAEGSNSESSDDDSEEAPSTSGMGFHAPKIGSNGVEMAAK
1	ľ		FPSGSQRARVVNTDHGSPEQLQIPVTDSGRHILEDSCAELGESK
1			EHMESRMVTETEETQEKKAESKEPIBEEPTGAGLNKDKETEERT
		1	DGERVAEVAPEERENVAVAKLQESQPGNAVIDKETIDLLAFTSV
			AELELLGLEKLKCELMALGLKCGGTLQ
5762	2	344	GSTGQTPLHSQGGGGGGGGRRRTPRGMPKEKYBPPDPRRMYTI
			MSSEBAANGKKSHWAELEISGKVRSLSASLWSLTHLTALHLSDN
1			SLSRIPSDIAKLHNLVYLDLSSNKIR
5763	3	429	LDKDTGLIMLIARLDYELIQRFTLTIIARDGGGEETTGRVRINV
			LDVNDNVPTFQKDAYVGALRENEPSVTQLVRLRATDEDSPPNNQ
			ITYSIVSASAFGSYFDISLYEGYGVISVSRPLDYEQISNGLIYL
	l		TVMAMDAGN
5764	19	441	VCARACGEMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK
7,04	1	***	LRSOLYOGDFVHAMEGKDFNYEYVOREALRVPLIFREKDGLGIK
	1		MPDPDFTVRDVKLLVGSRRLVDVMDVNTOKGTEMSMSOFVRYYE
	1		TPEAORDKL
F1 F1 F F	 	935	
5765	3	825	QKILRLNNSHQPPTSSSNSKDCGGPASSGAGATAALADGLKFAS
[VQASAPQGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS
			STGKRQEVQGRPGEATGMNSALGQSVSSGGSGNPNSNSTSTSTS
1			AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ
			GHQNGSGSQAPSGGHLYGFGAKSNGGGASPFHCGGTGSGSVAAA
			GEVSKSAPDSGLMGNSMLVKKEEEEEESHRRIKKLKTEKVDPLF
1			TVPAPPPHV
5766	1608	663	SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLILALVL
			AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE
1	1		PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD
	1		IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND
}			TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL
			RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG
1			SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV
1			1 1 1 1
	 	 	FGMYGR
5767	2	892	NFRATPRPPTRPELRTGTEVILWYLDWRALMKRKRMKANIKLVG
1	1		SGFPLPSSDLDDSLTEEIDEKIGFRNDANFDWQNVADFRDAGGS
L .		1	LTEVKVEEEERDPQSPEFEIEEEEEMLSSVIPDSRRENELPDFP

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Clubards Asid E Described and Color Es
NO:	location	1	Glutamic Acid, F=Phenylalanine, G=Glycine,
1		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	•	\=possible nucleotide insertion)
	 		HIDEFFTLNSTPSRSAYDEPHLLVNIEKQKLELEKRRLDIEAER
i		[LQVEKERLQIEKERLRHLDMEHERLQLEKERLQIEREKLRLQIV
	1		
	1	1	NSEKPSLBNELGQGEKSMLQPQDIETEKLKLERERLQLEKDRLQ
	<u> </u>		FLKFESEKLQIEKERLQVEKDRLRIQKEGHLQ
5768	3	476	SSRSRLSVSVSPPPPGIVELGPPFAWEFCSRLGSAVTSQRAGPA
			AAMVAKDYPFYLTVKRANCSLELPPASGPAKDAEEPSNKRVKPL
ļ			SRVTSLANLIPPVKATPLKRFSQTLQRSISFRSESRPDILAPRP
j	1	1	WSRNAAPSSTKRRDSKLWSETFDVC
5769	38	667	TKTKKGVKEKATDQSVKAFAEHCPELQYVGFMGCSVTSKGVIHL
			TKLRNLSSLDLRHITELDNETAMEIVKRCKNLISLNLCLNWIIN
			DRCVEVIAKEGQNLKELYLVSCKITDYALIAIGRYSMTIETVDV
1	1		
			GWCKEITDQGATLIAQSSKSLRYLGLMRCDKVNEVTVEQLVQQY
	 		PHITFSTVLQDCKRTLERAYQMGWTPNMSAASS
5770	1	484	DSRRYDVKTRKWSFLLEEHSKLIAKVRCLPQVQLDPLPTTLTLA
1	1		FASQLKKTSLSLTPDVPEADLSEVDPKLVSNLMPFQRAGVNFAI
1	1		AKGGRLLLADDMGLGKTIQAICIAAFYRKEWPLLVVVPSSVRFT
	<u> </u>		WEQAFLRWLPSLSPDCINVVVTGKDRLTA
5771	168	741	GLLPSACLRARSWREASEGPSSRACSNGSQDTFEACYSGTSTPS
			FHGSHCSGSDHSSLGLEQLQDYMVTLRSKLGPLEIOOFAMLLRE
			YRLGLPIQDYCTGLLKLYGDRRKFLLLGMRPFIPDQDIGYFEGF
	1		LEGVGIREGGILTDSFGRIKRSMSSTSASAVRSYDGAAQRPEAQ
1	ľ	ł	AFHRLLADITHDIE
5772	148	202	
3//2	148	383	EFNLALVSPSHPQIKAEDDQPLPGVLLSLSGGLFRSNLLTQDNG
			ILTFSNLVTCSAIYHLPVFPEREPGCSMRDLRVA
5773	2	723	PRVRSKHNFCFMEMNTRLQVEHPVTEMITGTDLVEWQLRIAAGE
			KIPLSQEEITLQGHAFEARIYAEDPSNNFMPVAGPLVHLSTPRA
[DPSTRIETGVRQGDEVSVHYDPMIAKLVVWAADRQAALTKLRYS
}	1	Į	LRQYNIVGLHTNIDFLLNLSGHPEFEAGNVHTDFIPQHHKQLLL
			SRKAAAKESLCQAALGLILKEKAMTDTFTLQAHDQFSPFSSSSG
1			RRLNISYTRNMTLKDGKNSK
5774	· 2	592	FVEEENIRVVRCGGSELNFRRAVFSADSKYIFCVSGDFVKVYST
1 3,	•	352	VTEECVHILHGHRNLVTGIQLNPNNHLQLYSCSLDGTIKLWDYI
ľ			
			DGILIKTFIVGCKLHALFTLAQAEDSVFVIVNKEKPDIFQLVSV
1			KLPKSSSQEVBAKELSFVLDYINQSPKCIAFGNEGVYVAAVREF
			YLSVYFFKKETTSRVTLSSS
5775	3	538	SSGCCDPAAPSSLAEAATMPVSKCPKKSESLWKGWDRKAQRNGL
1			RSQVYAVNGDYYVGEWKDNVKHGKGTQVWKKKGAIYEGDWKFGK
1			RDGYGTLSLPDQQTGKCRRVYSGWWKGDKKSGYGIQFFGPKEYY
			EGDWCGSQRSGWGRMYYSNGDIYEGQWENDKPNGEGMLRLSQNP
			RP
5776	2	484	RLPQDCVCQNLSESLGTLCPSKGLLFVPPDIDRRTVELRLGGNF
-/		•53	IIHISRQDFANMTGLVDLTLSRNTISHIQPFSFLDLESLRSLHL
1			
			DSNRLPSLGEDTLRGLVNLQHLIVNNNQLGGIADEAFEDFLLTL
	<u> </u>		EDLDLSYNNLHGPAVGLRGDAWVQPSTS
5777	2	949	GQDPEPGQDLFQPEREVDPSWGRGREPRLGKLRFQNDHLSVLKQ
1			VKKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG
i			GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV
1			YRGSEGSPTKPFINPLPKPRRTFKHAGEGDKDGKPGIGFRKEKR
1 -			NLPPLPSLPPPPLPSSPPPSSVNRRLWTGROKSSADHRKSYEFE
1	1		DLLQSSSESSRVDWYAQTKLGLTRTLSEENVYEDILDPPMKENP
1			YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTKQSLSKPAFFRQ
1	1		
5778		1912	NSERRNV
3//8	1	1210	QRRQSVSRLLLPVFLLEPPAEPGLEPPPEEEGGEPAGVAEEPGS
1			GGPCWLQLEEVPGPGPLGGGGPLRSPSSYSSDELSPGEPLTSPP
1	ĺ		WAPLGAPERPEHLLNRVLERLAGGATRDSAASDILLDDIVLTHS
1			LFLPTEKFLQELHQYFVRAGGMEGPEGLGRKQACLAMLLHFLDT
1			YQGLLQEEEGAGHIIKDLYLLIMKDESLYQGLREDTLRLHOLVE
	Į l		TVELKIPEENQPPSKQVKPLFRHFRRIDSCLQTRVAFRGSDEIF
			CRVYMPDHSYVTIRSRLSASVQDILGSVTEKLQYSEEPAGREDS
		1	LILVAVSSSGEKVLLQPTEDCVFTALGINSHLFACTRDSYEALV
	L		BADTATOOODER TODGE I EDCAL INDOINGENCIADSYEALV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
I	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion
<u> </u>	sequence		\=possible nucleotide insertion)
ı			PLPEEIQVSPGDTEIHRVEPEDVANHLTAFHWELPRCVHELEFV
			DYVFHGE
5779	138	1671	EAVQVLIKHSADVNARDKNWQTPLHVAAANKAVKCAEVIIPLLS
1			SVNVSDRGGRTALHHAALNGHVEMVNLLLAKGANTNAFDKKDPP
			ALHWAAYMGHLDVVALLINHGAEVTCKDKKGYTPLHAAASNGQI
			NVVKHLLNLGVEIDEINVYGNTALHIACYNGQDAVVNELIDYGA
İ			NVNQPNNNGFTPLHFAAASTHGALCLELLVNNGADVNIQSKDGK
1		•	SPLHMTAVHGRFTRSQTLIQNGGEIDCVDKDGNTPLHVAARYGH
		ı	ELLINTLITSGADTAKCGIHSMFPLHLAALNAHSDCCRKLLSSG
			QKYSIVSLFSNEHVLSAGFEIDTPDKFGRTCLHAAAAGGNVECI
			KLLQSSGADFHKKDKCGRTPLHYAAANCHFHCIETLVTTGANVN ETDDWGRTALHYAAASDMDRNKTILGNAHDNSEELERARELKEK
1			EATLCLEFLLQNDANPSIRDKEGYNSIHYAAAYGHRQCLELLLE
			RTNSGFEESDSGATKSPLHLAVSEMP
5780	154	624	QFFRVITCLPFKGPDYRLYKSEPELTTVAEVDESNGEEKSEPVS
			EIETSVVKGSHFPVGVVPPRAKSPTPESSTIASYVTLRKTKKMM
			DLRTERPRSAVEQLCLAESTRPRMTVEEOMERIRRHOOACLREK
5781			KKGLNVIGASDQSPLQSPSNLRDNP
3/81	19	941	RGSLGGHPWRPPMRAASQGCLPVSFVTGPHQERAYGGRGPGGAF
			PAPPVSGTCPPDLIYAPTPEKAEGGSQKNHQPPPGERAAHRDGE
1			QAPCRAGPTRKVAVAPRPPSCP*GPE\PGEEPRRPLDRSPPLGQ
			VQPHFTSQDAKSAEDEAPSRHLGKHQPRSAQVGSRLDALQGPKT QHS1HTVTCKSPRQKEDRSPKPPQAPKHPERHGRQS\QAPPPLP
			VAPSRTCGGC*TWDPALLVSP/PQGDSTPELPAP\QQPTGGPSR
			CRQALPPQG*RQQPRQRPR/PTGASRSHPAKAKGCQGPPKIRNY
			NIMD
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE
1			PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV
			SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPEPP
			PEPESSITLTPVESAVVABEHEVVPBRPVTCMVSETPAMSAEPT
			VLASEPPVMSETAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL
		1	EPSVVTVPEPPVVAEPDYVTI PVPVVSALEPSVPVLEPAVSVLQ
1 1	i		PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM
1			ILESSIMSSHVMKGINLSSGDQNLAPEIGMOEIALHSGEEPHAE
			EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE
}			IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD
	ľ		ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP
			SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTMEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD
1		Í	LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV
			\SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG
			EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRARKRSSKSKS
1		ŧ	HRS\QTRSRSRS/RDRRRRSSRSRSKSRGRRSVSKEKRKRSPKH
1 1			RSKSRERKRKRSSSRDNRKTVRARSRTPSRRSRSHTPSRRRRSR
1 1		1	SVGRRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRS
1 1			RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS
1 1			RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA
1 1			GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE
1		1	DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN
		1	KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM
ļ			LNRAQERIDAWAQLNSIPGQFTGSTGVQVLTQEQLANTGAQAWI
	ļ		KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV
	1		DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN
	j	}	KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR
5783	1693		Y
5.05	1073	698	DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM
		1	QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGEKSL
<u> </u>		11	NDLIEE/PI*SQ/PKILFQQP/LILKVALNMARGLKYLHQEKKL

Fredicted Predicted Predicted end Indication Indication Corresponding Correspond				
NO: nucleotide corresponding to first amino acid residue of sinst amino acid residue of sinst amino acid residue of sinst amino acid residue of sinst amino acid residue of sinst amino acid sequence seq	SEQ		Predicted end	Amino acid segment containing signal peptide
Cottston Cottston	ID			
corresponding to first anino acid recidue of anino acid recidue of anino acid recidue of anino acid sequence anino acid sequence companies and acid sequence companies anino acid sequence	NO:	nucleotide	location	
to first anino acid anino acid anino acid anino acid anino acid anino acid sequence Section Tuthreonine, V=Valine, W=Typtophan, Y=Tyrosine, X=Unknown, *=Stop Codon, \possible nucleotide deletion, \possible nucleotide inertion		location	corresponding	
amino acid residue of anino acid sequence codon, /=possible nucleotide deletion, /=possible nu		corresponding	to first	
reaidue of anino acid sequence (Codon, A-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide insertion) 1869		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence Codon, /-possible nucleotide deletion, /-possible nucleotide insertion)		amino acid	residue of	
amino acid sequence Codon, /-possible nucleotide deletion, /-possible nucleotide insertion)		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence Sequence		amino acid	sequence	
LHGDIKSSINVIKGDFETIKLCDVGSLILDENNTYTDPEACYT GTEPWRPKRAVERSUUTTEADIPAGLILDENNTIST IPHILIS MDDDDENKTDDSIDPDDENYMALATRPTIMBELDSSYGKVIE LPSVCTMEDPKORPSAANIVEALETIN 5784 2669 1388 FRVEREVERDHNYTSRTYGSBSASBDLWNILDOMENDEVKIH RMLTRITYGIAPLMANTDPSVSRSTVRYDNOTALJVVQNDHVHL GUNYMLGSFTPGATLHIDGRIIFGKSIKJEVLVTQISSFNIPVKV GLSDAPVVVWRIQGIDNVRRRITYSYLRVELQMSKITTISAVEM TPLPTCLOFFRGGDVSSGIPFOXGSKLJQRCSSGFBRIRDOM VDSGCDESSKEMCENTEPVSTYFLEPPOP*BROPPSSGS*LDP E/DAVTSGFFSLSTEDDIKLAHLKONGASTDDSASKKGGTL HAGLIVGILLULIVATATLUTYMYHHPTSAASIFFIERRPSR **PANKFRGSGRPAVAVEVPUGKEGISTIVSEC 5785 2669 1388 FRVERRUSTDNYTSRTYGSBSASRDLWNILDOMENDEVKIH RMLTRATQYIAPLMANTDPSVSRSTVRYEDNOTALJVVQNDHVHL GILSAPVVVWRIQGIPNVRRSTVYFDNOTALJVVQNDHVHL GRANDAPLVVWRIQGIPNVRRSTVYFDNOTALJVVQNDHVHL GRANDAPLVVWRIQGIPNVRRSTVYFDNOTALJVVQNDHVHL GRANDAPLVVWRIQGIPNVRRSTVYFDNOTALJVVQNDHVHL GRANDAPLVVWRIQGIPNVRRSTVYFDNOTALJVVQNDHVHL GRANDAPLVVWRIQGIPNVRRSTVYFDNOTALJVVQNDHVHL GLSDAPVVVRIQGIPNVRRSTVYFDNOTALJVVQNDHVHL GLSDAPVVVRIQGIPNVRRSTVYFDNOTALJVVQNDHVHL GLSDAPVVVRIQGIPNVRRSTVYFDNOTALJVVQNDHVHL GLSDAPVVVRIQGIPNVRRSTVYFDNOTALJVVQNDHVHL GLSDAPVVVRIQGIPNVRRSTVYFDNOTALJVVQNDHVHL GLSDAPVVVRRTQGIPNVRRSTVYFDNOTALJVVQNDHVHL HAGLIVGILLULIVATATLUTVYMYHHPTSAASIFFIERRPSR MPANKFRGSGRPAJAVEVPUGKESCHJCVSGC 5786 2532 1674 SYKLPAABRRASSGSOPPTPTRRRFAPAGRTSKGHFØM*SGTP APRPRARSTVSPASFIPKPRGGGGSSKJLORGSSGFTVSGC SYKLPAABRRASSGSOPPTPTRRRFAPAGRTSKGHFØM*SGTP SHPAKRRSGSGBAAFHEV**ROGGDSFTVSGC GRSMTTCTTRATTDFWARAASSCRPHRY**ROGGNSASKGGT SHPKRGSGRAFTGOALGSGSLSGSRST**P**PRRSPRPASFTPSFPTT**APPTSSPGST SHPKRGSGRAFTGOALGSGSLSGSRST**P**PRRSPRPASFTPSFPTT**APPTSSPGST GRSMTTCTTRATTDFWARAASSGSSOSSASGSSGSGSFRASFRSTVFTRGFTGALGT** SHPKRGSGRAFTGOALGSGSSASGSSSSSSSGSFRAGGATHARVFTCAGAC T\RYCCEIF\GDP\LEESP\TCP\LCKEPPRP\GSFPALTDFUT**APPTSSPGST GRSMTTCTTRATTDFUT**PRAFFRAGGTSTSFAGGTT** SHPKRGSGRAFTGOALGSGSSASGSSSSSSSSSGSGSGSTGTT** SHPKRGSGRAFTGOALGSGSSASGSSSSSSSSSSSSSSSSSSSSSSSSSSSS			504	
GTEPMKYREAVERSOVITIKADI PAPOLILLIEMMTLS I PHINDELDS SYLVIE DDDOENTPOSS PDDEAVYALATED Y PINMEDLESSY GVIE FEVERVEVENDHYNY ISTYGESSASABLUWNIOMENDKVKIH GILSHTIROAARVALSTOP PYCHILLITVATOGFI Y TOEVUH GILSHTIROAARVALSTOP PYCHILLITVATOGFI Y TOEVUH GILSHTIROAARVALSTOP PYCHILLITVATOGFI Y TOEVUH GILSHTYROAARVALSTOP PYCHILLITVATOGFI Y TOEVUH GILSHTYROAARVALSTOP PYCHILLITVATOGFI Y TOEVUH GILSHTYROAARVALSTOP PYCHILLITVATOGFI Y TOEVUH GILSHTYROAARVALSTOP PYCHILLITVATOGFI Y TOEVUH TPLETCLOF PROSPCUSSO I OFNOSKOSKILOROSSAS FRINTEVAN TPLETCLOF PROSPCUSSO I OFNOSKOSKILOROSSAS FRINTEVAN TPLETCLOF PROSPCUSSO I OFNOSKOSKILOROSSAS FRINTEVAN TPLETCLOF PROSPCUSSO I OFNOSKOSKILOROSSA FROSTORI BYCHTA PROSPCUSSO I OFNOSKOSKILOROSSA FROSTORI BYCHTA PROSPCUSSO I OFNOSKOSKILOROSSA FROSTORI BYCHTA POWNILLIAN TALLITVATA POWNIH PYSAAS I PIETERPS MEMAKYRROSSI PANALA ENDEPPYCHILLIA TALTOGFI Y TOEVUH GONINLIS PYCHTA TALLITVAT POWNIH PYSAAS I PIETERPS MEMAKYRROSSI PYOANILLIMORA I FOYKEI PILITVOI STANIPVAN GOLDAF VVUH ROOLD PROSPENS TALVENDOLA NOVANNIH PIPTALOFI PICHOFI POWNIH PIPTALOFI POWNIH PIPTALOFI PICHOFI PROSPCA SA COSTRIBOROS I LEP ADAVISOR PICHOROSSI PICHOROSSI LOROSSI PICHOROSSI LOROSSI PICHOROSSI LOROSSI PICHOROSSI LOROSSI PICHOROSSI LOROSSI PICHOROSSI LOROSSI PICHOROSSI LOROSSI PICHOROSSI PICHOROSSI LOROSSI PICHOROSSI LOROSSI PICHOROSSI LOROSSI PICHOROSSI LOROSSI PICHOROSSI LOROSSI PICHOR		sequence		
NDDDDENTTDSSPPDBEATYAALGTEPPINBELDESYQKVIE				
LPSVCTNEDFUNDRSAMITVEALETUV ST84 2669 1388 ENVERVENTENHYLSFTYGESSASSASMUNVILOMERDKVXIH GILSHTHROAREVALSFDEPPYCHFLEETVATGGFIYTGEVUH MILTATOYIA PHAMATEPSVSMSSTYUYFONTALVVQMCHVHL QDMYRLSSFTYGATLLMDGRIIFGVKBIPVLYTQISSTNHPVKY GLSDAFVVVHRIQQIPWCRRTIYEYIRVELQUSKITYISAVEM TPLPTCLOFFRIGGEVGSSQIOFNCSKSLQRCSSSGFRENRGDM VDSGCFEESKEMCENTEPVETYTLEPPOPT RRQPFSSGS1LPP E/DAVTSGFFTSLTEDOTKIALLKUNGASTDGSASKKGSTL HAGLIVGILIVLIVATAILVTYMYHHPTSASIFFIERPSR 5785 2659 1388 ERVERRUETUNTYTSRYYGESSASSBOLMWAIDOMERDKVKIH HAGLIVGILIVLIVATAILVTYMYHHPTSASIFFIERPSR MPAMKERGSGHPAYARVEPVGKEKGI IVSEQC GILSHTHROARWILSFPEPYCHIBLETTAVAGGFITTGEVVH RMLTATOYIAPLMANPDPSVSRNSTVRYEDMOTALVVQMDHVHL ODMYNLGSFTFGATLLMORRIFGYKSKIKVCSSGSFINEWKY GLSDAFVVVHRIQOIPNVRRTIYSYHRVELQMSKITTISAVEM TPLPTCLOFFRIGGEVSSGIFFICKSKOKLKGCSSGFBRADGM VDSGCFESSKEMCENTEPVETYFLEPPOPTERPROPESSGS1LEP B/DAVTSGFFTSLETDOTKALHLKUNGASTDDSASKKGGTL HAGLIVGILIVLIVATAILVTYMYHHPTSAASIFFIERRSR MPAMKERGSGHPAYAVEVPUGKSKGFINENGC 5786 2532 1674 25786 25786 25787 2669 25787 27460 APREPARSTYSASSFEPLEVRAGGGCSSGKIACGSSGFBRAGGT HAGLIVGILIVLIVATAILUTYMYHHPTSAASIFFIERRSR SPLAGSSGSASSGSSSSSSSTSPESSFRSAGSTERPG-SLAM S-H +KNILSGRSSMSRRFLSCARPHK-*ROGHTVARLFTTMK S-H +KNILSGRSSMSRRFLSCARPHK-*ROGHTVARLFTTMK S-H +KNILSGRSSMSRRFLSCARPHK-*ROGHTVARLFTTMK S-H +KNILSGRSSMSRRFLSCARPHK-*ROGHTVARLFTTMA S-H +KNILSGRSSMSRRFLSCARPHK-*ROGHTVARLFTTMA S-H +KNILSGRSSMSRRFLSCARPHK-*ROGHTVARLFTTMA S-H +KNILSGRSSMSRRFLSCARPHK-*ROGHTVARLFTTMA S-H +KNILSGRSSMSRRFLSCARPHK-*ROGHTVARLFTTMA S-H +KNILSGRSSMSRRFLSCARPHK-*ROGHTVARLFTTMA S-H +KNILSGRSSMSRRFLSCARPHK-*ROGHTVARLFTTMA S-H +KNILSGRSSMSRRFLSCARPHK-*ROGHTVARLFTTMA S-H +KNILSGRSSMSRRFLSCARPHK-*ROGHTVARLFTTMA S-H +KNILSGRSSMSRRFLSCARPHK-*ROGHTVARLFTTMA S-H +KNILSGRSSMSRRFLSCARPHK-*ROGHTVARLFTTMA S-H +KNILSGRSSMSRRFLSCARPHK-*ROGHTVARLFTTMA S-H +KNILSGRSSMSRRFLSCARPHK-*ROGHTVARLFTTMA S-H +KNILSGRSSMSRRFLSCARPHK-*ROGHTVARLFTTMA S-H +KNILSGRSSMSRRFLSCARPHK-*ROGHTVARLFTTMA S-H +KNILSGRSSMSRRFLSCARPHK-*ROGHTVARLFTMA S-H +KNILSGRSSMSRRFLSCARPHK-*ROGHTVARLFTMA S-H +KNILSGRSSMSR		Į.		
1366 PRVEPRVETOHNYYISETYOPSDEASRDLWNILDMEKDKYKY GILSNIHROARWINSTOPPYGETREITUATOGFTYTTEEVIH RMILTATOYIAPIMANEDPEYGETRIETUATOGFTYTTEEVIH RMILTATOYIAPIMANEDPEYGETRIETUATOGFTYTTEEVIH RMILTATOYIAPIMANEDPEYGETRIETUATOGFTYTTEEVIH RMILTATOYIAPIMANEDPEYGETRIETUATOGFTYTTEEVIH TPLIPTTCLOFTRICOPYGETOGTTALUMORITHISTERITUATOGFTYTTEEVIH TPLIPTTCLOFTRICOPYGETOGTTALUMORITHISTERITUATOGFTYTTEEVIH TPLIPTTCLOFTRICOPYGETOGTTALUMORITHISTERITUATOGFTYTTEEVIH TRUBETATOMIAPIMANEDPEYGETRICOPYGETYGFTYTTATOGFTYTTEEVIH TRUBETATOMIAPIMANEDPEYGETRICOPYGETYGFTYTTATOGFTYTTEEVIH RMILTATOYIAPIMANEDPEYGETRICOPYGETRICOPYGETYGFTYTTATOGFTYTTEEVIH RMILTATOYIAPIMANEDPEYGETRICOPYGETRIC				1
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### HAGLIVGILILVIIVATAILVTYWYHIPPSAASIFFIERRSS ### MPAMKERIGSCHPATAEVEDEKEGITIVEGEKEGITIVEGE 5785 2669 1388 PRVERFURTDHNYYISRIYGFSBASRDLWVNIDQMEKDKVKIH GILSNTHRQAARVNISFDFPFYGHILKEITVATGGITYTGGVYR RMLTAQVILAFLAMNEPDSVERRSTVYYFDNATALVVQMDHVHL QDMYNLGSFTFQATLLMOGRITIGYKEITVLTTGISTHTHYKV GLSDAFVVHRIQOIPNVRRTTYYHRVLDGMSKITNISAVEM TPLPTCLOFNRCGFCVSSGIGFNCSWCSKLQRCSSGFDRRRQDM VDSGCPESSKKKCENTEPVETTYFHREVLORGSTIDAAEKKGGTL HAGLIVGILILVILVATAILVTYWHYHPPSATSFFIERRPSR #PAMKFRRGSGHPAYAPVEPVGEKEGFIVSEQC 5786 2532 1674 SYKLPAAERRASSGSOFFTFRERSRAGSTFFRECSSTF* ***PYMAKFRRGSGHPAYAPVEPVGEKEGFIVSEQC ***PYMAKFRRGSGHPAYAPVEPVGEKEGFIVSEQC ***SYKLPAAERRASSGSOFFTFTRERNFAAGRTSRGHRPQM*SGTF APPPARSTVAPSAELPEPPRAGCGSRRFASGSTFFREC*SILN** **S*PLACSTCOAACKSGLISSGRST**PERRSRGSFPASFSTFREC*SILN** **S*PLACSTCOAACKSGLISSGRST**PERRSPCPASFPONTAIP* SLAPSSRF/FRGRPCTWIPSRFPASPTAPPTT**AFTSSFST GRSMTCTPTRATTATPWSARASSFSPNNFT**APTSSFST GRSMTCTPTRATTATPWSARASSFSPNNFT**APTSSFSTST GRSMTCTPTRATTATPWSARASSFSPNNFT**APTSSFSTST GRSMTCTPTRATTATPWSARASSFSPNNFT**APTSSFSTST GRSMTCTPTRATTATPWSARASSFSPNNFT**APTSSFSTSTST** **TYCKSIP**QFDLUBESP**LCP**LCKEPFFP**GSFFRNNQLANV VENIERLGLVSTLGJGEBDVCCPHGEKI**FFCEDDEWGLGVVCR BAGGRATHTHRFLEDAA\PYRAGIHKCLKLIKEREE*QGELGVVCR RENERMQVLLTOVSTKRQQVISEFAHLKELEEQOSILLAGLES* QDGGILRRQRBFPLLVAGGI**CRFSALIFELEEKERRPRAELLTI IRSTLIRCSTKCRKPVAVSPELGQRIRDFPQQALPLQREMMF LEKLCFELDYBPAHTSLDFOTSHFLLLASSGNFSYSKGSTCSSSTLISS TRADALLSSGAVDVCLHVLKSLLEYNKSOARSSFSTGSSSTLISS **STPONGFRATUTTDLGGBCBWGGADINLLAGAPSYKWONS** PDNPQRPDRATCVLAHTVTDLGGBCBWGGADINLLAGAPSYKWONS** PSPONGFFRATCVLAHTVTDLGGBCBWGGADINLLAGAPSYKWONS** PSPONGFFRATCVLAHTVTDLGGBCBWGGADINLAGAPSYKWONS** PSPONGFFRATCVLAHTVTDLGGBCBWGGADINLAGAPSYKWONS** PSPONGFFRATCVLAHTVTDLGGBCBWGADINLAGAPSYKWONS** PSPONGFFRATCVLAHTVTDLGGBCBWGADINLAGAPSYKWONS** PSPONGFFRATCVLAHTVTDLGGBCBWGADILTAGHANGAPTTWRQFCTKADGVLY **STPONGFFRATCVLAHTVTDLGGBCBWGADILTAGHANGAPTTWRQFCTKADGVLY **STPONGFFRANGAPSYFULGARAFTYNGKPCTKNDGVLY** PSPONGFFRANGAPSYFULGARAFTYNGKPCTKNDGVLY** PSPONGFFRANGAPSYFULGARAFTYNGKPCTKNDGVLY** PSPONGFFRAN	ļ	}		VDSGCPBESKEKMCENTEPVET\FLEPPQP*ERQPPSSGS*LPP
### PAMKERROSCHPAYAEVEPVGEKEGFIVSEQC \$785 1388 PRVEREVENTYLSETYTGEDSAEDLWWILDQMEKDKVKIH GLISNTHRQARVMLSPDFPFYGHFLREITVATOGFIYTGEVVH RMITATQYIAELMANFDFSVGRNSTVRYFDNSTALLVVQDHVHL QDMYNLGSFTFQATLLMOGRIFGGFUSSGGSTGFUSGWSCKGSGFPBHRQDW VDSGCFBESKEKMCENTEPVET\PLEPPQP*ERQPFSSGS*LDP E/DAYTSGPFTSLPTEDPFYTALHLENGRGSGSFPBHRQDW VDSGCFBESKEKMCENTEPVET\PLEPPQP*ERQPFSSGS*LDP E/DAYTSGPFTSLPTEDPFTALHLENGRGSFFPBHRQDW VDSGCFBESKEKMCENTEPVET\PLEPPQP*ERQPFSSGS*LDP E/DAYTSGPFTSLPTEDPFTTALHLENGRGSSFFPBHRQDW VDSGCFBESKEKMCENTEPVET\PLEPPQP*ERQPFSSGS*LDF E/DAYTSGPFTSLPTEDPFTTALHLENGRGSSFFFFSSGS*LDF E/DAYTSGPFTSLPTEDPFTTALHPADATGSTFFFFSSGS*LDF E/DAYTSGPFTSLPTEDPFTTREWPAPGGTSGGHRPQOF*SGFF ### PAMENGSSSSMSMSTRSLSCAPHRP*GTSGGHRPQOF*SGFF APRPPARSTVSPASPLPKFRAGGGSGPFSAGSTFFPC*SIN*M S*H*ERNLSQRSSSMSMSTRSLSCAPHRP*RGGLTVARAELPTMA S*PLACSFCOADOKSGSLSGRSTR*PEERMSFTA\SPPEDPT SLAPSSRP*PKRSPDGSSBSMSTR*PEERMSFTA\SPPEDPT SLAPSSRP*PKRSPDGSSBSSMSGFHRPQSTSCHRPQOF*SGFTA- SFH*ENTATATPWSARASSSPRNWPTP*WRPSGRLSTV*RA TGGSTATAPPREFFRWMPMAB ### SASASVIELDBENCPQ*LCCGFFGEK!FFCEDDEMQLCVVCR EAGHATHTMR*PLEDAA\APPREGINKCLKCL.IKEREFIQETOS RENTRMQVLLTOVSTKRQOVISEFALHEEQOGSILLAQLES QDGDILRQRDEFDLLVAGEICRFSALIEELEEKNERPARELLTD IRSTLIRCETRRCKRVAVSPELGQRIRDFFQALEDQBEMCHVCV EAGHATHTMR*PLEDAA\APPREGITSHEKLLEEQOGSILLAQLES QDGDILRQRDEFDLLVAGEICRFSALIEELEEKNERPARELLTD IRSTLIRCETRRCKRVAVSPELGQRIRDFFQALEDQBEMCHV LEKLCFELDYBPAHISLDPGTSHEKLLIEEDQGSILLAQLES QDGSFSLSS DOVGKSGLERLPFESGWAVRILABGFVSALIGEGNTATHVOST DEDVGRKGELREPESGWAVRILABGFVSALIGEGNTATHVOST DEDVGRKGELREPESGWAVRILAGGSSSTYNGAGSTCTGVVS SDOVGKSGLERLPFESGWAVRILAGGFVSALIGEGNTATHVOSTCHONGVT RAFTMOVILUTTDLDCGEDEXDCALDLNLSQLIAELGMKMDV SKNBERSALNEVHLVVMRLLSVFWSRTKSGSSSSTGLIKDFTTTTGHQEGDG SCGGGGGSTEGDVBTSNRLHWYRTKKSGSKSSTGLIKDFTTTTGHQEGDG SCGGGSSFLUGUNTTTDLDSCHEXCKSVRJALAASSGSSSALS SPAPAVASSGQATTGSKSSTKKSKREKEKSDGETFGSSGBDQ LCTALVNOLUTKSLLEYMFGTANGATTNOCHTCMDSVLUT FILQVSFLUKKLESGSTALGSSTKKSKKBEKEKSDGTFTGSGSDDQ LCTALVNOLUTKSLLEYMFGTANGATTNOCHTCMDSVLUT FILQVSFLUKKLESDPCLVCNNETYSTTTOQVVKLI GSHTISKVTVIKIGGLKKTURPTTTNOVVKLI GSHTISKV		1		E/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAAEKKGGTL
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GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS	1			
RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS	1			
	1		1	
				<u></u>

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l wo:	location		
İ		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LCNACGFCKYARFDFMLYAKPCCAVDPIENEEDRKKAVSNINTL
			LDKADRVYHQLMGHRPQLENLLCKVNEAAPEKPODDSGTAGGIS
			STSASVNRYILQLAQEYCGDCKNSFDELSKIIQKVFASRKELLE
			YDLQQREAATKSSRTSVQPTFTASQYRALSVLGCGHTSSTKCYG
}			
1		1	CASAVTEHCITLLRALATNPALRHILVSQGLIRELFDYNLRRGA
	1		AAMREEVRQLMCLLTRDNPEATQQMNDLIIGKVSTALKGHWANP
	l,	1	DLASSLQYEMLLLTDSISKEDSCWELRLRCALSLFLMAVNIKTP
1	ſ		VVVENITLMCLRILQKLIKPPAPTSKKNKDVPVEALTTVKPYCN
	į.		EIHAQAQLWLKRDPKASYDAWKKCLPIRGIDGNGKAPSKSELRH
1	}	,	LYLTEKYVWRWKQFLSRRGKRTSPLDLKLGHNNWLRQVLFTPAT
			QAARQAACTIVEALATIPSRKQQVLDLLTSYLDELSIAGECAAE
	1	1	YLALYQKLITSAHWKVYLAARGVLPYVGNLITKEIARLLALEEA
}	1		TLSTDLQQGYALKSLTGLLSSFVEVESIKRHFKSRLVGTVLNGY
	i		LCLRKLVVQRTKLIDETQDMLLEMLEDMTTGTESETKAFMAVCI
1			ETAKRYNLDDYRTPVFIFERLCSIIYPEKNEVTEFFVTLEKDPO
i	1		QEDFLQGRMPGNPYSSNEPGIGPLMRDIKNKICQDCDLVALLED
J)		DSGMELLVNNKIISLDLPVAEVYKKVWCTTNEGEPMRIVYRMRG
1			LLGDATEEFIESLDSTTDEEEDEEEVYKMAGVMAQCGGLECMLN
		İ	
		1	RLAGIRDFKQGRHLLTVLLKLFSYCVKVKVNRQQLVKLEMNTLN
1			VMLGTLNLALVAEQESKDSGGAAVAEQVLSIMEI\IQAEPNVEP
i			LSEDKGNLLLTGDKDQLVMLLDQINSTFVRSNPSVLQGLLRIIP
			YLSFGEVEKMQILVERFKPYCNFDKYDEDHSGDDKVFL\DCFCK
			IAAGIK\NNSNGHQL\KDL\ILQKGITQNALD\YMKKHIP/SAA
1		ļ	RIWDADI\WKSFCLRPALPFILRLLRGLAIQHPGTQVLIGTDSI
	,		PNLHKLEQVS\SDEGIGTLA\ENL\LESLREHPDVNKKIDA\AR
1	ł		RETRAEKKRMAMAMRQKALGTLG\MTTNEKGQVVD/TRTALLEA
	i		DWEELIEEP\GLTCCICREGYKFQPTKVLGIYTFTKRVVLGGVW
1			ENKPRETSRATSTVSHFNIVHYDC\HLA\AVSLARGREEWESAA
1			LQNANTKCNGLLPVWGPHVPESAFATCLARHNTYLQECTGOREP
1			TYQLNIHDIKLLFLRFAMEQSFSADTGGGGRESNIHLIPYIIHT
			GLYVLNTTRATSREEKNLQGFLEQPKEKWVESAFEVDGPYYFTV
	[-		·-
			LALHILPPEQWRATRVEILRRLLVTSQARAVAPGGATRLTDKAV
İ			KDYSAYRSSLLFWALVDLIYNMFKKVPTSNTEGGWSCSLAEYIR
	-		HNDMPIYEAADKALKTFQEEFMPVETFSEFLDVAGLLSEITDPE
			SFLKDLLNSVP .
5789	1	2407	LPLHAVEKTGRPGQPALKMPGKLRSDAGLESDTAMKKGETLRKQ
			TEEKEKKEKPKSDKTEEIAEEEETVFPKAKQVKKKAEPSEVDMN
			SPKSKKAKK\KEEPSQNDISPKTKSLRKKKEPIEKKVVSSKTKK
1			VTKNEEPSEEEIDAPKPKKMKKEKEMNGETREKSPKLKNGFPHP
			EPDCNPSEAASEESNSEIBQEIPVEQKEG\AFSNFPISEETIKL
1			LKGRGVTFLFPIQAKTFHHVYSGKDLIAQARTGTGKTFSFAIPL
1			IEKLHG\ELQDRKRGRAPQVLVLAPTRELANQVSKDFSDITKKL
1			SVACFYGGTPYGGQFERMRNGIDILVGTPGRIKDHIQNGKLDLT
1			KLNHVVLDEVDQMLDMGFADQVEEILSVAYKKDSEDNPQTLLFS
			ATCPHWVFNVAKKYMKSTYBQVDLIGKKTQKTAITVEHLAIKCH
1			WTQRAAVIGDVIRVYSGHOGRTIIFCETKKEAOELSONSAIKOD
1) · · · · · · · · · · · · · · · · · · ·
			AQSLHGDIPQKQREITLKGFRNGSFGVLVATNVAARGLDIPEVD
			LVIQSSPPKDVESYIHRSGRTGRAGRTGVCICFYQHKEEYQLVQ
1			VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK
1			QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM
1			ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF
			DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ
1			REGSRGFRGQRDGNRRFRGQREGSRGPRGQRSGGGNKSNRSQNK
			GQKRSFSKAFGQ
5790	3786	1585	ARRORDPLQALRRRNOELKOOVDSLLSESQLKEALEPNKROHIY
			QRCIQLKQAIDENKNALQKLSKADESAPVANYNORKEEEHTLLD
			KLTQQLQGLAVTISRENITEVGAPTEEEEESESEDSEDSGGEEE
			DAEEEEEKEENESHKWSTGEEYIAVGDFTAQQVGDLTFKKGEI
			LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEEGQESSEE
			GSEEDVEAVDETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN
L	l		HVSFCYLIVLMRNRMETVEDTNGSETGFRAWNVQSRGRIFLVSK

Deginning				
No: location corresponding to first anino acid residue of residue of anino acid residue of anino acid residue of anino acid sequence corresponding to first anino acid residue of anino acid residue of anino acid sequence corresponding to first anino acid sequence corresponding to first anino acid residue of anino acid sequence corresponding to first anino acid sequence corresponding to the sequ	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
corresponding to first amino acid residue of amino acid amino acid sequence property	(
to first anino acid residue of anino acid sequence sequ	NO:		1	Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid sequence PULQUITVPULTIMORINE, X-UNKNOWN, *=Stop Codon, /-possible nucleotide deletion, V-possible nucleotide insertion) PULQUITVPULTIMORINGENERSISTISLIALINISCHIPLE GMIGUISRIVALLE/DEMORVISIALINITANGENERSISTISLIALINISCHIPLE GMIGUISRIVALLE/DEMORVISIALINITANGENERSISTISLIALINISCHIPLE GMIGUISRIVALLE/DEMORVISIALINITANGENERSISTISLIALINISCHIPLE GMIGUISRIVALLE/DEMORVISIALINITANGENERSISTISLIALINISCHIPLE GMIGUISRIVALLE/DEMORVISIALINITANGENERSISTISLIALINISCHIPLE GMIGUISRIVALLE/DEMORVISIALINITANGENERSERISLIALINISCHIPLE GMIGUISRIVALLE/DEMORVISIALINITANGENERSERISLIALINISCHIPLE GMIGUISRIVALLE/DEMORVISIALINISMINGENERSERISLIALINISCHIPLE GMIGUISRIVALLE/DEMORVISIALINISMINGENERSERISLIALINISCHIPLE GMIGUISRIVALINITANGENERSERISLIANGENERSISLIALINISCHIPLE GMIGUISRIVALINITANGENERSISTISLIALINISCHIPLE GMIGUISRIVALINITANGENERSISTISLIALINISCHIPLE GMIGUISRIVALINITANGENERSISTISLIALINISCHIPLE GMIGUISRIVALINITANGENERSISTISLIALINISCHIPLINITANGEN GMIGUISRIVALINITANGENERSISTISLIALINISCHIPLINITANGEN GMIGUISRIVALINITANGENERSISTISLIALINISCHIPLINITANGEN GMIGUISRIVALINITANGENERSISTISLIALINISCHIPLINITANGEN GMIGUISRIVALINITANGENERSISTISLIALINISCHIPLINITANGEN GMIGUISRIVALINITANGENERSISTISLIALINISCHIPLINITANGEN GMIGUISRIVALINITANGENERSISTISLIALINISCHIPLINITANGEN GMIGUISRIVALINITANGENERSISTISLIALINISCHIPLINITANGEN GMIGUISRIVALINITANGENERSISTISLIALINISTISLIALININITANGEN GMIGUISRIVALINITANGENERSISTISLIALININISTISLIALININI GMIGUISRIVALINITANGENERSISTISLIALINININISTISLIALININI AMANISTISLIALININISTISLIALINININISTISLIALINININISTISLIALINININISTISLIALINININISTISLIALINININISTISLIALINININISTISLIALINININISTISLIALINININISTISLIALINININISTISLIALINININISTISLIALINININISTISLIALINININISTISLIALINININISTISLIALINININISTISLIALINININISTISLIALINININISTISLIALININININISTISLIALINININININISTISLIALININININISTISLIALINININININISTISLIALININININININININISTISLIALINININININISTISLIALININININININININININININININININININ	1			
amino acid residue of amino acid sequence Codon, /=possible nucleotide deletion,			l .	
menio acidi sequence ### Aryptophan, Y-Tyrosine, X-Unknown, *-Stop Codon, /-possible nucleotide deletion, Vepossible nucleotide deletion, Vepossible nucleotide insertion #### PEMPSGLAPERLMERGERSTEISGLICHENOPPANYFLO PELMPSGLAPERLMERGERSTEISGLICHENOPPANYFLO PELMPSGLAPERLMERGERSTEISGLICHENOPPANYFLO PELMPSGLAPERLMERGERSTEISGLICHENOSPENTEIGE BLSCOMPYLLIPERGLAPERSPESTISGLICHENOSPENTEIGE BLSCOMPYLLIPERGLAPERSPESTISGLICHENOSPENTEIGE BLSCOMPYLLIPERGLAPERSPESTISGLICHENOSPENTEIGE BLSCOMPYLLIPERGLAPERSPESTISGLICHENOSPENTEIGE BLSCOMPYLLIPERGLAPERSPESTISGLICHENOSPENTEIGE BLSCOMPYLLIPERGLAPERSPESTISGLISHMANTSPELL LEGEDVMDALRSSNAGGSSTURGERSKAY PERFLUYER GOMESTILLIPERGLAPERGLAPERGERTEITHELL LEGEDVMDALRSSNAGGSSTURGERSKAY GOM/GOLL/HAPPERGLAPERGERTEINFEITHERSHVGTELLORDEN GALQALLSPEGNHEFFERSSETTISGLISHMANTSHVGTESLEPDLV NRIGOGPOFFILLICHENOSPHASETTISHTEINTEPETISHTEINFEITHE BRANCHTEIGESNVGLKLTIVATTGGGOINNESSYGPIVUY BLAGGFORTLICKETTISHTEINTEPETISHTEINFEITHEIN	1			
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Sequence N=possible nucleotide insertion	l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
PVLOOINTYUVITHMAIT PROFEST LIGHTLEEGNOPERNEYELD PELMESGIAPRILAMOTEGTISES PEST SILITURES (CEMPIL) GMSIQULSERUVALCI PRONKYLSINITHYVRATWOP KYPETYTESP OVTRILLPOLLDEDGET, ERNSNAS POLISE LEGATION THE STORKE BLSCGWVELLEDASGYPI PARTYSELFLINGGTYPERG TEUDES I GRAGGSYFVOLTHMRROPOLLVKERLSINGERSNALLSETLI GOMMSIHLLI PYROILGDVILLKORNSLOSTOLLSHEMLATERIL LEOPDWALLSSHANGOSEN TLASSER PAREAUS PERLEVYER GALQALLS PROWINGEN JENSERY PAREAUS PELLUYEN GALQALLS PROWINGEN JENSERY PAREAUS PELLUYEN GALQALLS PROWINGEN JENSERY PAREAUS PELLUYEN GALQALLS PROWINGEN JENSERY PAREAUS PELLUYEN GALQALLS PROWINGEN JENSERY PAREAUS PAREAUS PAREAUS TO KYGKOL ANS SQUADDELINER PREDINGGANGER PLOYAU NESTOGGE CENTLIC VOETS TO KENTLINGS HOW PERSELPODLY NYKLRAOTYPLOES HOUSE CHARLES AND THE AND THE SENSER PENSEL PAREAUS PAR	l	amino acid	sequence	Codon, /=possible nucleotide deletion,
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RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ FGFSEKDADEVKGI FVDTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKSMIGMSTKAVLWRCFSTVVI FLFILLDEQTSLLIVLVP AGVGAAIELWKVKKALKMTI FWRGLMPEFQPGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNI KYKSWYSWLINSFVNGV YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD 5794 1 5016 MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPGMQGPEGPQGPPGQKGDTGEPGLPG TKGTRGPPGASGYPGNPGLPGI PGQDGPPGPPGI PGCNGTKGER GPLGPPGLPGFAGNPGPPGLPGHKGDPGEI LGHVPGMLLKGERG GPLGPPGLPGFAGNPGPPGLPGHKGDPGEILGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGVVGPPGTTGPPGPPGPPGERGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEFGKPGPRGKPGKDGNGEKGSPGFPGEPG YPGLIGRQGP\QBKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGFFGFFGFPGPPGPPGTTNGIVECQPGPP GPGFPGTSLPGPSGRDCLPGPPGSPGPPGTTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPQG	1		1	
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ISFWKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAPGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD 5794 1 5016 MGPRLSVWLLLLPAALLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPGMQGPEGPQGPPGQKGDTGEPGLPG TKGTRGPPGASGYPGNPGLPGIPGQDGPPGPPGPPGPPGP GPLGPPGLPGFAGNPGPPGLPGHPGPPGPPGPPGPPGPPGPFGPPGPPGPPGPPGPPGPPGPP		İ	I	
AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YARGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD 5794 1 5016 MGPPLSVWLDLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGBRGLPGLQGVIGFPGMQGPEGPQGPPGLPGG TKGTRGPPGASGYPGNPGLPGIPGQDGPPGPPGLPGGRGRGR GPLGPPGLPGFAGNPGPPGLPGHPGPGPPGPPGPPGPPGPPGP TKGTRGPPGASGYPGNPGLPGPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPG	1		1	
DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD 5794 1 5016 MGPRLSVWLLLLPAALLLHEEHSRAAKGGCAGSGCGKCDCHGV KGQKGBRGBPGLPGLQGVIGFFBMQGPBGPPGCNGTKGBR TKGTRGPPGASGYPGNPGLPGIPGQDGPPGPPGLPGCNGTKGBR GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGBRG FPGIPGTPGPPGLPGLQGVUGPPGFTGPPGPPGPPGEKGQM GLSFQGPKGDKGDQGVGPPGFTGPDGPPGPPGEKGQM GLSFQGPKGDKGDQGVGPPGPQQQVVDEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGRKPGKDGKGEKGSPGFPGEPG YPGLIGRQGP\QBEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGFPGFFGFPGPPGPPGPPGTTNGIVECQPGPP GPGPGFPGFPGFPGFPGFPGFPGFPGFPGFPGTTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPQG			1	
YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD 5794 1 5016 MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPGMQGPEGPPGQKGDTGEPGLPG TKGTRGPPGASGYPGNPGLPGIPGQDGPPGPPGLPGGNGTKGER GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG GPLGPPGLPGFAGNPGPPGLPGPGPPGPPGPPGPPGEKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGPRGKPGKDGKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPVIGTGPLGEKGERGYPGT PGPRGEPGFPGFFGFPGPPGPPGPPGPPGPPGPFGFERGEKGD RGFPGTSLPGPSGRDCLPGPPGSPGPPGTYNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPQG	1		1	-
IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD 5794 1 5016 MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPGMQGPEGPQGPPGQKGDTGEPGLPG TKGTRGPPGASGYPGNPGLPGIPGQDGPPGPPG1PGCNGTKGER GPLGPPGLPGFAGNPGPPGLPGHQGNGDPGETLGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGPPGEKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEFGKPGPRGKPGKDGKGGKGSPGFPGEPG YPGLIGRQGP\QBKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGFPGFPGLPGPGPPGDPGPPGJPGFFGERGEKGD RGFPGTSLPGPSGRDGLPGPPGSPGPGPTTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGQQG			[
EKATRAPHTD 5794 1 5016 MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGBRGLPGLQGVIGFPGMQGPEGPQGPPGQKGDTGEPGLPG TKGTRGPPGASGYPGNPGLPGIPGDGPPGPPGIPGCNGTKGER GPLGPPGLPGFAGNPGPPGLPGLMGDPGETLGHVPOMLLKGERG FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGPPGEKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGPRGKPGKDGNGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPSGRDCLPGPPGSPGPTNTGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGQG				
1 5016 MGPRLSVWLLLLPAALLLHEEHSRAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPGMQGPEGPQGPPGQKGDTGEPGLPG TKGTRGPPGASGYPGNPGLPGIPGQDGPPGPPGIPGCNGTKGER GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGYGPPGPPGPPGPPGPPGPBGKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGKPGKPGKDGDKGEKGSPGFPGPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTOFLGEKGERGYPGT PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPCERGEKGD RGFPGTSLPGPSGRDGLPGPPGSPGPPGTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGQG	1			
KGQKGBRGLPGLQGVIGFPGMQGPEGPQGPPGQKGDTGEPGLPG TKGTRGPPGASGYPGNPGLPGIPGQDGPPGPGPGLPGCNGTKGER GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGBRG FPGIPGTPGPPGLPGLQGPVGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPG		L		
TKGTRGPPGASGYPGNPGLPGIPGCPGPPGIPGCNGTKGER GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGEKGQM GLSFQGPKGDKGDQVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGKPGKDGKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPSGRDGLPGPPGSPGPPGTTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGQG	5794	1	5016	
GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGEKGQM GLSFQGPKGDKGDQGVGGPGPVGQAQVQBKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGKPGKDGKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPFGFFGPFGPPGDPPGDPAGAPGFPGERGEKGD RGFPGTSLPGPSGRDGLPPPGSPGPGTTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGQG]	KGQKGERGLPGLQGVIGFPGMQGPEGPQGPPGQKGDTGEPGLPG
GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGEKGQM GLSFQGPKGDKGDQGVGGPGPVGQAQVQBKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGKPGKDGKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPFGFFGPFGPPGDPPGDPAGAPGFPGERGEKGD RGFPGTSLPGPSGRDGLPPPGSPGPGTTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGQG	1			TKGTRGPPGASGYPGNPGLPGIPGQDGPPGPPGIPGCNGTKGER
FPGIPGTPGPPGLPGLQGPVGPPGFPGPPGPPGPPGEKGQM GLSFQGPKGDKGDQVGQPGPPGVPGPPGPPGEKGQM GLSFQGPKGDKGDQVGPGPPGPPGPPGPPGEPGPGPGPGPGPGPGPGEPGGPGPGPGPGPGPGPGPGPGEPGGPGPGPGPGPGPGEPGGPGPGPGPGPGPGPGPGPGPGPGFGERGEKGD RGFPGTSLPGPSGRDGLPGPPGSPGPPGTPGTVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGQG	1	İ		
GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPSGRDGLPGPPGSPGPPGYTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGQG			[
EPGFQGMPGVGEKGEPGKPGPRGKPGKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPPGPAGAAAPGFPGERGEKGD RGFPGTSLPGPSGRDGLPGPPGSPGPPGYTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGQG			1	
YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPSGRDGLPGPPGSPGPPGQPGYTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGQG	1			
PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPSGRDGLPGPPGSPGPPGQPGYTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPQG	1			
RGFPGTSLPGPSGRDGLPGPPGSPGPPGQPGYTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPQG				
GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPQG				1
			}	1
PPGEIGFPGOPGAKGDRGLPGRDGVAGVPGPOGTPGLIGOPGAK	1			1
		<u> </u>		PPGEIGFPGQPGAKGDRGLPGRDGVAGVPGPQGTPGLIGQPGAK

SEO	Predicted	Dyadiated and	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
""	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			GEPGEFYFDLRLKGDKGDPGFPGQPGMPGRAGSPGRDGHPGLPG
		}	PKGSPGSVGLKGERGPPGGVGFPGSRGDTGPPGPPGYGPAGPIG
			DKGQAGFPGGPGSPGLPGPKGEPGKIVPLPGPPGAEGLPGSPGF
ı			PGPQGDRGFPGTPGR\PGL\PGEKGAVG\OPGIGFPGPPGPKGV
1		1	DGLPGDMGPPGTPGRPGFNGLPGNPGVOGOKGEPGVGLPGLKGL
			PGLPGIPGTPGEKGSIGVPGVPGEHGAIGPPGLOGIRGEPGPPG
1			LPGSVGSPGVPGIGPPGARGPPGGQGPPGLSGPPGIKGEKGFPG
İ			FPGLDMPGPKGDKGAQGLPGITGQSGLPGLPGQQGAPGIPGFPG
1	Ì		SKGEMGVMGTPGQPGSPGPWGAPGLPGEKGD\HGFPGSSGPRGD
1			PGLKGDKGDVGLPGKPGSMDKVYMGSMKGQKGDQGEKGQIGPIG
İ			EKGSRGDPGTPGVPGKDGQAGQPGQPGPKGDPGISGTPGAPGLP
	1		GPKGSVGGMGLPGTPGEKGVPGIPGPQGSPGLPGDKGAKGEKGQ
1	1		AGPPGIGIPGLRGEKGDQGIAGFPGSPGEKGEKGSIGIPGMPGS
			PGLKGSPGSVGYPGSPGLPGEKGDKGLPGLDGIPGVKGEAGLPG
			TPGPTGPAGQKGEPGSDGIPGSAGEKGEPGLPGRGFPGFPGAKG
			DKGSKGEVGFPGLAGSPGIPGSKGEQGFMGPPGPQGQPGLPGSP
ļ			GHATEGPKGDRGPQGQPGLPGLPGPMGPPGLPGIDGVKGDKGNP
			GWPGAPGVPGPKGDPGFQGMPGIGGSPGITGSKGDMGPPGVPGF
			QGPKGLPGLQGIKGDQGDQGVPGAKGLPGPPGPPGPYDIIKGEP
			GLPGPEGPPGLKGLQGLPGPKGQQGVTGLVGIPGPPGIPGFDGA
			PGQKGEMGPAGPTGPRGFPGPPGPDGLPGSMGPPGTPSVDHGFL
			VTRHSQTIDDPQCPSGTKILYHGYSLLYVQGNERAHGQDLGTAG
			SCLRKFSTMPFLFCNINNVCNFASRNDYSYWLSTPEPMPMSMAP
			ITGENIRPFISRCAVCEAPAMVMAVHSQTIQIPPCPSGWSSLWI
	l		GYSFVMHTSAGAEGSGQALASPGSCLEEFRSAPFIECHGRGTCN
			YYANAYSFWLATIERSEMFKKPTPSTLKAGELRTHVSRCQVCMR
			RT
5795	1192	61	
		01	STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE
			PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL
			VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN
			FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH
1			KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR
5796	2	1078	
''	_	*070	GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF
			FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE
			RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP
			GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE
			LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGPLHL
1			GALGTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ
	1		NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK+R
	1	İ	EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG
5797		0.03	QHRDPG
	•	891	PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE
	Ì		VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR
1 1			KHSAEKEALLEETNSFLKAIERANKKMQAAEISLEEKDQRIGEL
1	ĺ	ţ	DRLIERMEKERHQLQLLEHBTEMSGELTDSDKERYQQLEEAS
1 I	ļ	i	ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLOOKOLLILO
1 1		i	LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP
F700			SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT
5798	644	115	KILGSRWKSMSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR
			TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGOOPOIPITTGTG
			VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIOSTYGMKT
			DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN
5799	2679	1435	LLSTYIKFINLFPETKATIOGVLRAGSOLRNADVELOORAVEYL
		ļ	TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL
			DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP
1		,	PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP
]		1	EADBLLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN
]]		J	KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL
j [ſ	NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM
		i	AAQDFFQRWKQLSLPQQEAQKIFKANHPMDAEVTKAKLLGFGSA
			~ · · · · · · · · · · · · · · · · · · ·

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	1		
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
,	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
{			
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
		bequeene	
	sequence		\=possible nucleotide insertion)
	1		LLDNVDPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTL
1			RTSKEPVSRHLCELLAQQF
5800	2679	1435	LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELOORAVEYL
3000	2075	1 1435	
Ì		l	TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL
	!		DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP
		i	PASAGAGNLLVDVFDGPAAQPSLGPTPREAFLSPGPEDIGPPIP
		1	EADELLNKFVCKNNGVLFENQLLQIGVKSEFRONLGRMYLFYGN
ł	ł	1	
		1	KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL
		{	NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM
			AAQDFFQRWKQLSLPQQEAQKIFKANHPMDAEVTKAKLLGFGSA
1.			
ľ			LLDNVDPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTL
			RTSKEPVSRHLCELLAQQF
5801	3	1413	FPRLYHLIPDGEITSIKINRVDPSESLSIRLVGGSETPLVHIII
			QHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLROP
I			_ · · ·
1	1		CQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEE
1	1		QLGIKLVRKVDEPGVFIFNVLDGGVAYRHGQLEENDRVLAINGH
İ			DLRYGSPESAAHLIQASERRVHLVVSRQVRQRSPDIFQEAGWNS
			NGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVA
l		i	GGASHREWDLPIYVISVEPGGVISRDGRIKTGDILLNVDGVELT
1	1	1	
1	1	4	EVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNH
1		(NMAPPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVG
i	į.	ł	GYEEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSG
		1	MIHACLARLLKELKGRITLTIVSWPGTFL
5802	3	290	CFSLYQIMERIMDLPTLLRHAFREMFSVGGLFWMFRIRIILCLM
1	1	1	GAFFYLISPLDFVPEALFGILGFLDDFFVIFLLLIYISIMYREV
ł			ITQRLTR
5803	2234	1299	EAQFGTTAEIYAYREEQDFGIEIVKVKAIGRORFKVLELRTOSD
3003	2234	***	
			GIQQAKVQILPECVLPSTMSAVQLESLNKCQIFPSKPVSREDQC
)	ł	SYKWWQKYQKRKFHCANLTSWPRWLYSLYDAETLMDRIKKQLRE
		!	WDENLKDDSLPSNPIDFSYRVAACLPIDDVLRIOLLKIGSAIOR
			LRCELDIMNKCTSLCCKQCQETEITTKNEIFSLSLCGPMAAYVN
1			
			PHGYVHETLTVYKACNLNLIGRPSTEHSWFPGYAWTVAQCKICA
1			SHIGWKFTATKKDMSPQKFWGLTRSALLPTIPDTEDEISPDKVI
			LCL .
5804	2	1707	EMEKOROEEORKRTEEERKRRIEODMLEKRKIORELAKRAEOIE
1		1	1
1			DINNTGTESASEEGDDSLLITVVPVKSYKTSGKMKKNFEDLEKE
1			RBEKERIKYEEDKRIRYEEQRPSLKEAKCLSLVMDDEIBSEAKK
1			ESLSPGKLKLTFEELERQRQENRKKQAEEEARKRLEEEKRAFEE
1			ARROMVNEDEENQDTAKIFKGYRPGKLKLSFEEMERQRREDEKR
į			KAEEEARRRIEEEKKAFAEARRNMVVDDDSPEMYKTISOEFLTP
1			
1	1		GKLEINFEELLKQKMEEEKRRTEEERKHKLEMEKQEFEQLRQEM
1	1	1	GEEEEENETFGLSREYEELIKLKRSGSIQAKNLKSKFEKIGQLS
1	1		EKEIQKKIEEERARRRAIDLEIKEREAENFHEEDDVDVRPARKS
1			EAPFTHKVNMKARFEQMAKAREEEEQRRIBEOKLLRMOFEOREI
1			
1			DAALQKKREEEEEEGSIMNGSTAEDEEQTRSGAPWFKKPLKNT
1		l	SVVDSEPVRFTVKVTGEPKPEITWWFEGEILQDGEDYQYIERGE
i			TYCLYLPETFPEDGGEYMCKAVNNKGSAASTCILTIESKN
5805	3	776	YISDTLGQVYKSKIRWWIEENGGNGNISVDDLIALLDLAEHASS
1 2003	1	l ''°	
1			AFKESQQQSEDREYEVKERLYPKSKRRYDTYNIAGYQGEIEVGL
1			YTIQILQLIPFFDNKNELSKRYMVNFVSGSSDIPGDPNNEYKLA
1	•	1	LKNYIPYLTKLKFSLKKSFDFFDEYFVLLKPRNNIKONEEAKTR
1			RKVAGYFKKYVDIFCLLEESQNNTGLGSKFSBPLQVERCRRNLV
l	ł	1	
			ALKADKFSGLLEYLIKSQEDAISTMKCIVNEYTFLLK
5806	1257	877	AVFTFHNHGRTANLYSLHSWLGITTVFLFACQRFLGFAVFLLPW
1			ASMWLRSLLKPIHVFFGAAILSLSIASVISGINEKLFFSLKNTT
			i l
L	 		RPYHSLPSEAVFANSTGMLVVAFGLLVLYILLASSWKRP
5807	2267	1302	RFSKKTFRRPMAVDIQPACLGLYCGKTLLFKNGSTEIYGECGVC
	1		PRGORTNAOKYCOPCTESPELYDWLYLGFMAMLPLVLHWFFIEW
1			YSGKKSSSALFQHITALFECSMAAIITLLVSDPVGVLYIRSCRV
1			1
L	<u></u>		LMLSDWYTMLYNPSPDYVTTVHCTHEAVYPLYTIVFIYYAFCLV

SEQ Predicted beginning nucleotide nucleotide location nucleotide location corresponding to first amino acid segment containing signal pept to first amino acid residue of amino acid sequence s	E=
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence sequ	
location corresponding to first amino acid residue of amino acid sequence Sequence Coden	•
corresponding to first amino acid residue of samino acid residue of amino acid sequence Sequence Sequence Sequence Sequence Separate Separate Separate Sequence Sequence Sequence Sequence Separate Sequence Seque	
to first amino acid residue of sequence Sequence Codon, /=possible nucleotide deletion, sequence EpyrAppyIILVLSLVTLAVYMSASEIENCYDLLVRKKAL FSHWLLHAYGIISISRVDKLEQDLPLLALVPTPALFYLFTA EPSRILSEGANGH 5808 2 433 SLPDSGVVEYLSNGVADNHKDFGELRYNECLMNFSCNGKN EGRITHGFQLKSAYENNLMPYTNYTFDFKGVIDYIFYSKTH LGVLGPLDPQWLVENNITGCPHPHIPSDHFSLLTQLELHPP LVNGVHLPNRR 5809 464 2422 ILVPGFQGILHPGVYCALQSQHQAQELVADIDECEVSGLCR	
amino acid residue of residue of residue of amino acid sequence S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=St Codon, /=possible nucleotide deletion, \text{ =possible nucleotide insertion} LMLLRPLLVKK1ACGLGKSDRFKS1YAALYFFP1LTVLQA GLLYYAFPY11LVLSLVTLAVYMSASB1ENCYDLLVRKKRL FSHWLLHAYG11S1SRVDKLEQDLPLLALVPTPALFYLFTA EPSR1LSEGANGH 5808 2 433 SLPDSGVVEYLSNGGVADNHKDFGELRYNECLMNFSCNGKN EGRITHGFQLKSAYENNLMPYTTYTFDFKGV1DY1FYSKTH LGVLGPLDPQWLVENN1TGCPHPH1PSDHFSLLTQLELHPP LVNGVHLPNRR 5809 464 2422 ILVPGFQG1LHPGVYCALQSQHQAQELVADIDECEVSGLCR	
residue of amino acid sequence Codon, /=possible nucleotide deletion, /=possible nucleotide insertion) LMMLLRPLLVKKIACGLGKSDRFKSIYAALYFFPILTVLQA GLYYAFPYIILVLSLVTLAVYMSASBIENCYDLLVRKKRL FSHWLLHAYGIISISRVDKLEQDLPLLALVPTPALFYLFTA EPSRILSEGANGH S808 2 433 SLPDSGVVEYLSNGGVADNHKDFGELRYNECLMNFSCNGKN EGRITHGFQLKSAYENNLMPYTNYTFDFKGVIDYIFYSKTH LGVLGPLDPQWLVENNITGCPHPHIPSDHFSLLTQLELHPP LVNGVHLPNRR 5809 464 2422 ILVPGFQGILHPGVYCALQSQHQAQELVADIDECEVSGLCR	
amino acid sequence Codon, /=possible nucleotide deletion, =possible nucleotide insertion	
amino acid sequence Codon, /=possible nucleotide deletion, -possible nucleotide insertion	go
sequence \=possible nucleotide insertion) LMMLLRPLLVKKIACGLGKSDRFKSIYAALYFFPILTVLQA GLLYYAFPYIILVLSLVTLAVYMSASBIENCYDLLVRKKRL FSHWLLHAYGIISISRVDKLEQDLPLLALVPTPALFYLFTA EPSRILSEGANGH 5808 2 433 SLPDSGVVEYLSNGGVADNHKDFGELRYNECLMNFSCNGKN EGRITHGFQLKSAYENNLMPYTNYTFDPKGVIDYIFYSKTH LGVLGFLDPQWLVENNITGCPHPHIPSDHFSLLTQLELHPP LVNGVHLPNRR 5809 464 2422 ILVPGFQGILHPGVYCALQSQHQAQELVADIDECEVSGLCR	•
LMMLLRPLLVKKIACGLGKSDRFKSIYAALYFFPILTVLQA GLLYYAFPYIILVLSLVTLAVYMSASBIENCYDLLVRKKRL FSHWLHAYGIISISRVDKLEQDLPLLALVPTPALFYLFTA EPSRILSEGANGH 5808 2 433 SLPDSGVVEYLSNGGVADNHKDFGELRYNECLMNFSCNGKN EGRITHGFQLKSAYENNLMPYTNYTFDPKGVIDYIFYSKTH LGVLGPLDPQWLVENNITGCPHPHIPSDHFSLLTQLELHPP LVNGVHLPNRR 5809 464 2422 ILVPGFQGILHPGVYCALQSQHQAQELVADIDECEVSGLCR	
GLLYYAFPYIILVLSLVTLAVYMSASBIENCYDLLVRKKRL FSHWLLHAYGIISISRVDKLEQDLPLLALVPTPALFYLFTA EPSRILSEGANGH 5808 2 433 SLPDSGVVEYLSNGGVADNHKDFGELRYNECLMNFSCNGKN EGRITHGFQLKSAYENNLMPYTNYTFDPKGVIDYIFYSKTH LGVLGPLDPQWLVENNITGCPHPHIPSDHFSLLTQLELHPP LVNGVHLPNRR 5809 464 2422 ILVPGFQGILHPGVYCALQSQHQAQELVADIDECEVSGLCR	VCC
FSHWLLHAYGIISISRVDKLEQDLPLLALVPTPALFYLFTA EPSRILSEGANGH 5808 2 433 SLPDSGVVEYLSNGGVADNHKDFGELRYNECLMNFSCNGKN EGRITHGFQLKSAYENNLMPYTNYTFDPKGVIDYIFYSKTH LGVLGPLDPQWLVENNITGCPHPHIPSDHFSLLTQLELHPP LVNGVHLPNRR 5809 464 2422 ILVPGFQGILHPGVYCALQSQHQAQELVADIDECEVSGLCR	
EPSRILSEGANGH 5808 2 433 SLPDSGVVEYLSNGGVADNHKDFGELRYNECLMNFSCNGKN EGRITHGFQLKSAYENNLMPYTNYTFDPKGVIDYIFYSKTH LGVLGPLDPQWLVENNITGCPHPHIPSDHFSLLTQLELHPP LVNGVHLPNRR 5809 464 2422 ILVPGFQGILHPGVYCALQSQHQAQELVADIDECEVSGLCR	
5808 2 433 SLPDSGVVEYLSNGGVADNHKDFGELRYNECLMNFSCNGKN EGRITHGFQLKSAYENNLMPYTNYTFDFKGVIDYIFYSKTH LGVLGPLDPQWLVENNITGCPHPHIPSDHFSLLTQLELHPP LVNGVHLPNRR 5809 464 2422 ILVPGFQGILHPGVYCALQSQHQAQELVADIDECEVSGLCR	K.F.T.
EGRITHGFQLKSAYENNLMPYTNYTFDFKGVIDYIFYSKTH LGVLGPLDPQWLVENNITGCPHPHIPSDHFSLLTQLELHPP LVNGVHLPNRR 5809 464 2422 ILVPGFQGILHPGVYCALQSQHQAQELVADIDECEVSGLCR	
IGVLGPLDPQWLVENNITGCPHPHIPSDHFSLLTQLELHPP LVNGVHLPNRR 5809 464 2422 ILVPGFQGILHPGVYCALQSQHQAQELVADIDECEVSGLCR	GSS
LVNGVHLPNRR 5809 464 2422 ILVPGFQGILHPGVYCALQSQHQAQELVADIDECEVSGLCR	MNV
5809 464 2422 ILVPGFQGILHPGVYCALQSQHQAQELVADIDECEVSGLCR	LLP
	HGG
EVPDGYIIGNYTSSLGSQVRYACREGFFSVPEDTVSSCTGL	
ESPKLHCQEINCGNPPEMRHAILVGNHSSRLGGVARYVCOE	
SPGGKITSVCTEKGTWRESTLTCTEILTKINDVSLFNDTCV	
INSRRINPKISYVISIKGQRLDPMESVREETVNLTTDSRTP	_
LALYPGTNYTVNISTAPPRRSMPAVIGFQTAEVDLLEDDGS	
SIFNETCLKLNRRSRKVGSEHMYQFTVLGQRWYLANFSHAT	
FTTREQVPVVCLDLYPTTDYTVNVTLLRSPKRHSVQITIAT	
VKQTISNISGFNETCLRWRSIKTADMEEMYLFHIWGQRWYQ	
AQEMTFNISSSSRDPEVCLDLRPGTNYNVSLRALSSELPVV	
TTQITEPPLPEVEFFTVHRGPLPRLRLRKAKEKNGPISSYQ	
LPLALQSTFSCDSEGASSFFSNASDADGYVAAELLAKDVPD	DAM
EIPIGDRLYYGEYYNAPLKRGSDYCIILRITSEWNKVRRHS	CAV
WAQVKDSSLMLLQMAGVGLGSLAVVIILTFLSFSAV	
5810 3 1641 KVFGTHKDHEVSTLDTAISAVKVQLAEFLENLQEKSLRIEA	FVS
BIESFFNTIEENCSKNEKRLEEONEEMMKKVLAOYDEKAOS	FER
VKKKKMEFLHEOMVHFLOSMDTAKDTLETIVREAEELDEAV	FLT
SFEEINERLLSAMESTASLEKMPAAFSLFEHYDDSSARSDO	
QVAVPQPPRLEPQEPNSATSTTIAVYWSMNKEDVIDSPQVY	
BPODDOEVNELVEEYRLTVKESYCIFEDLBPDRCYQVWVMA	
TGCSLPSERAIFRTAPSTPVIRAEDCTVCWNTATIRWRPTT	
TETYTLEYCRQHSPEGEGLRSFSGIKGLQLKVNLQPNDNYF	
RAINAFGTSEQSEAALISTRGTRFLLLRETAHPALHISSSG	
SFGERRRLTEIPSVLGEELPSCGQHYWETTVTDCPAYRLGI	
SAVQAGALGQGETSWYMHCSEPQRYTFFYSGIVSDVHVTER	
VGILLDYNNQRLIFINAESEQLLFIIRHRFNEGVHPAFALE	KPG
KCTLHLGIBPPDSVRHK	
5811 1918 851 AAALADPLPEDKWSAEKRRPLKSSLGYEITFSLLNPDPKSH	
WDIEGAVRRYVQPFLNALGAAGNFSVDSQILYYAMLGVNPR	FDS
ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVP	ELA
HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASV	ĻPV
RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEG	
WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDV	
VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDP	
HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWR	
KTD	
5812 5204 2744 GGRORCORGRSCGAREBEVEPGTARPPPAASAMDASLEKIA	nnm nnm
5812 5204 2744 GGRQRCQRGRSCGAREREVEPGTARPPPAASAMDASLEKTA LAEMGKNLKEAVKMLEDSORRTEEENGKKLISGDIPGPLOG	
	_
DMVSILQLVQNLMHGDEDEEPQSPRIQNIGEQGHMALLGHS	
YISTLDKEKLRKLTTRILSDTTLWLCRIFRYENGCAYFHBE	
GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARPG	_
YLCNQLGLPFPCLCRVPCNTVFGSQHQMDVAFLEKLIKDDI	
RLPLLLVANAGTAAVGHTDKIGRLKELCEQYGIWLHVEGVN	LAT
LALGYVSSSVLAAAKCDSMTMTPGPWLGLPAVPAVTLYKHD	DPA
LTLVAGLTSNKPTDKLRALPLWLSLQYLGLDGFVERIKHAC	QLS
QRLQESLKKVNYIKILVEDELSSPVVVFRFFQELPGSDPVF	_
PVPNMTPSGVGRERHSCDALNRWLGEOLKOLVPASGLTVMD	
EGTCLRFSPLMTAAVLGTRGEDVDQLVACIESKLPVLCCTL	
EGTCLRFSPLMTAAVLGTRGEDVDQLVACIESKLPVLCCTL EEFKQEVEATAGLLYVDDPNWSGIGVVRYEHANDDKSSLKS	
EGTCLRFSPLMTAAVLGTRGEDVDQLVACIESKLPVLCCTL EEFKQEVEATAGLLYVDDPNWSGIGVVRYEHANDDKSSLKS GENIHAGLLKKLNELESDLTFKIGPEYKSMKSCLYVGMASDI	ፖ አሮ
EGTCLRFSPLMTAAVLGTRGEDVDQLVACIESKLPVLCCTL EEFKQEVEATAGLLYVDDPNWSGIGVVRYEHANDDKSSLKS	

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	i .	Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1		residue of	S=Serine, T=Threonine, V=Valine,
ľ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-Ston
	amino acid	sequence	Codon, /=possible nucleotide deletion.
	Bequence		\=possible nucleotide insertion)
			TEPIYVYKAQGAGVTLPPTPSGSRTKORLPGOKPFKFSLPGCDA
ĺ			LSETSSVSHIEDLEKVERLSSGPEQITLEASSTEGHPGAPSPQH
		ĺ	TDQTEAFQKGVPHPEDDHSQVEGPESLR
5813	2936	699	HRDGVSGSLERPLTDRSRTGAFAQQRGKMATAGGGSGADPGSRG
1			LLRLLSPCVLLAGLCRGNSVERKIYIPLNKTAPCVRLLNATHQI
1			GCQSSISGDTGVIHVVEKEEDLQWVLTDGPNPPYMVLLESKHFT
			RDLMEKLKGRTSRIAGLAVSLTKPSPASGFSPSVQCPNDGFGVY
1			SNSYGPEFAHCREIQWNSLGNGLAYEDFSFPIFLLEDENETKVI
Í	1		KOCYODUNI SONCEADTEDI CAMOL ESIMANI
			KQCYQDHNLSQNGSAPTFPLCAMQLFSHMAWLSFSTAT\CMRRS
			SIQSTFSINPKIVCDPLSDYNVWSMLKPINTTGTLKPDDRVVVA
1			ATRLDSRSFFWNV\APGAESAVASFVTQLAAAEALQKAPDVTTL
	{		PRNVMFVFFQGETFDYIGSSRMVYDMEKGKFPVQLENVDSFVEL
1 :			GQVALRTSLELWMHTDPVSQKNESVRNQVEDLLATLEKSGAGVP
			AVILRRPNQSQPLPPSSLQRFLRARNISGVVLADHSGAFHNKYY
			QSIYDTAENINVSYPEWLEPLKE/ETWNFG*QDTAKALADVATV
			LGRALYELAGGTNFSDTVQADPQTVTRLLYG\FLIKANNSWFQS
			ILQGRDLRSYLG*RGLFQH\YIAV\SSPTNTIYV/VLQYALANL
			TGTVVNLTREQCQDPSKVPSENKDLYEYSWVOGPLHSNETDBLD
			RCVRSTARLARALSPAFELSOWSSTEYSTWTESRWKDIDADIDI
J			IASKELELITLTVGFGILIFSLIVTYCINAKADVLFIAPREPGA
5814			VSY
2014	8500	432	ALKCRPRRVLAILVGPVQPDRMAEEGAVAVCVRVRPLNSREESL
			GETAQVYWKTHNNVIYPVDGSKSFNFDRVLHGNETPKNVVFA\T
			AAPIIDSAIQGYNGTIFA\YGOT\ASGKTYTMMGSEDHLGVIDO
			GQFHGHFSQKI*EVFLDREFLLRVSYMEIYNETITDLLCGTOKM
1			KPLIIREDVNRNVYVADLTEEVVYTSEMALKWITKGEKSPHYGE
			TKMNQRSSRSHTIFRMILESREKGEPSNCEGSVKVSHLNLVDLA
1 1			GSERAAQTGAAGVRLKEGCNINRSLFILGQVIKKLSDGQVGGFI
1 1			NYRDSKLTRILQNSLGGNPKTRIICTITPVSFDETLTALQFAST
1 1			AKYMKNTPYVNEVSTDEALLKRYRKEIMDLKKQLEEVSLETRAQ
l i	•		AMEKDQLAQLLEEKDLLQKVQNEKIENLTRMLVTSSSLTLQQEL
	1		KAKRKRRVTWCLGKINKMKNSNYADQFNIPTNITTKTHKLSINL
			LREIDESVCSESDVFSNTLDTLSEIBWNPATKLLNQENIESELN
			SLRADYDNLVLDYEQLRTEKEEMELKLKEKNDLDEFEALERKTK
1			KDQEMQLIHEISNLKNLVKHREVYNQDLENELSSKVELLREKED
			QIKKLQEYIDSQKLENIKMDLSYSLESIEDPKQMKQTLFDAETV
			ALDAKRESAFLRSENLELKEKMKELATTYKQMENDIQLYQSQLE
1 1		i	AKKKMQVDLEKELQSAFNEITKLTSLIDGKVPKDLLCNLELEGK
1 1			ITDLQKELNKEVBENEALRBEVILLSBLKSLPSEVERLRKEIQD
1 1			KSEELHIITSEKDKLFSEVVHKESRVQGLLEEIGKTKDDLATTQ
1 1			SNYKSTDQEFQNFKTLHMDFEQKYKMVLEENBRMNQEIVNLSKE
1 1		ŀ	AQKFDSSLGALKTELSYKTQELQEKTREVQERLNEMEQLKEQLE
1			NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL
			QIERDQLKSDIHDTVNMNIDTQEQLRNALESLKQHQETINTLKS
1		ļ	KISEEVSRNLHMBENTGETKDEFQQKMVGIDKKQDLEAKNTQTL
1	1	J	TADVKONE I FOODKI FOI TO EVERY COMPONENT OF THE TADVKONE I FOODKI F
1		İ	TADVKDNEIIEQQRKIFSLIQEKNELQQMLESVIAEKEQLKTDL KENIEMTIENQEELRLLGDELKKQQEIVAQEKNHAIKKEGELSR
1			TCDPLAEVEEKI.VPVCOOLOBVOOCTANDEKNHAIKKEGELSR
j i	ł	ł	TCDRLAEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINBIE
		ļ	NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVL
[[į	KELQKSFETERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE
	1	İ	TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP
, ,		f	NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRLNEKF
			QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE
			SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG
	}		LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV
		1	AKHLETEEELKVAHCCLKEQEBTINELRVNLSEKETEISTIQKQ
		1	LEAINDKLQNKIQEIYEKEEQLNIKOISEVOEKVNELKOFKFHD
1			KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMKRVOFA
		1	LQIERDQLKENTKEIVAKMKESOEKEYOFLKMTAVNRTOFKMOF
		į.	IEHLKEQFETQKLNLENIETENIRLTOILHENLEEMRSVTKERD
L			DLRSVEETLKVERDQLKENLRETITRDLBKQEELKIVHMHLKEH

	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:		_	H=Histidine, I=Isoleucine, K=Lysine,
1	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
ļ	corresponding	to first	
Ì	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence		\=possible nucleotide insertion)
			QETIDKLRGIVSEKTNEISNMQKDLEHSNDALKAQDLKIQEELR
		1	IAHMHLKEQQETIDKLRGIVSEKTDKLSNMQKDLENSNAKLQEK
		1	IOELKANEHOLITLKKDVNETOKKVSEMEQLKKQIKDQSLTLSK
			LEIENLNLAQKLHENLBEMKSVMKERDNLRRVEETLKLERDQLK
ì			ESLOETKARDLEIQQELKTARMLSKEHKETVDKLREKISEKTIQ
1			ISDIQKDLDKSKDELQKKIQELQKKELQLLRVKEDVNMSHKKIN
Į	i		EMEQLKKOFEPNYLCKCEMDNFQLTKKLHESLEEIRIVAKERDE
	1		
į.		•	LRRIKESLKMERDQFIATLREMIARDRQNHQVKPEKRLLSDGQQ
i	1		HLMESLREKCSRIKELLKRYSEMDDHYECLNRLSLDLEKEIEFH
1			RIMKKLKYVLSYVTKIKEEQHBCINKFEMDFIDEVBKQKELLIK
1	1		IQHLQQDCDVPSRELRDLKLNQNMDLHIEEILKDFSESEFPSIK
			TEFQQVLSNRKEMTQFLEEWLNTRFDIEKLKNGIQKENDRICQV
			NNFFNNRIIAIMNESTEFEERSATISKEWEQDLKSLKEKNEKLF
			KNYQTLKTSLASGAQVNPTTQDNKNPHVTSRATQLTTEKIRELE
1		1	NSLHEAKESAMHKESKIIKMOKELEVTNDIIAKLQAKVHESNKC
			LEKTKETIOVLODKVALGAKPYKEEIEDLKMKLGKIDLEKMKNA
			KEFEKEISATKATVEYQKEVIRLLRENLRRSQQAQDTSVISEHT
			DPOPSNKPLTCGGGSGIVONTKALILKSEHIRLEKEISKLKOON
1			EQLIKQKNELLSNNQHLSNEVKTWKERTLKREAHKQVTCENSPK
ł			SPKVTGTASKKKOITPSOCKERNLODPVPKESPKSCFFDSRSKS
}			LPSPHPVRYFDNSSLGLCPEVQNAGAESVDSQP\GPWARLFQGK
1			
			DVP\ECKTQ
5815	23	1460	SELVMWTVQNRESLGLLSFPVMITMVCCAHSTNEPSNMSYVKET
			VDRLLKGYDIRLRPDFGGPPVDVGMRIDVASIDMVSEVNMDYTL
l			TMYFQQSWKDKRLSYSGIPLNLTLDNRVADQLWVPDTYFLNDKK
1	1		SFVHGVTVKNRMIRLHPDGTVLYGLRITTTAACMMDLRRYPLDE
		ł	QNCTLEIESYGYTTDDIEFYWNGGEGAVTGVNKIELPQFSIVDY
1		1	KMVSKKVEFTTGAYPRLSLSFRLKRNIGYFILQTYMPSTLITIL
i	1		SWVSFWINYDASAARVALGITTVLTMTTISTHLRETLPKIPYVK
	1	1	AIDIYLMGCFVFVFLALLEYAFVNYIFFGKGPQKKGASKQDQSA
	1		NEKNKLEMNKVQVDAHGNILLSTLEIRNETSGSEVLTSVSDPKA
Ĭ	1	1	TMYSYDSASIQYRKPLSSRE\A*GRAPDRHGVPSKGRIRRRAS\
1	1	1	OLKVKIPDLTDVNSIDKWSRMFFPITFSLFNVVYWLYYVH
		ļ	TSSRSRAAAOEGDAETPGSVERRGRRAGAEDGMSQAPGAQPSPP
5816	861	191	
	1	i	TVYHERQRLELCAVHALNNVLQQQLFSQEAADBICKRLAPDSRL
1	1	4	NPHRSLLGTGNYDVNVIMAALQGLGLAAVWWDRRRPLSQLALPQ
	· L	İ	VLGLILNLPSPVSLGLLSLPLRRRHLRWPCARL/VTVSYYNLDS
1			K\LRAPEGPGGLRTE*GPFLAAALAQGLCEVLLVVTKEVEEKG
		1	SWLRTD
5817	851	118	RLFRGPGANRGRSCRGCSGGREPSGGALPKRHCPC*PPSPPAAD
			VMSNTTVPNAPQANSDSMVGYVLGPFFLITLVGVVVAVVMYVQK
			KKRVDRLRHHLLPMYSYDPAEELHEAEQELLSDMGDPKVV\QAG
		1	RVATSTSGCHCWMSRRDLTPLPHPSBPGVLDCLGPCHLLPLLSP
i			GSPCWVLGLHPSLHPPSAASASHALTITSLPPGLLPFVGVELTA
1			HPOALMGRGFPSGMAAAGRHLCFL
E03.0		3918	QALRDKLWIFLVQSFYAVRHTESWKLMSTDDQQKIQAAAFDKGD
5818	3	2270	DRRLGKKPIFSSSOORKOVSDSGDIKIKSWRGNNKKECWSYLST
1			
1			NKKMKSDGLGASGHSSSTNRNSINKTLKQDDVKEKDGTKIASKI
1		1	TKELKTGGKNVSGKPKTVTKSKTENGDKARLENMSPRQVVERSA
1			TAAAAATGQKNLLNGKGVRNQEGQISGARPKVLTGNLNVQAKAK
1	1		PLKKATGKDSPCLSIAGPSSRSTDSSMEFSISTECLDEPKENGS
1			TEEEKPSGHKLSFCDSPGQMMKNSVDSVKNSTVAIKSRPVSRVT
1			NGTSNKKSIHEQDTNVNNSVLKKVSGKGCSEPVPQAILKKRGTS
	1		NGCTAAQQRTKSTPSNLTKTQGSQGESPNSVKSSVSSRQSDENV
1			AKLDHNTTTEKQAPKRKMVKQVHTALPKVNAKIVAMPKNLNQSK
			KGETLNNKDSKQKMPPGQVISKTQPSSQRPLKHETSTVQKSMFH
			DVRDNNNKDSVSEQKPHKPLINLASEISDAEALQSSCRP\DPQK
			PLNDOEKEKLALECQNISKLDKSLKHELESKQICLDKSETKFPN
			HKETDDCDAANICCHSVGSDNVNSKFYSTTALKYMVSNPNENSL
l			NSNPVCDLDSTSAGQIHLISDRENQVGRKDTNKQSSIKCVEDVS
		!	
L	<u> </u>	<u> </u>	LCNPERTNGTLNSAQEDKKSKVPVEGLTIPSKLSDESAMDEDKH

SEQ	Predicted	Predicted end	Lating add government control
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	_	\=possible nucleotide insertion)
	· · · · · · · · · · · · · · · · · · ·		ATADSDVSSKCFSGQLSEKNSPKNMETSESPESHETPETPFVGH
1			WNLSTGVLHQRESPESDTGSATTSSDDIKPRSEDYDAGGSQDDD
			GSNDRGISKCGTMLCHDFLGRSSSDTSTPEELKIYDSNLRIEVK
			MKKQSSNDLFQVNSTSDDEIPRKRPEIWSRSAIVHSRERENIPR
ļ		Į	GSVQFAQEIDQVSSSADETEDERSEAENVAENFSISNPAPQQFQ
1			GIINLAFEDATENECREFSANKKFKRSVLLSVDECEELGSDEGE
	1		VHTPFQASVDSFSPSDVFDGISHEHHGRTCYSRFSRESEDNILE
1			CKQNKGNSVCKNESTVLDLSSIDSSRKNKQSVSATEKKNTIDVL
	}	1	SSRSRQLLREDKKVNNGSNVENDIQQRSKFLDSDVKSQERPCHL
			DLHQREPNSDIPKNSSTKSLDSFRSQVLPQEGPVKESHSTTTEK
j			ANIALSAGDIDDCDTLAQTRMYDHRPSKTLSPIYEMDVIEAFEQ
			KVESETHVTDMDF*DDQHFAKQDWTLLKQLLSEQDSNLDVTNSV
	1		PEDLSLAQYLINQTLLLARDSSKPQGITHIDTLNRWSELTSPLD
	1		SSASITMASFSSEDCSPQGEWTILELETQH
5819	1	5557	AAAGLLGALHLVMTLVVAAARAEKEAFVQSESIIEVLRFDDGGL
	ļ		LQTETTLGLSSYQQKSISLYRGNCRPIRFEPPMLDFHEQPVGMP
			KMEKVYLHNPSSE*TITLVSIFATTSHFHASFFQNRKILPGGNT
1			SFDVS/VFLARVVGNVENTLFINTSNHGVFTY\QVFGVGVPNPY
			RLRPFLGARVTVNSSFSPIINIHNPHSEPLQVVEMYSSGGDLHL
			ELPTGQQGGTRKLWEIPPYETKGVMRASFSSREADNHTAFIRIK
ĺ			TNASDSTEFIILPVEVEVTTAPGIYSSTEMLDFGTLRTODLPKV
		1	- ·
			LNLHLLNSGTKDVPITSVRPTPQ\NDAITVHFKPITLKAS\ESK
j			YTKVASISFDASKAKKPSQFSGKITVKAKEKSYSKLEIPYQAEV
ì			LDGYLGFDHAATLFHIRDSPADPVERPIYLTNTFSFAILIHDVL
ł			LPEEAKTMFKVHNFSKPVLILPNESGYIFTLLFMPSTSSMHIDN
1			NILLITNASKFHLPVRVYTGFLDYFVLPPKIEERFIDFGVLSAT
1			EASNILFAIINSNPIELAIKSWHIIGDG\LSIELVAVDRGNRTT
1			IISSLPECEKSSSSDQSSVTLASGYF\AVFRVKLTAKKL\EGIH
1			DGAIQITTDYEILTIPVK\AVIAVGSLTCSPKHVVLPPSFPGKI
1			VHQSLNIMNSFSQKVKIQQIRSLSEDVRFYYKRLRGNKEDLEPG
1		•	KKSKIANIYFDPGLQCGDHCYVGLPFLSKSEPKVQPGVAMQEDM
			WDADWDLHQSLFKGWTGIKENSGHRLSAIFEVNTDLQKNIISKI
}			TAELSWPSILSSPRHLKFPLTNTNCSS\EEEITLENP/SQDVPV
1			YVQFIPLALYSNPSVFVDKLVSRFNLSKVAKIDLRTLEFQVFRN
1			SAHPLQSSTGFMEG\LSPHLILNLILKPGEKKSVKVK\FTPVHN
i .			RTVSSLIIVRNNLTVMDAVMVQGQGTTENLRVAGKLPGPGSSLR
1			FKITEALLKDCTDSLKLREPNFTLKRTFKVENTGQLQIHIETIE
1			ISGYSCEGYGFKVVNCQEFTLSANASRDIIILFTPDFTASRVIR
1	1		ELKFITTSGSEFVFILNASLPYHMLATCAEALPRPNWELALYII
1			ISGIMSALFLLVIGTA\YLEAQGIWBP\FRRRLS\FEASNPPFD
1			VGRPFDLRRIVGISSEGNLNTLSCDPGHSRGFCGAGGSSSRPSA
			GSHKQ*GPSGHPHSSHSNRNSADVDDVRAYNSGRTSSMTSAQAA SSQPANKTRPLVLDSNTGAQGHSAGRKSKGAKQSQHGSQHHAHS
1			PLECHPOPPLPPPVPQPQEPQPERLSPAPLAHPSHPERASSARH
1			SSEDSDITSLIRAMDKDFDHHDSPALEVFTEQPPSPLPKSKGKG
1			KPLORKVKPPKKQEEKEKKGKGKPQEDELKDSLADDDSSSTTTE
l			TSNPDTEPLLKEDTEKQKGKQAMPEKHESEMSQVKQKSKKLLNI
1			KKEIPTDVKPSSLELPYTPPLESKQRRNLPSKIPLPTAMTSGSK
1			SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEKDSP
			PPEWDSVPVHKPGSSTDSLYKLSLQTLNADIFLKQRQTSPTPAS
1			PSPPAAPCPFVARGSYSŚIVNSSSSSDPKIKQPNGSKHKLTKAA
	İ	i	SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSLGIS
	ļ		HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNLTGE
			VFSKLGLSRSCNQASQRSWNBFNSGPSYLWESPATDPSPSWPAS
			SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFTTPAN
			TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSPTIGR
			RSSDPWSNSHFPHEN
5820	310	1270	RVSLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSRGPIQ
		12,0	
			SSGPTIQ\VI*IDQGLPGKK*KSN*KRKRK/DSKALAEFEEKMN
		J	ENWKKELEKHREKLLSGSESSSKKRQRKKKEKKKSW*\DSSSS\
L			SSSSDSSSSSSDSEDEDKKQGKRRKKKNRSHKSSESSMSETES

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L-Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1 1	residue of amino acid	amino acid sequence	Codon, /=possible nucleotide deletion,
1		sequence	\=possible nucleotide insertion)
	sequence		DSKDSLKKKKKSKDGTEKEKDIKGLSKKRKMYSEDKPLSSESLS
1			ESEYIEEVRAKKKKSSEEREKATEKTKKKKKKKKKKKKKKAA
1			SSSPDSP*H*EKSGFPYKESAMSEEISTVKTTTYLLKCMNFLVF
1 1			GIIPGLFSSHSDATV
5821	179	915	KWRNQSWRWPKPGTNWMLSCSVCWRRVTWTGSVWMRKLGKHPQT
	-17		PT/IKDCSIAATGKRPSARFPHQRRKKRREMDDGLAEGGPQRSN
1			TYVIKLFDRSVDLAQFSENTPLYPICRAWMRNSPSVRERECSPS
1			SPLPPLPEDEEG\SEVTNSKSR*CVQACPPTHTPGGQPKNACR\
			SRIPSPLAALRMQGTP*RWSPFEPEPSPSTLIYRNMQRWKRIRQ
1			RWKEASHRNQLRYSESMKILREMYERQ
5822	464	4379	QTLKEMPIVMARDLEETASSSEDBEVISQEDHPCIMWTGGCRRI
			PVLVFHADAILTKDNNIRVIGERYHLSYKIVRTDSRLVRSILTA
			HGFHEVHPSSTDYNLMWTGSHLKPFLLRTLSEAQKVNHFPRSYE
			LTRKDRLYKNIIRMQHTHGFKAFHILPQTFLLPAEYAEFCNSYS
1 1			KDRGPWIVKPVASSRGRG\VYLINNPNQISLEENILVSRYINNP LLIDDFKFDVRLYVLVTSYDPLVIYLYEEGLARFATVRYDQGAK
1			NIRNOFMHLTNYSVNKKSGDYVSCDDPEVEDYGNKWSMSAMLRY
1			LKQEGRDTTALMAHVEDLIIKTIISAELAIATACKTFVPHRSSC
1			FELYGFDVLIDSTLKPWLLEVNLSPSLACDAPLDLKIKASMISD
1			MFTVVGFVCQDPAQRASTRPIYPTFESSRRNPFQKPQRCRPLSA
1		i	SDABMKNLVGSAREKGPGKLGGSVLGLSMEEIKVLRRVKEENDR
1			RGGFIRIFPTSETWEIYGSYLEHKTSMNYMLATRLFQDRMTADG
! !			APELKI*SLNSKAKLHAALYERKLLSLEVRKRRRRSSRLRAMRP
1 1			KYPVITQPAEMNVKTETESEEEEEVALDNEDEEQEASQEESAGF
		ļ	LRENQAKYTPSLTALVENTPKENSMKVREWNNKGGHCCKLETQE
1			LEPKFNLMQILQDNGNLSKMQARIAFSAYLQHVQI\RLMKDSGG
			QTFSASWAAKEDEQMELVVRFLKRASNNLQHSLRMVLPSRRLAL
1			LERTRILAHQLGDFIIVYNKETEQMAEKKSKKKVEEEEEDGVNM
			ENFORFIROASEAELEEVLTFYTQKNKSASVFLGTHSKISKNNN
1 1			NYSDSGAKGDHPETIMEEVKIKPPKQQQTTEIHSDKLSRFTTSA EKEAKLVYSNSSSGPTATLQKIPNTHLSSVTTSDLSPGPCHHSS
1 1		ļ	LSQIPSAIPSMPHQPTILLNTVSASASPCLHPGAQNIPSPTGLP
1 1			RCRSGSHTIGPFSSFOSAAHIYSOKLSRPSSAKAGSCYLNKHHS
1			GIAKTQKEGEDASLYSKRYNQSMVTAELQRLAEKQAARQYSPSS
1 1			HINLLTQQVTNLNLATGIINRSSASAPPTLRPIISPSGPTWSTQ
1			SDPQAPENHSSSPGSRSLQTGGFAWEGEVENNVYSQATGVVPQH
1			KYHPTAGSYQLQFALQQLEQQKLQSRQLLDQSRARHQAIFGSQT
			LPNSNLWTMNNGAGCRISSATASGQKPTTLPQKVVPPPSSCASL
		1	VPKPPPNHEQVLRRATSQKASKGSSAEGQLNGLQSSLNPAAFVP
			ITSSTDPAHTKIMNHKHTEKQPVHHSWVHD
5823	42	2293	LLTALSMEGGGGRDEPSACRAGDVNMDDPKKEDILLLADEKFDF
1 1		1	DLSLSSSSANEDDEVFFGPFGHKERCIAASLELNNPVPEQPPLP
1 1		1	TSESPFAWSPLAGEKFVEVYKEAHLLALHIESSSRNQAAQAAKP EDPRSOGVERFIOESKF\KINLFEKEKEMKKSPTSLKRETYYLS
		Į.	DSPLLGPPVGEPRLLASSPALPSSGAOARLTRAPGPPHSAHALP
		1	RESCTAHAASOAATORKPGTKLLLPRAASVRGRGIPGAAEKPKK
			EIPASPSRTKIPAEKESHRDVLPDKPAPGAVNVPAAGSHLGOGK
		İ	RAIPVP\NKLGLKKTLLKAPGSYSN\LORKSSSGA\VWSGASSA
			CTPOPVAKAKSSEFASIPAN*LPGLCPNISKS\GRMGPAMLRPA
			L\PAGPVG\ASSWQAKRVDVSELAAEQLTAPP\SASPTQPQTPE
1			GGG\QWLNSSCAWSESSQLNKTRSIRRRDSCLNSKTKVMPTPTN
			QFKIPKFSIGDS\PDSSTPKLSRAQRPQSCTSVGRVTVHSTPVR
			RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPKTMPRAVGS
			PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDSR\LVDVSPDR
			GSPPSRVPQALNFSPEESDSTFSKSTATEVAREEAKPGGDAAPS
1			EALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPEAHVAVGSE
			SRPLIDLMTNTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPEADK
		1	ENVDSPLLKF
5004			
5824	42	2293	LLTALSMEGGGGRDBPSACRAGDVNMDDPKKEDILLLADEKFDF
5824	42	2293	

SEQ	Predicted	Predicted end	I amino agid compant containing
	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1 1	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1 1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1 1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1 1	sequence	2042000	\=possible nucleotide insertion)
			EDPRSQGVERFIQESKF\KINLFEKEKEMKKSPTSLKRETYYLS
1			DSPLLGPPVGEPRLLASSPALPSSGAQARLTRAPGPPHSAHALP
1 1			RESCTAHAASQAATQRKPGTKLLLPRAASVRGRGIPGAAEKPKK
1			EIPASPSRTKIPAEKESHRDVLPDKPAPGAVNVPAAGSHLGQGK
			RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSGASSA
ŀ			CTPQPVAKAKSSEFASIPAN*LPGLCPNISKS\GRMGPAMLRPA
1 1	j		L\PAGPVG\ASSWQAKRVDVSELAAEQLTAPP\SASPTQPQTPE
1 1			GGG\QWLNSSCAWSESSQLNKTRSIRRRDSCLNSKTKVMPTPTN
1 1			QFKIPKFSIGDS\PDSSTPKLSRAQRPQSCTSVGRVTVHSTPVR
1 1			RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPKTMPRAVGS
[PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDSR\LVDVSPDR
			GSPPSRVPQALNFSPEESDSTFSKSTATEVAREEAKPGGDAAPS
			EALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPEAHVAVGSE
1 1			SRPLIDLMTNTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPEADK
			ENVDSPLLKF
5825	2	4210	FLQIESASPAPFSSGFLAAHPHSPGGSLATKGRSRLSAPGMLHL
			SAAPPAPPPEVTATARPCLCSVGRRGDGGKMAAAGALERSFVEL
1 1			SGAERERPRHFREFTVCSIGTANAVAGAVKYSESAGGFYYVESG
1			KLFSVTRNRFIHWKTSGDTLELMEESLDINLLNNAIRLKFQNCS
1 1			VLPGGVYVSETQNRVIILMLTNQTVHRLLLPHPSRMYRSELVVD
			SQMQSIFTDIGKVDFTDPCNYQLIPAVPGISPNSTASTAWLSSD
1			GEALFALPCASGGIFVLKLPPYDIPGMVSVVELKQSSVMQRLLT
1			GWMPTAIRGDQSPSDRPLSLAVHCVEHDAFIFALCQDHKLRMWS
1 1			YKEQMCLMVADMLEYVPVKKDLRLTAGTGHKLRLAYSPTMGLYL
			GIF\MHAPKRGQFCIFQLVSTESNRYSLDHISSLFTSQETLIDF
			ALTSTDIWALWHDAENQTVVKYINFEHNVAGQWNPVFMQPLPEE
i l			EIVIRDDQDPREMYLQSLFTPGQFTNEALCKALQIFCRGTERNL
			DLSWSELKKEVTLAVENELQGSVTEYEFSQEEFRNLQQEFWCKF YACCLQYQEALSHPLALHLNPHTNMVCLLKKGYLSFLIPSSLVD
1 1			HLYLLPYENLLTEDETTISDDVDIARDVICLIKCLRLIEESVTV
			DMSVIMEMSCYNLQSPEKAAEQILEDMITIDVENVMEDICSKLO
1 1	1		EIRNPIHAIGLLIREMDYETEVEMEKGFNPAQPLNIRMNLTQLY
			GSNTAGYIVCRGVHKIASTRFLICRDLLILQQLLMRLGDAVIWG
			TGQLFQAQQDLLHRTAPLLLSYYLIKWGSECLATDVPLDTLESN
1			LQHLSVLELTDSGALMANRFVSSPQTIVELFFQEVARKHIISHL
			FSQPKAPLSQTGLNWPEMITAITSYLLQLLWPSNPGCLFLECLM
1 .			GNCQYVQLQDYIQLLHPWCQVNVGSCRFMLGRCYLVTGEGOKAL
}	•		ECFCQAASEVGKEEFLDRLIRSEDGEIVSTPRLQYYDKVLRLLD
1			VIGLPELVIQLATSAITEASDDW\KSQATL\RTCIFKHHL\DLG
1	ĺ		\HNSQAYGSL*PQIPDSSRQLDCLRQLVVVLCERSQLQDLVEFS
1 1			YVNLHNEVVGIIESRARAVDLMTHNYYELLYAFHIYRHNYRKAG
1			TVMFEYGMRLGREVRTLRGLEKQGNCYLAALNCLRLIRPEYAWI
			VQPVSGAVYDRPGASPKRNHDGECTAAPTNRQIEILELEDLEKE
[]			CSLARIRLTLAQHDPSAVAVAGSSSAEEMVTLLVQAGLFDTAIS
1 1			LCQTFKLPLTPVFEGLAFKCIKLQFGGEAAQARAWAWLAANQLS
			SVITTKESSATDEAWRLLSTYLERYKVQNNLYHHCVINKLLSHG
			VPLPNWLINSYKKVDAAELLRLYLNYDLLDLTPYQVIRICGC
5826	3	871	KSQLLRDHSAPPPKPCTSVGAMGC*PRQ/SPKEQQRQLKKQKNR
			AAAQRSRQKHTDKADALHQQHESLEKDNLALRKEIQSLQAELAW
Į l			WSRTLHVHERLCPMDCASCSAPGLLGCWDQAEGLLGPGPQGQHG
1			CREQLELFQTPGSCYPAQPLSPGPQPHDSPSLLQCPLPSLSLGP
1			AVVAEPPVQLSPSPLLFASHTGSSLQGSSSKLSALQPSLTAQTA
			PPOPLELEHPTRGKLGSSPDNPSSALGLARLQSREHKPALSAAT
			WQGLVVDPSPHPLLAFPLLSSAQVHF
5827	194	2287	GMGSENSALKSYTLREPPFTLPSGLAVYPAVLQDGKFASVFVYK
1 1			RENEDKVNKAAKVP++HLKTLRHPCLLRFLSCTVEADGIHLVTE
			RVQPLEVALETLSSAEVCAGIYDILLALIFLHDRGHLTHNNVCL
ļ			SSVFVSEDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPP
			EEMSPEFTTLPECHGHARDAFSFGTLVESLLTILNEQVSADVLS
1 f	1		SFQQTLHSTLLNPIPKWRPALCTLLSHDFFRNDFLEVVNFLKSL
1	ſ		TLKSEEEKTEFFKFLLDRVSCLSEELIASRLVPLLLNQLVFAEP

<u> </u>	Dung's at = 3	Predicted end	Amino acid segment containing signal peptide
SEQ ID	Predicted beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	location		L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	
]	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1 1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			VAV\KSFLPYLLGPKKDHAQGETPCLLSPALFQSRVIPVLLQLF
i i		Į.	EVHEEHVRMVLLSHIEAYVGALSLREQLKKV\IL\PQVLLG\LR
1 1			D\TSDSIVAITLHSLAVLVSLLGPEVVVGGERTKIFKRTAP\SF
l i			TK\NTDLSLEGDPFSQPIKFPINGLSDVKNTSEDSENFPSSSKK
1 1		1	SEEWPDWSGPE\EPENQTVNI\QIWP\REP\CDDVKSQCTTLDV
i i			EESSWDDCEPSSLDTKVNPGGGITATKPVTSGEQKPIPALLSLT
		1	EESMPWKSSLPQKISLVQRGDDADQIEPPKVSSQERPLKVPSEL
1			GLGEEFTIQVKKKPVKDPEMDWFADMIPEIKPSAAFLILPELRT
1 1		1	· ·
			EMVPKKDDVSPVMQFSSKFAAAEITEGEAEGWEEEGELNWEDNN
			W
5828	2	257	AREGGSLGAVAACGELSYSCDFCPARPHTSWLTRFVKMEFQAVV
į l			MAVGGGSRMTDLTSSIPKPLLPVGNKPLIWYPLNLLERVGFEEV
}			IVVTTRDVQKALCABFKMKMKPDIVCIPDDADMGTADSLRYIYP
Į			KLKTDVLVLSCDLITDVALHEVVDLFRAYDASLAMLMRKGQDSI
1		1	BPVPGQKGKKKAVEQRDFIGVDSTGKRLLFMANEADLDEELVIK
1			GSILQKHPRIRFHTGLVDAHLYCLKKYIVDFLMENG\SITSIRS
1 1			BL\IPYLV/RGKQFSSASSQQGTRKEKEGGSKGKRGLKSFRISY
			SFY*KEANYTGTGAPY\D\ACWI
5829	260	1259	PDGRLIVSCSEDKTIKIWDTTNKQCVNNFSDSVGFANFVDFNPS
1 3023	200	1233	GTCIASAGSDOTVKVWDVRVNKLLQHYQVHSGGVNCISFHPSGN
			YLITASSDGTLKILDLLKGRLIYTLQGHTGPVFTVSFSKGGELF
İ		i	ASGGADTQVLLWRTNFDELHCKGLTKRNLKRLHFDSPPHLLDIY
		1	PRTPHPHERKVETVEDFFLHLLRLIOSLR*SICRSLLPLLWISF
1			
1 .			LLILPQQQKPVVGLCQTRVKRPVDIS*TLP*CHQNVCQQPRKRK
			QKT+VTSPVKVK/VSIPLAVTDALEHIMEQLNVLTQTVSILEQR
		<u> </u>	LTLTEDKLKDCLENQQKLFSAVQQKS
5830	4496	3139	GGKMAAPEERDLTQEQTEKLLQFQDLTGIESMDQCRHTLEQHNW
			NIEAAVQDRLNEQEGVPSVFNPPPSRPLQVNTADHRIYSYVVSR
			PQPRGLLGWGYYLIMLPFRFTYYTILDIFRFALRFIRPDPRSRV
{		1	TDPVGDIVSFMHSFEEKYGRAHPVFYQGTYSQALNDAKRELRFL
		1	LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLFWACSTNKPE
Į.		İ	GYRVSQALRENTYPFLAMIMLKDRRE*PV\VGRLEGLI\QPDDL
	}		INQLTFIMDANQTYLVSERLEREERNQTQVLRQQQDEAYLASLR
}	ľ		ADQEKERKKREERERKRRKKEEVQQQKLAEERRRQNLQEEKERK
			LECLPPEPSPDDPESVKIIFKLPNDSRVERRFHFSQSLTVIHDF
		1	LFSLKESP\EKFOIEA\NFPRR\VLPCIPSEE\WPNPPTLQE\A
1		1	GLSHTEVLFVQDLTDE
5831	71	2897	FCSKDKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSERQVKD
5551	'-	1	TDDIESPKRSIRDSGYIDCWDSERSDSLSPPRHGRDDSFDSLDS
ļ.			FGSRSROTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDDMS
1		1	ARRISHGEPKSAVPFNOYLPNKSNOTAYVPAPLRKKKABREEYR
{			KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMRCEE
i			EAAVQPHSRARQEQLQLINNQLRBEDDKWQDDLARWKSRKRSVS
1		1	
			QDLIKKEEERKKMEKLLAGEDGTSERRKSIKTYREIVQEKERRE
			RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPKILE
			RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIARAS
1			VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTFK
i			VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFEGVARVH
			GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQEDKND
1			GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQLKND
1			VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFPFLD
1			KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEERRR
	1		QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEBRRY
			YEEEP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNKIDL
1			GNCODEKODRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTEGAL
1			AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQTSN
1			PTHSSBDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSSCGL
1			PIGSSBOVKPKIDPBDGSINNQIESFSEKKKSISGKKECSSCOB PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDVRIR
	1		•
	1		
<u> </u>	2754	630	NGLLNCNDCYMRSRSAGQPTTL
5832	2454	829	PGRRFRHGSCAFOKQCIMLHICQYFLQGECKFGTSCKRSHDFSN SENLEKLEKLGMSSDLVSRLPTIYRNAHDIKNKSSAPSRVPPLF

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	1	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	1	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			VPQGTSERKDSSGSVSPNTLSQEEGDQICLYHIRKSCSFQDKCH
[1		RVHFHLPYRWQFLDRGKWEDLDNMELIEEAYCNPKIERILCSES
ì	ŧ		
}	1		ASTFHSHCLNFNAMTYGATQARRLSTASSVTKPPHFILTTDWIW
ŀ			YWSDEFGSWQEYGRQGTVHPVTTVSSSDVEKAYLAY/WYTGV*R
ł			PGSHLEVPGRKAQLRVRFQSLRSEKPGLWHN*KGLPQTQIR\AP
	i		QDVTTMQTCNTKFPGPKSIPDYWDSSALPDPGFQKITLSSSSEE
1			YQKVWNLFNRTLPFYFVQKIERVQNLALWEVYQWQKGQMQKQNG
1			GKAVDERQLFHGTSAIFVDAICQQNFDWRVCGVHGTSYGKGSYF
			ARDAAYSHHYSKSDTQTHTMFLARVLVGEFVRGNASFVRPPAKE
			GWSNAFYDSCVNSVSDPSIFVIFEKHQVYPEYVIQYTTSSKPSV
			TPSILLALGSLFSSRQ
5833	170	3289	SILCLLSPCVVQFGKPVVSILSSRSRHSPCTKKGWEGMRKHLHT
			RQGHK*VHVEISKALWVYRDDYFIRHSISVSAVIVRAWITHKYR
ŀ		,	GRDWNVKWEENLLHAVAKNYTLLQTIPPFERPFKDHQVCLEWNM
			GYIWNLRANRIPQCPLENDVVALLGFPYASSGENTGIVKKFPRF
	f		RNRELEATRRORMDYPVFTVSLWLYLLHYCKANLCGILYFVDSN
		•	EMYGTPSVFLTEEGYLHIQMHLVKGEDLAVKTKFIIPLKEWFRL
			DISFNGGQIVVTTSIGQDLKSYHNQTISFREDFHYNDTAGYFII
i			GGSRYVAGIEGFFGPLKYYRLRSLHPAQIFNPLLEKQLAEQIKL
			YYERCAEVQEIVSVYASAAKHGGERQEACHLHNSYLDLQRRYGR
			PSMCRAFPWEKELKDKHPSLFQALLEMDLLTVPRNQNESVSEIG
1			GKIFEKAVKRLSSIDGLHQISSIVPFLTDSSCCGYHKASYYLAV
}			FYETGLNVPRDQLQGMLYSLVGGQGSERLSSMNLGYKHYQGIDN
1			YPLDWELSYAYYSNIATKTPLDQHTLQGDQAYVETIRLKDDEIL
1			KVQTKEDGDVFMWLKHEATRGNAAAQQRLAQMLFWGQQGVAKNP
			EAAIEWYAKGALETEDPALIYDYAIVLFKGQGVKKNRRLALELM
1			KKAASKGLHQAVNGLGWYYHKFKKNYA\KAAKYWLKA\EE\MGN
			PDASYNLGVLHLDGIFPGVPGRNQTLAGEYFHKAAQGGHMEGTL
			WCSLYYITGNLETFPRDPEKAVVWAKHVAEKNGYLGHVIRKGLN
1	i		AYLEGSWHEALLYYVLAAETGIEVSQTNLAHICEERPDLARRYL
			GVNCVWRYYNFSVFQIDAPSFAYLKMGDLYYYGHQNQSQDLELS
}			VQMYAQAALDGDSQGFFNLALLIEEGTIIPHHILDFLEIDSTLH
	i i		
	,		SNNISILQELYERCWSHSNEESFSPCSLAWLYLHLRLLWGAILH
			SALIYFLGTFLLSILIAWTVQYFQSVSASDPPPRPSQASPDTAT
5834	17	1000	STASPAVTPAADASDQDQPTVTNNPEPRG
3034	17	4020	RFRRGGGRVFPGAFPASPSDSLGQGNSQGPPRTPKPPRT/QECG
			SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV
1			TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR
į .			NAFVTGIARYIEQATVHSSMNEMLEEGQEYAVMLYTWRSCSRAI
			PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC
			GEVRRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV
			KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ
			QQLEVISGYEELLADIVNLCVDYYENRMYLTPSEKHMLLKVMGF
		1	GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI
			ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM
			RFISELARYSNSEVVTGSGRQEAQKTDAEYRKLFDLALQGLQLL
			SQWSAHVMEVYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS
			EEKFALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDFSQ
			VTLMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAL
			RGEKDPKSG*DIKVPRRAVGPSSTQLYMVRTMLBSLIADKSGSK
]			
			KTLRSSLEGPTILDIEKFHRESFFYTHLINFSETLQQCCDLSQL
1			WFREFFLELTMGRRIQFPIEMSMPWILTDHILETKEASMMEYVL
1 1			YSLDLYNDSAHYALTRFNKQFLYDEIEAEVNLCFDQFVYKLADQ
1			IFAYYKVMAGSLLLDKRLRSECKNQGATIHLPPSNRYETLLKQR
1		-	HVQLLGRSIDLNRLITQRVSAAMYKSLELAIGRFESEDLTSIVE
1			LDGLLEINRMTHKLLSRYLTLDGFDAMFREANHNVSAPYGRITL
1			HVFWELNYDFLPNYCYNGSTNRFVRTVLPPSQEFQRDKQPNAQP
1			QYLHGSKALNLAYSSIYGSYRNFVGPPHFQVICRLLGYQGIAVV
;			MEELLKVVKSLLQGTILQYVKTLMEVMPKICRLPRHEYGSPGIL
[[1	ľ	EFFHHQLKDIVEYAELKTVCFQNLREVGNAILFCLLIEQSLSLE
!	J		EVCDLLHAAPFQNILPRVHVKEGERLDAKMKRLESKYAPLHLVP
			

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Ţ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
į	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	 		LIERLGTPQQIAIAREGDLLTKERLCCGLSMFEVILTRIRSFLD
ł			DPIWRGPLPSNGVMHVDECVEFHRLWSAMOFVYCIPVGTHEFTV
1	ì		EQCFGDGLHWAGCMIIVLLGQQRRFAVLDFCYHLLKVOKHDGKD
			EIIKNVPLKKMVERIRKFQILNDEIITILDKYLKSGDGEGTPVE
			HVRCFQPPIHQSLASS
5835	4209	1904	SGNIRMAQGSHQIDFQVLHDLRQKFPEVPEVVVSRCMLQNNNNL
			DACCAVLSQESTRYLYGEGDLNFSDDSGISGLRNHMTSLNLDLO
Ì	1		SQNIYHHGREGSRMNGSRTLTHSISDGQLQGGQSNSELFQQEPQ
			TAPAQVPQGFNVFGMSSSSGASNSAPHLGFHLGSKGTSSLSOOT
			PRFNPIMVTLAPNIQTGRNTPTSLHIHGVPPPVLNSPQGNSIYI
	ĺ		RPYITTPGGTTRQTQQHSGWVSQFNPMNPQQVYQPSQPGPWTTC
	ŀ		PASNPLSHTSSQQPNQQGHQTSHVYMPISSPTTSQPPTIHSSGS
			SQSSAHSQYNIQNISTGPRKNQIEIKLEPPORNNSSKLRSSGPR
			TSSTSSSVNSQTLNRNQPTVYIAASPPNTDELMSRSQPKVYISA
İ			NAATGDEQVMRNQPTLFISTNSGASAASRNMSGQVSMGPAFIHH
			HPPKSRAIGNNSATSPRVVVTQPNT\EYTFKITVSPNKPPAVSP
			GVVSPTFELTNLLNHPDHYVETENIHHLTDPTLAHVDRISETRK
]	LSMGSDDAAYTQDI*RISNSWLGMVAHACNSSALGGQDGRII*A
		Ì	QEFETSWGNIWRLRLYRRF*NYAGMVAHTCSPSYSVD*ALLVHQ
			KARMERLQRELBIQKKKLDKLKSEVNEMENNLTRRRLKRSNSIS
			QIPSLEEMQQLRSCNRQLQIDIDCLTKEIDLFQARGPHFNPSAI
			HNFYDNIGFVGPVPPKPKDQRSIIKTPKTQDTEDDEGAQWNCTA
			CTFLNHPALIRCEOCEMPRHF
5836	361	2303	FHITMCGICCSVNFSAEHFSQDLKEDLLYNLKQRGPNSSKQLLK
		367	SDVNYQCLFSAHVLHLRGVLTTQPVEDERGNVFLWNGEIFSGIK
		1	VEAEENDTQILFNYLSSCKNESEILSLFSEVQGPWSFIYYQASS
1			HYLWFGRDFFGRRSLLWHFSNLGKSFCLSSVGTQTSGLANOWOE
			VPAS\DFSELILSLLSFPDALFYNCILGNIFLGRILLKKMLIA*
			VKFQQTYQHLYQR*QMKPNCILKNLLFL*I*CCHKLHWRLIAVI
			FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR
			DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPLDE
	1	Ì	PIDLLNVAFIAEEKTMPTTFNREGNKQKNKCEIPSEEFSKDVAA
			AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSME
1			ELQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAOEG
1			VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM
1			MELGRISSRNLGRDDRVIGDHGKEARFPFLDENVVSFLNSLPIW
			EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA
}		1	KMEKINEKASDKCGRLQIMSLENLSIEKETKL
5837	4792	903	NGNAVAQAPVTNCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL
			KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT
	1	1	QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD
1	1		RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG
		1	MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT
	1	1	DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE
		1	GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY
		1	KLPVHTBISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH
1	1	1	HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQOCSPFTCHNLKNC
}	1	1	P*KAAPESPSDPLQSPYRTPPQGHTAQDYPVWAWEPHIH*WEGL
		1	VFCFPIDGYSPGCWD\AFPGKEAPVAIFRG\HOGRLLCVAWSPL
1			DPDCIYSG\ADDFCVHKWLTSMODHSRPPOGKKSIELEKKRLSO
1			PKAKPKKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGVSDO
	1	1	EGEEQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV
		1	ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHODCL
	1		VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG
1	1	[HLENGHPELFHOLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA
1	1		GYHVWLWAVEAFAKOLCFODOYVKAASHLLSIHKVYRAVELLKS
			NHFYREAIAIAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK
İ			CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA
1	1		LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE
1			BKQLSEGKSSSSYHTWNTGTEGPFVERVTAVWKSIFSLDTPEQY
	1	1	QEAFQKLQNIKYPSATNNTPAKQLLLHICHDLTLAVLSQQMASW
	<u> </u>	J	F F F F F F F F

CRO	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ			
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ı	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1			1
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
	Bequeince		
			DEAVQALLRAVVRSYDSGSFTIMQEVYSAFLPDGCDHLRDKLGD
1			HQSPATPAFKSLEAFFLYGRLYEFWWSLSRPCPNSSVWVRAGHR
1	1		TLSVEPSQQLDTASTEETDPETSQPEPNRPSELDLRLTEEGERM
		Ī	LSTFKELFSEKHASLONSORTVAEVQETLAEMIRQHQKSQLCKS
1		1	TANGPDKNEPEVEAEQPLCSSQSQCKEEKNEPLSLPELTKRLTE
i			
	ł		ANQRMAKFPESIKAWPFPDVLECCLVLLLIRSHFPGCLAQEMQQ
		ŀ	QAQELLQKYGNTKTYRRHCQTFCM
5838	110	98	KTMPHLLVTFRDVAIDFSQEEWECLDPAQRDLYRDVMLENYSNL
		}	ISLDLESSCVTKKLSPEKEIYEMES\PSGRIWGNVSTITFQYNG
1			
1			LGDNMECKGNLEGQVSKSEGLYMCVKITCEEKATESHSTSSTFH
ì		}	RII/HYQGKIVKCKECRQGFSYLSCLIQHEENHNI*KCSEVNKH
1			RNTFSKKPSYI*HQ\KFRLGEKPYECMECGKAFGRTSDLIQHQK
1		İ	IHTNEKPYQCNACGKAFIRGSQLTEHQRVHTGEKPYDCKKCGKA
1	1	1	FSYCSQYTLHQRIHSGEKPYECKDCGKAFILGSQLTYHQRIHSG
1		1	EKPYECKECGKAFILGSHLTYHORVHTGEKPYICKECGKAFLCA
		1	
1		ļ	SQLNEHQRIHTGEKPYECKECGKTFFRGSQLTYHLRVHSGERPY
1		1	KCKECGKAFISNSNLIQHQRIHTGEKPYKCKECGKAFICGKQLS
			EHORIHTGEKPFECKECGKAFIRVAYLTQHEKIHGEKHYECKEC
1			GKTFVRATQLTYHQRIHTGEKPYKCKECDKAF/HLWLTILSEHQ
1	f		RIHRGEKPYECKQCGR/LFIRGSHL/NEHLRTHTGEKPYECKEC
İ			
]	GRAFSRGSEHTLHQRIHTGEKPYTCVQCGKDFRCPSQLTQHTRL
			HN*EYSSHKICMHSIALASLDFAHLQEKNPEN
5839	1	2425	GRPFPRPPRALPRLPLRGRRQDGRWTVDFEECLKD\SPRFRAAL
	1		EEVEGDVAELELKL\DKLVKLCIA\MIDTGKAFCVANKQFMNGI
		i .	RD\LAQNS\NNDA\VVETKFAPSFLDSLQEMINFHTIL/L*PNS
1	1	ŀ	1 ' = ' '
			EIN*GHSFQNFVKEDLRKFKDAKKQFENSQ*KRKKIALVKNAPV
-	ļ		PSRPASLEL*KPPNILTATRKCFRHIALDYVLQINVLQSKRRSE
Ì	1		ILKSMLSFMYAHLAFFHQGYDLFSELGPYMKDLGAQLDRLVGDA
			AKEKREMEQKHSTIQQKDFSRDDSKLKYNVDAANGIVMEGYLFK
			RASNAFKTWNRRWFSIQNNQVVYQKKFKDNPTVVVEDLRLCTVK
		1	
	1	1	HCEDIERRFCFEVVSPTKSCMLQADSEKLRQAWIKAVQTSI\AT
			AYREKDDESEKLDKKSSPSTGSLDSGNESKEKLLKGESALQRVQ
	l l		CIPGNASCCDCGLADPRWASINLGITLCIECSGIHRSLGVHFSK
1	ļ		VRSLTLDTWEPELLKLMCELGNDVINRVYEANVEKMGIKKPQPG
İ	1	ľ	QRQEKEAYIRAKYVERKFVDKIFL*SLSPP\EQQKK\FVSKSSE
l.			EKRLSISKFGP\GDQVRASAQSSVRSNDSGIQQSSDDGRESLPS
	1		
1	,		TVSANSLYEPEGERQDSSMFLDSKHLNPGLQLYRASYEKNLPKM
1			AEALAHGADVNWANSEENKATPLIQAVLGGSLVTCEFLLQNGAN
1			VNQRDVQGRGPLHHATVLGHTGQVCLFLKRGANQHATDEBGKDP
1			LSIAVEAANADIVTLLRLARMNEEMRESEGLYGQPGDETYQDIF
1			RDFSQMASNNPEKLNRFQQDSQKF
5840	600	2610	KHLHLPROHLTTLWOISSPRWRSPORAFMSALSKTOTOSAPALO
5840	698	3610	
1	1		GLSSLLQSVTGNPVPASEAASQSTSASPANTTVYTIKGRNLPSS
1	1		AQPFIPKSFNYSPNSSTSEVSSTSASKASIGQSPGLPSTAFKLP
1	1		SNTKGFTATHNTSPAAPPTEVTICQSSEVSKPKL\ESESTSPSL
1	1		\EMKIHNFLKGNPGFSVA*NLKHPNPAGSLGSSAPSESHPSDFO
			RGPTSTSIDNIDGTPVRDERSGTPTQDEMMDKPTSSSVDTMSLL
I	1		<u> </u>
1			SKIISPGSSTPSSTRSPPPGRDESYPRELSNSVSTYRPFGLGSE
1	1		SPYKQPSDGMERPSSLMDSSQEKFYPDTSFQEDEDYRDFEYSGP
		1	PPSAMMNLQKKPAKSILKSSKLSDTTEYQPILSSYSHRAQEFGV
1		1	KSAFPPSVRALLDSSENCDRLSSSPGLFGAFSVRGNEPGSDRSP
1	1		SPSKNDSFFTPDSNHNSLSOSTTGHLSLPOKOYPDSPHPVPHRS
}	1		LFSPONTLAAPTGHPPTSGVEKVLASTISTTSTIEFKNMLKNAS
			=
	1		RKPSDDKHFGQAPSKGTPSDGVSLSNLTQPSLTATDQQQQEEHY
1			RIETRVSSSCLDLPDSTEBKGAPIETLGYHSASNRRMSGEPIQT
			VESIRVPGKGNRGHGREASRVGWFDLSTSGSSFDNGPSSASELA
			SLGGGGSGGLTGFKTAPYKERAPQFQESVGSFRSNSFNSTFEHH
1			
1		1	LPPSPLEHGTPFQREPVGPSSAPPVPPKDHGGIFSRDAPTHLPS
			VDLSNPFTKEAALAHAAPPPPPGEHSGIPFPTPPPPPPGEHSS
1	1	l	SGGSGVPFSTPPPPPPPPVDHSGVVPFPAPPLAEHGVAGAVAVFP
			DOODO TITLE TELEVISION TO TH
			KDHSSLLQGTLAEHFGVLPGPRDHGGPTQRDLNGPGLSRVRESL

SEQ	Predicted	1.6	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
100:	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
Ī	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	sequence	\=possible nucleotide deletion,
		 	TLPSHSLEHLGPPHGGGGGGGSNSSSGPPLGPSHRDTISRSGII
1			LRSPRPDFRPREPFLSRDPFHSLKRPRPPFARGPPFFAPKRPFF
1]	PPRY
5841	1908	762	
5512	1 2000	/02	GLRLFLVLTVWPMMKPSWLSRTEFSKRLLCRTLWCQSGWSSRSY
			TRSMLKMTTSINRRSRTSTKSTRTSARPGLTATVSIGLSDSPTW
			RHCWMTARSCSGEKGGHWAPRQVGVYLLPGRVGCVSSRVSPSFP GDGLDSGLARRGSAVSALASGLVEEPMLGPPFHPTPRFKAVSAK
ł			SVEDI VSOCEMBERT PROTESTED TO THE PROTEST OF THE PR
			SKEDLVSQGFTEFTIEDFHNTFMDLIEQVEKQTSVADLLASFND
}	İ		QSTSDYLVVYLRLLTSGYLQRESKFFEHFIEGGRTVKEFCQ\QE \VEPMCKESDHIHIIALAQGLQRVHPGWBYMGPRPRAATTNPHI
1	ł	ļ	FP+GLPSPKVYLLYRPG\HYDILYKIGLGSSPLGCPGCPLLARA
			LGHCYRGFSVVVKWSYFTPFFLSHDPPPMFY
5842	307	1918	QEPTADFKLRSTCGCGREMTCPDKPGQLINWFICSLCVPRVRKL
		1710	WSSRRPRTRRNLLLGTACAIYLGFLVSQVGRASLQHGQAAEKGP
1	1		HRSRDTAEPSFPEIPLDGTLAPPESQGNGSTLQPNVVYITLRSK
1			RSKPANIRGTVKPKRRKKHAVASAAPGQEALVGPSLQPQEA\EG
1			KLML*HLGTLREQTWLRLESDPGGWCGVRE/WRAGGPDFLQPSS
1	1		RESNIRIYSESAPSWLSKDDIRRMRLLADSAVAGLRPVSSRSGA
	1		RLLVLEGGAPGAVLRCGPSPCGLLKQPLDMSEVFAFHLDRILGL
1			NRTLPSVSRKAEFIQDGRPCPIILWDASLSSASNDTHSSVKLTW
			GTYQQLLKQKCWQNGRVPKPESGCTEIHHHEWSKMALFDFLLQI
			YNRLDTNCCGFRPRKEDACVQNGLRPKCDDQGSAALAHIIQRKH
			DPRHLVFIDNKGFFDRSEDNLNFKLLEGIKEFPASAVYVLKSOH
			LRQKLLQSLFLDKGYWESQGGRQGIEKLIDVIEHRAKILITYIN
			AHGVKVLPMNE
5843	500	1453	GTARLVTCWVLHGQ*VKKPAWEPGVVWL*Q*RCRPKGWGLGAGM
1			RGSRMSQPPQCLRRAQSSCCHFMVKLLDDGTFMIPGEKVAHTSL
ì			DALVTFHQQKPIEPRRELLTQPCRQKDPANVDYEDLFLYSNAVA
-			EEAACPVSAPEEASPKPVLCHQSKERKPSAEM/RQNNHQGSHFL
1	ŀ		LPPKIPSWRDPPETLEEPQNAPRERPEGPAAAKKPPRHCELVVT
Ī			LGCPEIHGDLRPWDRKRQPRSLRGSHLGGQRLHGSLCGHISQKP
1	1		LTAPGTKRQKGPHQEGREVGQLH*GDPRGQELAPNGSESPILPG
	i		VQARAPGLGRA
5844	202	2471	FDSAVLSSINVMAVLPGPLQLLGVLLTISLSSIRLIQAGAYYGI
			KPLPPQIPPQMPPQIPQYQPLGQQVPHMPLAKDGLAMGKEMPHL
		•	OYGKEYPHLPQYMKEIQPAPRMGKEAVPKKGKEIPLASLRGEQG
			PRGEPGPRGPPGPPGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM
			PGKPGAMGMPGAKGEIGQKGEIGPMGIP*PQGPPGPHGLPGIGK
]			PGGPGLPGQPGPKGDRGPKGLPGPOGLRGPKGDKGFGMPGAPGV
			KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\OGPLGK\PGAPGEP
			GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGGKGEQGL
j i			PGLPGPPGLPGIGKPGFPGPKGDRGMGGVPGALGPRGEKGPIGA
1			PGIGGPPGEPGLPGIPGPMGPPGAIGFPGPKGEGGIVGPOGPPG
			PKGEPGLQGFPGKPGFLGEVGPPGMRGFPGPIGPKGEHGOKGVP
	,		GLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGI
			PGPKGEPGLPGPPGFPGIGKPGVAGLHGPPGKPGALGPOGOPGL
			PGPPGPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDGVKPPHAYG
	•		AKKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRONY
			NPQTGIFTCEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYD
			EYKKGFLDQASGSAVLLLRPGDRVFLQMPSEQAAGLYAGQYVHS
			SFSGYLLYPM
5845	215	2061	HASNKSASLQDKMANPKEKTAMCLVNELARFNRVQPQYKLLNER
ļ i	1		GPAHSKMFSVQLSLGEQTWESEGSSIKKAOOAVGNKALTESTLP
	ł		KPI+KPPKSNVNNNPGCITPTVELNGLAMKRG\KPAIHRPLDPK
[[1	Í	PFPNNRANYNFQVMYNQRYHCPIPKIFYVOLTVGNNBFFGEGKT
	ľ		RQAARHNAAMKALQALQNEPIPERSPONGESGKDMDDDKDANKS
]	EISLVFEIALKRNMPVSFEVIKESGPPHMKSFVTRVSVGEFSAE
			GEGNSKKLSKKRAATTVLQELKKLPPLPVVEKPK\HFFKKRPKT
	1		IVKAGPEYGQGMNPISRLAQIQQAKKEKEPDYVLLSERGMPRRR
	t		EFVMQVKVGNEVATGTGPNKKIAKKNAAEAMLLQLGYKASTNLO
L			DQLEKTGENKGWSGPKPGFPEPTNNTPKGILHLSPDVYQEMEAS
		l	- THE TENED TO THE PERSON OF T

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
- 1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W-Truntonhan V-Truntonhan V-Truntonhan V-Truntonhan
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
		 	RHKVISGTTLGYLSPKDMNQPSSSFFSISPTSNSSATIARELLM
ĺ		1	NGTSSTAEAIGLKGSSPTPPCSPVQPSKQLEYLARIQGFQVHYC
1	1		DRQSGKECVTCLTLAPVQMTFHAIGSSIEASHDQV*YATAILLC
			YGPARKWKAIKMEAMCAHAALLSLIHYLLAPSARLEKSKLFALG
			N.
5846	1126	456	FSKLIMKTFIIGISGVTNSGKTTLAKNLQKHLPNCSVISQDDFF
	ĺ		KPESEIETDKNGFLQYDVLEALNMEKMMSAISCWMESARHSVVS
			TDQESAEEIPILIIEGFLLFNYKPLDTIWNRSYFLTIPYEECKR
			RRSTRVYQPPDSPGYFDGHVWPMYLKYRQEMQDITWEVVYLDGT
1	İ		KSEEDLFLQVYEDLIQELAKQKCLQVTA*RRNTTNPS/CK*IRK
			LQGVI
5847	2769	505	APEMEDLSSPDSTLLQGGHNLLSSASFQESVTFKDVIVDFTQEE
1			WKQLDPGQRDLFRDVTLENYTHLVSIGLQVSKPDVISQLEQGTE
			PWIMEPSIPVGTCADWETRLENSVSAPEPDISEEELSPEVIVEK
			HKRDDSWSSNLLESWEYEGSLERQQANQQTLPKEIKVTEKTIPS
			WEKGPVNNEFGKSVNVSSNLVTQEPSPEETSTKRSIKQNSNPVK
			KEKSCKCNECGKAFSYCSALIRHORTHTGEKPYKCN*/CVEKAR
1	}		SRSENLINHQRIHTGDKPYKCDOCGKGFIEGPSLTOHORIHTGR
			KPYKCDECGKAFSQRTHLVOHORIHTGEKPYTCNECGKAFSODG
			HFMEHQKIHTGEKPFKCDECDKTFTRSTHLTOHOKIHTGEKTVK
]		CNECGKAFNGPSTFIRHHMIHTGEKPYECNECGKAFSOHSNITO
1			HQKTHTGEKPYDCAECGKSFSYWSSLAOHLKIHTGEKPYKCNEC
1			GKAFSYCSSLTQHRRIHTREKPFECSECGKAFSYLSNLNOHOKT
1			HTQEKAYECKECGKAFIRSSSLAKHERIHTGEKPYOCHECGKTE
			SYGSSLIQHRKIHTGERPYKCNECGRAFNONIHLTOHKRIHTGA
ŀ			KPYECAECGKAFRHCSSLAQHQKTHTEEKPYOCNKCEKTFSOSS
ĺ			HLTQHQRIHTGEKPYKCNECDKAFSRSTHLTOHORIHTGEKPVK
			CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN
5848	22	2061	KHQRLHPGI
3313		2961	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK
			GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL
			DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG
			YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV
1 1			GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL
1 !		•	VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV
! [SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY
1	İ		PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA
			SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN
ł i		i	APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD
			TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ
			APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL
1			CSVPTRALLLSTYIKFVNLFPEVKPTIQDVLRSDSQLRNADVEL
]]	ĺ		QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK
			GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG
'			LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA
			RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL
		1	NFTPTLICSDDLQPNLNLQTKPVDPTVEGGAOVOOVVNIECUSD
			FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASODERO
			RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLERUDD
		[NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV
6040		<u> </u>	SQRLCELLSAQF
5849	3545	1895	KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ
		}	P*DPCMSLSPPCFTEEDRFSLEALOTIHKOMDDDKDCGTEVERS
ľ	1	1	DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVLING
			TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI
		1	COL KI CDDCHDOW OF MAY DIME DOOR
		i	SQUATSDASHAQALQLKALDVVLFGPLTRPPHNWMKDFIJ.TVST
ē		ļ	SQLKISDRSHRQKLQLKALDVVLFGPLTRPPHNWMKDFILTVSI VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQER
=		. 1	VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQER LEKAQEENRNVAVEKQNL+RKMMDEINYAKEEACRLRELREGAE
÷			VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQER LEKAQEENRNVAVEKQNL*RKMMDEINYAKEEACRLRELREGAE CELSRRQYAEQELEQVRMALKKABKEFELRSSWSVPDALOKWLO
-			VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQER LEKAQEENRNVAVEKQNL+RKMMDEINYAKEEACRLRELREGAE

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Clutaria haid E Phanalala in a care
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	· ·		H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			AHSSSLDEVDHKILEAKKALSELTTCLRERLFRWQQIEKICGFQ
			IAHNSGLPSLTSSLYSDHSWVVMPRVSIPPYPIAGGVDDLDEDT
	1		DDIVCOEDCEMY ADDOCT ADDOCT COORDOL COO
			PPIVSQFPGTMAKPPGSLARSSSLCRSRRSIVPSSPQPQRAQLA
1			PHAPHPSHPRHPHHPQHTPHSLPSPDPDILSVSSCPALYRNEEE
1			EEAIYFSAEKQWEVPDTASECDSLNSSIGRKQSPP/SKPRDIPN
			IIS/DERYQEMRCP*RIPSGGIL
5850	3	1895	KAVLNFSASGSVISLTGSNPMHDASMWHLKKNGIIVYLDVPLLN
			LICRLKLMKTDRIVGQNSGTSMKDLLKFRRQYYKKWYDARVFCE
}			SGASPEEVADKVLNAIKRYQDVDSETFISTRHVWPEDCEQKVSA
1		1	EFFIEAVIEGLASDGGLFVPAKEFPKLSCGEWKSLVGATYVERA
1			QILLERCIHPADIPAARLGEMIETAYGENFACSKIAPVRHLSGN
1			QFILELFHGPTGSFKDLSLQLMPHIFAQCIPPSCNYMILVATSG
			DTGSAVLNGFSRLNKNDKQRIAVVAFFPENGVSDFQKAQIIGSQ
1			DIGSAVENGES STEERANDROKTAVVAFFPENGVSDFQKAQIIGSQ
Ì			RENGWAVGVESDFDFCQTAIKRIFNDSDFTGFLTVEYGTILSSA
1			NSINWGRLLPQVVYHASAYLDLVSQGFISFGSPVDVCIPTGNFG
1			NILAAVYAKMMGIPIRKFICASNQNHVWTDFIKTG\HYDLRGKB
			N*AQTFFTVQ*IFLPNLSNLERHLHLMANKDGQLMTELFNRLES
			QHHFQIEKALVEKLQQDFVADWCSEGECLAAINSTYNTSGYILD
1			PHTAVAKVVADRVQDKTCPVIISSTAHYSKFAPAIMQALKIKEI
1			NETSSSQLYLLGSYNALPPLHEALLERTKQQEKMEYQVCAADMN
1			VLKSHVEQLVQNQFI
5851	3120	1802	RCYLQFLALLLTSTSARAAAAIAAAEEPAGSPSVMTRAGDHNRQ
			RGCCGSLADYLTSAKFLLYLGHSLSTWGDRMWHFAVSVFLVELY
			CNCLLI TANYCI MACCHINI CATTORININA PARTICIPATI
1			GNSLLLTAVYGLVVAGSVLVLGAIIGDWVDKNARLKVAQTSLVV
			QNVSVILCGIILMMVFLHKHELLTMYHGWVLTSCYILIITIANI
			ANLASTATAITIQRDWIVVVAGEDRSKLANMNATIRRIDQLTNI
i			LAPMAVGQIMTFGSPVIGCGFISGWNLVSMCVEYVLLWKVYQKT
			PALAVKAGLKEEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIH
			ELEHEQEPTCASQMAEPFRTFRDGWVSYYNQPVF/LGWHGSCFP
i	ĺ		LYDCPGL*LHHHRVRLHSGTEWFHPQYFDGSISYNWNNGNCSFY
			LATSKMWFGSDRSDLRIGTAFLFDLVCDLCIHAWKPPGLVRFSF
5852	1	422	KTTFPSSLCPLRQLPEVRGYSGQPLTDPLISLCRSHKCRGKGWG
			SSSYPSLPALLRARSAPGHCTHRSCGPEWRIDSISRLEMQGARR
	1		SGWAQAQPTILLLVPRLRKSLPSIWG/SLMGPFITSGPG/WFRQ
			VVERTCCDU+UI DEECDRUGGAADDGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
			YYFFISGRH*VLFTESDPYYVAMDFGGHGLSSHYSPGVPYYLQT
1			FVSBIRRVVAGKKQSVYFRRCGGCSRAPPLITGGGVGSRKQRWP
FOES	000		ESGAWALAPGLPAIHGRSWES
5853	223	1346	RLLGLSRVKGLHGPAASAWISDPETRGDPGGPWGMWRGSDLRPR
1			PVSLTGLTLVCK*AAQGPQV\HSVKLCFGLGG\PCLL\FPIFRP
			LLLHPRRPRLHPGTRGVAVEPHALRVVHVAHGEEAGIRAAGPGH
			GGVEIPQG/VGSLGARRGLRPSRPSSRHRNRVPAPPPGRPLATP
			HRRRFPPDPALTCPGLGQDQGPREQQKQGSGRHDTILGDWGESE
1			SRWVRGNFRTGTAATLIGFSRNPTLNGSENWGSLVSIQEEGPDT
			GWEREKRNPAEMGNPQRWASPIHTPPLGPEILRAMPEALRAMPE
			ALGLRPDPATSVPSALS/QTF/PESWPRSCLRNQGETLGMGPVP
	į į		LSSLCITESPSQNWTPCLLLLTCPRGLF
5854	86	938	
5551		٥٤٥	KGRNTAPEKKGAALNNRENASS*NGY/SRWKQDIRRIENHIIQE
			LKHLCAMIKRVLLERLENTRKLRELTEGRTLDWPQNRITEVSAK
			RQIVTEYREKGKRN*EEKKRDLEGRSRRYNLCIIGIPETEDRAS
ľ			GAETIKDLLE/ENFPELKNELDLQMEKAHRIPLKFNEKKAASRH
1			IRVTFL/KFQRRNILQASSQRKQVTYKGAKVRLTSDFSPAILNA
			RRQW/N/PISRVLRENNFEPRIIYSAKLSFLYKGNWKTFLDIQG
1			LGKYINQELSLKILLKDLLQLTENLN
5855	536	2391	LRSYGCKAPSRISHLHK\FLFLLLPSLLMGYSESPPPITDSWAP
			FISLTHHVLSQSQSPLSSNCWICLSTHTQ*FTALPADLLTWTQS
[.			MUCLUICAT VIDEL VECETATOR ALCONOMIC TOTAL A PROPERTY AND THE MINISTER AND
[]			NVSLHISYLATPFLADSFLKPV/L*PGNSAKHLSFKLSSLSMVS
[GRAVALLHLIASGLTSIQTNTASSKPPIWGY\LSTQTSFISPPP
			LCLSRTYPNPAHATMVGQVPQSLCGLIFTL/RTPCRPSILHPNY
1		ļ	KIISTSAWQKVLCPSGSPTIHTSLHLTTGSSFLSFHPIPGFPAA
L			NSALYVSSLKGPPGKNVTIPSPVTGT*QPPHRGSN/RLTVDKDN

Doginning Coction Coction Coction Coction Corresponding Coffict Samino acid Security Secur	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Noticetide Corresponding to first maino acid residue of maino acid residue of maino acid residue of maino acid sequence Helistidine, I=Isolauvine, K-Lywine, L=Ieucine, M-Methionine, N-Apparagine, P=Proline, Q-Glutamine, R-Asignine, S-Serine, T-Throndine, V-Valine, maino acid sequence S-Serine, T-Throndine, V-Valine, M-Typtophan, Y-Tyrosine, X-Unknown, *-Stop Codon, /-possible nucleotide deletion, \ \ \ \ \ \ \ \ \ \ \ \ \	_			
corresponding to first anino acid amino acid residue of anino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid acquence Prof. Codm. Y-Pytophan, Y-Tytosine, X-Unknown, *-Stop Codm. Y-Pytophan, Y-Tytosine, X-Unknown, *-Stop Codm. Y-Pytosine, X-Unknown, *-Stop Codm. Y-Pytosine, X-Unknown, *-Stop Codm. Y-Pytosine, X-Unknown, *-Stop Codm. Y-Pytosine, X-Unknown, *-Stop Codm. Y-Pytosine, X-Unknown, *-Stop Codm. Y-Pytosine, X-Unknown, *-Stop Codm. Y-Pytophan, Y-Tytosine, X-Unknown, *-Stop Codm. Y-Pytosine, X-Unknown, *-Stop Cod	1		5	
to first maino acid residue of amino acid residue of amino acid sequence ### Serine, T-Thronnine, V-Valine, ### Serine, T-Thronnine, ### Serine, T-Thronnine, ### Serine, T-Thronnine, ### Serine, T-Thronnine, ### Serine, T-Thronnine, ### Serine, T-Thronnine, ### Serine, T-Thronnine, ### Serine, T-Thronnine, ### Serine, T-Thronnin			1	
to first amino acid residue of amino acid residue of amino acid amino acid sequence ##Tryptophan, %=Tyrosine, X=Unknown, *=Stop Coden, %-possible nucleotide deletion, %-possible nucleotide deletion, %-possible nucleotide intertion) ##Tryptophan, %=Tyrosine, X=Unknown, *=Stop Coden, %-possible nucleotide intertion) ##Tryptophan, %=Tyrosine, X=Unknown, *=Stop Coden, %-possible nucleotide intertion) ##Tryptophan, %=Tyrosine, X=Unknown, *=Stop Coden, %-possible nucleotide intertion) ##Tryptophan, %=Tyrosine, X=Unknown, *=Stop Coden, %-possible nucleotide intertion) ##Tryptophan, %=Tyrosine, X=Unknown, *=Stop Coden, %-possible nucleotide intertion) ##Tryptophan, %=Tyrosine, X=Unknown, *=Stop Coden, %-possible nucleotide intertion) ##Tryptophan, %=Tyrosine, X=Unknown, *=Stop Coden, %-possible nucleotide intertion) ##Tryptophan, %=Tyrosine, X=Unknown, *=Stop Coden, %-possible nucleotide intertion) ##Tryptophan, %=Tyrosine, X=Unknown, *=Stop Coden, %-possible nucleotide intertion) ##Tryptophan, %=Tyrosine, X=Unknown, *=Stop Coden, %-possible nucleotide intertion) ##Tryptophan, %=Tyrosine, X=Unknown, *=Stop Coden, %-possible nucleotide intertion) ##Tryptophan, %-Tyrosine, X=Unknown, *=Stop Coden, %-possible nucleotide intertion) ##Tryptophan, %-Tyrosine, X=Unknown, *=Stop Coden, %-possible nucleotide intertion) ##Tryptophan, %-Tyrosine, X=Unknown, *=Stop Coden, %-possible nucleotide intertion) ##Tryptophan, %-Tyrosine, X=Unknown, *=Stop Coden, %-possible nucleotide intertion Composition				
amino acid residue of amino acid amino acid amino acid amino acid acquence Seguence				
main acid anino acid acquence Sequence			1	
amino acid sequence Codon, /=possible nucleotide deletion,	1			
### Requence Specific mucleotide insertion		residue of	amino acid	
FFLSERRISHIGLESQ YEVQALTGARLAGSYPT WERENTYLESH PETTINFICLISTIST, PELCOTIN YLLC LABMASGICTLY POPPIN ILPROTILISUSASISSE JIRKKARLHLITLLIGIATTARIGT GIAGITYSTISTOYOLF TURNIVERHITSTISKOROLDELIGVOY LONNRYLDLLITTEGGTCIYLOBECCE COVESGITUTAL VERLHID RABEL HOVADSWINGSSLIKHT PRAVPLEMPT LINTEG CIRLUSSE ISGRINGFIOASOKHIDN I FHILCHV*YQSLRGNH SEAPEPR 5856 173 1137 PRIMELGISAVELEYL*/VYTFILVGGIILLLIFTS INGILIYK FOULLY PEPOPSSEL VYPHOTO I PEHRIF I TITKTOGI TRILLII I TRYTONSEY SET I I YFHONAGHIGHEL PINILLIM (VANILLII I TRYTONSEY SET I I YFHONAGHIGHEL PINILLIM (VANILLII UNDROYCKSEGGABARLIVADHOTO I PEHRIF I TITKTOGI TRILLII I TRYTONSEY SET I I YFHONAGHIGHEL POPPATALE POPPATALE POPPATALE POPPATALE PHASTILESE POPPATALE POPPA		amino acid	sequence	Codon, /=possible nucleotide deletion,
PTETTNPCLSTSIPPLCDTN***LCLPANMSGTCTL/POAPTISI LLPPNOTTLISTEMS ISSSPIRMSKALINLITLATIGATIATAGE GIAGITTS ITSYQTLETTLSINTVENMSTSITSLQRQLDFL/WOV LQNMSVLDLITTESGTCTV/LQBECCOWASGIVILAVBRIMD RABEL*HQVADSWQGSSLURFPVAPPVAPPLOPLITEFILLMIGG CITNLYSEFISQRINCFTQASMQKHTDNIFPLCHV**YQSLGNIH SEAPERPR 5856 173 1137 PPLMSLIGSANPLPYL**/VVTFRLYGGITLLLLIFISIAGILYK FOUVLLYPPEQPSSSILVTENPTQGITLLLLIFISIAGILYK FOUVLLYPPEQPSSSILVTENPTQGITLLLLIFISIAGILYK FOUVLLYPPEQPSSSILVTENPTQGITLLLLIFISIAGILYK RIGGGAAAIHASDNSRISAHWEMTFISITPHARSTLSFPP RRILEGECYNNETS STRKISQCOMPSILSTSICSDDLYD PYMWK LTILDSFSTRKISQCOMPSILSTSICSDDLYD PYMWK LTILDSFSTRKISQCOMPSILSTSICSDDLYD PYMWK LTILDSFSTRKIAITPDGTHNDTWQCQYFTALSQFIKEVVSK RRILGQAAAIHASDNSRISAHWEMTFISITPHARSTLSFPP RRILEGECYNNETSSTRKISQCOMPSILSTSICSDDLYD PYMWK LTILDSFSTRKIAITPDGTHNDTWQCQYFTALSQFIKEVVSK RRILGQAAAIHASDNSRISAHWEMTFISITPHARSTLSFSPP RRILGQCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		sequence	ł	\=possible nucleotide insertion)
PTETTNPCLSTPSLPFLCDTN***LCLPANMSGTCTLVPQAPTISH LLPPNCTILISWASSSPIRMALINILITATIOLITATION GIACITTS ITSYQTLETTLSNTVERMITSITSLQRQLDFLWOVI LQNMWLDLITTESGTCTVLQEBCCCWASGTVILAVERLHD RABEL*HQVADSWQGSSLRWIPWVAPPLGPLIFLFLLMIGG CIPNLWSRFISGRINCFTQASMQKHIDNIFHLCHV**YQSLRGINH SEAPERPR 5856 173 1137 PPLMENICISANEPPLP,VVFPHLYGGIILLLLIPISIANIIYK FOUVLLYPPEQPSSSRLVYPHPYGGIILLLLIPISIANIIYK POUVLLYPPEQPSSSRLVYPHPYGGIILLLLIPISIANIIYK RYCOKOSEGSABERGUIVLGSAVLOYMISPDLDKTXILIAG RIGGGAAAIHASDNSRISAHWZMYTEISITPHRASTISPSPP MRILEGKYNKHEISKRISGCRPBISITSGDDLUPHWKX LYLDESPSTRKISGCRPBISITSGDDLUPHWKX LYLDESPSTRKISGCRPBISITSGDDLUPHWKX LYLDESPSTRKISGCRPBISITSGDDLUPHWKX LYLDESPSTRKISGCRPBISITSGDDLUPHWKX LYLDESPSTRKISGCRPBISITSGDDLUPHWKX LYLDESPSTRKISGCRPBISITSGDDLUPHWGSPTSPKPG WRAGHCYNKHEISKRIAIPPDGTHRNTWGCOYFTALEOPTIKEVVKSR MRILGKVULISVVADAWAAAVEPGPALGSEPMILGSPTSPKPG WRAGHCYNKHEISKRIAIPPDGTHRNTWGCOYFTALEOPTIKEVVKSR WRAGHCYNKHEISKRIAIPPDGTHRNTWGCOYFTALEOPTIKEVVKSR VROGENCONSTRASTIGGGRPSGGRAFALSSPTLTSRRQPHIS SPEDMAKTSSRVTIC GDSLTSEGNLODSWAGAARAASKETICSSPTUGGRPCHAGAGS PPOPVVPAHKDKSGAPPVTTGCRSISGSPVAVMERRSPLLAGGS PPOPVVPAHKDKSGAPPVTTGCRSISGSPVAVMERRSPLLAGGS PPOPVVPAHKDKSGAPPVTTGCRSISGSPVAVMERRSPLLAGGS PPOPVVPAHKDKSGAPPVTTGCRSISGSPVAVMERRSPLLAGGS PPOPVVPAHKDKSGAPPVTTGCRSISGSPVAVMERRSPLLAGGS PPOPVVPAHKDKSGAPPVTTGCRSTCATCHTSTVATP GDSLTSEGNLODSWAGAARAASKETLCTGTTGTTGTCTC DKSVMESSORCALSSPSLATTPPIKTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT		 		FFLSPKPNSLHOLPSO\TPYQALTGAALAGSYPIWENENTLSWL
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VDTRGGKSBGEASEGUYLDISEAVLDYVMTSPIDLEKTILISER RSLG\GARAHLLASDNSHISATAMYRTHESIPHMASTLPSFPP MRYLPLWCYKNKFLSYRKISQCRMPSLFISGLSDQLIPPVMKQ LYSLSPSRTKRLAIPPDGTHNDTWQCQCYFTALDGPIKEVVKSH SPEMAKTSSNVTII 5857 563 KLIGKKULVLSVVADANAAFAVEPQGPALGSEPMMLGSPTSPKPG VNAQFLPCFLMGGLPAPVTPQPRSIGGSPGVAVEMRSPLLAGGS PPQPVVPAHKDKSGAPPVRSTYDDISSPGLGSTPLTSRRQPNTS VMQSPLVGVTSTFOTGOSMSPFASIGGPTSLFSPROUTS WGSPLVGVTSTFOTGOSMSPFASIGGPTSLFSPROUTS WGSPLVGVTSTFOTGOSMSPFASIGGPTSLFSPROUTS UMMASTICNMWHIRVGNAGARKALSKORJESPMLTSPADLDPFYTQ GDSLTSEDH\LDDSWGDCTMGFLKASA\SYILL\QPAQYGGIS- NMMMSTGMWHIRVGNAGARKALSKORJESPMLTSPADLDPFYTQ GDSLTSEDH\LDDSWGDCTMGFLKASA\SYILL\QPAQYGGIS- NMMMSTGMWHIRVGNAGARKALSKORJESSINAFTHMPP LATAYKASTSDYQVISDRQTTKKODSSLVSKAMEYMMGD FRESOVPTTPQPAGGPPPPPPQPGSSKPVVAQGGGPAPEVGSAP PASSSAPPATPFTSGAPPGGSGCPGTTFPPRAVTSAPPGAPPPTT PSSGVPTTPQAGGPPPPPAVPGCGGPGPGGRGKMM GGPKPGGGGGISTTGGHPKPPHRGGGEPRGGCGMHPPYTQGHHG GPPPGGGGGGISTTGGHPKPPHRGGGEPRGGCGMHPPYTQGHHG GGPKPGGGGGISTTGGHPKNPPHRGGEPRGGCTGHKGKMG GGPKPGGGGGGSKEKIGGRGGFANSLSLFLALSSCVISPP MFPQ*NCMGRKPPPNLGPHLKGAVCNRWDDEWEGPTGKGHCN FAS ALA*NCPKBEGG*YTP*GGGCPCSSLFSTKAKDSEPTILESR ALA*NCPKBEGG*YTYSGDFTCHSVSTTSGGGVYKKETSPLLR RTFIGKTTPHETINKFSSNLSASPSYLARSLADVPREYGSSGFTV EVSFAVENCDSGSRYYYSDMFFDGGKPAFTGLASCSVGNGSGFTV EVSFAVENCDSGSRYYYSDMFFDGKRPLGDEAHEDVRYYEYN HDLPQRMPDGGRHASGIGGVAATSLGALTVSEDLPLPPGWS VDWTMGRKYYIHMTTHMSIPLEREGLPCWBRVESSSFFGT YYVDHTNKKAQY\RHCAPTTSV*ATTSALDVPREYGSSGFTV YVDHTNKKAQY\RHCAPTSV*ATTSALDVPREYGSSGFTV YVDHTNKAQY\RHCAPTTSV*ATTSACHLAPPTTIOT SWEKHGKSSGTVAVHHPQYGFSVGGEYGGRVLPNYSLINATT TLINIGFSBGKKYICKAVTPLANGARVSKCLIEVMETITQI SWEKHGKSSGTVAVHHPQYGFSVGGEYGGRVLPNYSLINATT TLINIGFSBGKKYICKAVTPLANGARVSKCLIEVMETITQI SWEKHGKSSGTVAVHHPQYGFSVGGEYGGRVLPNYSLINATT TLINIGFSBGKKYICKAVTPLANGARVSKCLIEVMETITQI SWEKHGKSSGTVAVHHPQYGFSVGGEYGGRVLPNYSLINATT TLINIGFSBGKKYICKAVTPLANGARVSKCLIEVMETITQI SWEKHGKSSGTVAVHHPQYGFSVGEYGGRVLVKRGLECHTCVCHPLETT TLINIGFSBGKKYICKAVTPLANGARVYLCEPHYDFPLLLLFP NETATIIGQYTHFPLANGARVYLCEPHYLANGARVYLCEPHYLL PSPLSTLIATITGPTHYPHTTTHNSCPLAGGCGCPCCGWWYKC VHTPTCDDSSGKYICKANAATASDALAFENY	ļ		1	FODVLLYFPEOPSSSRLYVPMPTGIPHENIFIRTKDGIRLNLIL
VDTRGGKSBGEASEGUYLDISEAVLDYVMTSPIDLEKTILISER RSLG\GARAHLLASDNSHISATAMYRTHESIPHMASTLPSFPP MRYLPLWCYKNKFLSYRKISQCRMPSLFISGLSDQLIPPVMKQ LYSLSPSRTKRLAIPPDGTHNDTWQCQCYFTALDGPIKEVVKSH SPEMAKTSSNVTII 5857 563 KLIGKKULVLSVVADANAAFAVEPQGPALGSEPMMLGSPTSPKPG VNAQFLPCFLMGGLPAPVTPQPRSIGGSPGVAVEMRSPLLAGGS PPQPVVPAHKDKSGAPPVRSTYDDISSPGLGSTPLTSRRQPNTS VMQSPLVGVTSTFOTGOSMSPFASIGGPTSLFSPROUTS WGSPLVGVTSTFOTGOSMSPFASIGGPTSLFSPROUTS WGSPLVGVTSTFOTGOSMSPFASIGGPTSLFSPROUTS UMMASTICNMWHIRVGNAGARKALSKORJESPMLTSPADLDPFYTQ GDSLTSEDH\LDDSWGDCTMGFLKASA\SYILL\QPAQYGGIS- NMMMSTGMWHIRVGNAGARKALSKORJESPMLTSPADLDPFYTQ GDSLTSEDH\LDDSWGDCTMGFLKASA\SYILL\QPAQYGGIS- NMMMSTGMWHIRVGNAGARKALSKORJESSINAFTHMPP LATAYKASTSDYQVISDRQTTKKODSSLVSKAMEYMMGD FRESOVPTTPQPAGGPPPPPPQPGSSKPVVAQGGGPAPEVGSAP PASSSAPPATPFTSGAPPGGSGCPGTTFPPRAVTSAPPGAPPPTT PSSGVPTTPQAGGPPPPPAVPGCGGPGPGGRGKMM GGPKPGGGGGISTTGGHPKPPHRGGGEPRGGCGMHPPYTQGHHG GPPPGGGGGGISTTGGHPKPPHRGGGEPRGGCGMHPPYTQGHHG GGPKPGGGGGISTTGGHPKNPPHRGGEPRGGCTGHKGKMG GGPKPGGGGGGSKEKIGGRGGFANSLSLFLALSSCVISPP MFPQ*NCMGRKPPPNLGPHLKGAVCNRWDDEWEGPTGKGHCN FAS ALA*NCPKBEGG*YTP*GGGCPCSSLFSTKAKDSEPTILESR ALA*NCPKBEGG*YTYSGDFTCHSVSTTSGGGVYKKETSPLLR RTFIGKTTPHETINKFSSNLSASPSYLARSLADVPREYGSSGFTV EVSFAVENCDSGSRYYYSDMFFDGGKPAFTGLASCSVGNGSGFTV EVSFAVENCDSGSRYYYSDMFFDGKRPLGDEAHEDVRYYEYN HDLPQRMPDGGRHASGIGGVAATSLGALTVSEDLPLPPGWS VDWTMGRKYYIHMTTHMSIPLEREGLPCWBRVESSSFFGT YYVDHTNKKAQY\RHCAPTTSV*ATTSALDVPREYGSSGFTV YVDHTNKKAQY\RHCAPTSV*ATTSALDVPREYGSSGFTV YVDHTNKAQY\RHCAPTTSV*ATTSACHLAPPTTIOT SWEKHGKSSGTVAVHHPQYGFSVGGEYGGRVLPNYSLINATT TLINIGFSBGKKYICKAVTPLANGARVSKCLIEVMETITQI SWEKHGKSSGTVAVHHPQYGFSVGGEYGGRVLPNYSLINATT TLINIGFSBGKKYICKAVTPLANGARVSKCLIEVMETITQI SWEKHGKSSGTVAVHHPQYGFSVGGEYGGRVLPNYSLINATT TLINIGFSBGKKYICKAVTPLANGARVSKCLIEVMETITQI SWEKHGKSSGTVAVHHPQYGFSVGGEYGGRVLPNYSLINATT TLINIGFSBGKKYICKAVTPLANGARVSKCLIEVMETITQI SWEKHGKSSGTVAVHHPQYGFSVGEYGGRVLVKRGLECHTCVCHPLETT TLINIGFSBGKKYICKAVTPLANGARVYLCEPHYDFPLLLLFP NETATIIGQYTHFPLANGARVYLCEPHYLANGARVYLCEPHYLL PSPLSTLIATITGPTHYPHTTTHNSCPLAGGCGCPCCGWWYKC VHTPTCDDSSGKYICKANAATASDALAFENY	ĺ		1	IRYTGDNSPYSPTIIYFHGNAGNIGHRLPNALLMLVNLKVNLLL
RSIG/GARAIHLASIDNSHRISAIMURTFISIPMYMKK NRYLPIMCKINKELSYRKISCKRMSLISICSLODLIPPYMKK LYELSPSRTKRLAIPPDGTHNDTWQCQYFTALEQPIKEVVKSH SPERMAKTSSNUTII 5857 563 KLIGKULVLSVVADANAAFAVEPQGFALGSEPMMLGSPTSPKPG VNAQFLPGFLMGDLRAPVTPQFRSIGGSEPMMLGSPTSPKPG VNAQFLPGFLMGDLRAPVTPQFRSIGGSEPMMLGSPTSPKPG VNAQFLPGFLMGDLRAPVTPQFRSIGGSEPVMLGSPTSPKPG VNAQFLPGFLMGDLRAPVTPQFRSIGGSEPVGVMEMRSPJLLAGGS PPQPVVPARHKDKSGAPPVRSITYDISSPGSTPLTSRRQPNIS VMGSPLVGVTSTPGTGGSMFSPASIGQPRKTTLSPAQLDPFYTO GDSLTSEBH/LDDSWGDCLMGFLKASAS, SYLLAYGRSIS- NMMSNTGNWMHIRVQSKLQARKALSKDGRIFGESIMIGVKPGI DKSVMSSSDRCALSSPSLAPTPPIKTLATPTQGSSTPMISTMAR 5858 355 1419 PPHQPAANSTSKPQCQOFPFPPDSSKPVVAQGFGBPAGVGSAP GRPKGGGGGGGSSPGTSPGGNFTPHRGGGEPFAVISAPPGAPPTT PSSGVPTTPPQAGGPPFPPDSSRPVVAQGFGBPGVGSAPPTT PSSGVPTTPPQAGGPPPPPDAVPGPGGPGFGGGGHBPPHQGHH GPPPGGPGGRSEEKISGPRGFKANLSLLRRPGEKTYTTQRCPC LLGIYLLISRMMSRRLPAKIMENGKPLSTTKAKDSEFIKLDSR ALA-NCPKEELG-YTPY-GGRQLDSSLPFTHACDPLSCGVIFSPP MFPQ*NCMGKPPRPNLGPHLKGAVCNRWDDFPGGTKGRGCUN FAS 5859 307 1503 GGSSASPRASSRMLSRKKTNNEVSKPAEVGKYVKKETSPLLR HDLPGRMPQNQGRBASGIGGVAATSLGALTHACDPLSCGVIFSPP MFPQ*NCMGRHSPTIRRGTPTSTGDGVVSRNQSFL RTPIQRTPHEIMRRESNRLSAPSYLARSLADVPREVGSSQSFVT EVSPAVENGDSGSTYYSDMFPTGGRRAPLGDBAABEDRYTYETN HDLPGRMPQNQGRBASGIGVXAATSLGALTHAGSBDLPLPPGMS VDMTMRGRKYYIDHTNTTHHSRIPLERGGLPGWBRVESSSFGT YYUDHTNKKAQY\RHCATYTCSV-4STTSCHLAFS-GLADUTREVGSCQMYAD- YQMMLKLLPMFLEGGSKYICAM-TPLCANGACHLAFLED- YQMMLKLLPMFLEGGSKYICAM-TPLCANGACHLAFLED- YQMMLKLLPMFLEGGSKYICAM-TPLCANGACHLAFLED- TIRNIEGFBLGGGKLAGLSASLLLGAGLLLQPPTPPPLLLLLFP LLLEFSRLGGALAGPIIVERPHVTAVMGNVSLKCLIEVMETTIQI SWEKHGKSSGTVAVHHPQYGFSVGGEYGGRVLPKNYSLINDATI TLINIIGFSBEGKYICAM-TPLCANGASTVTULPPTYSLIK PDSLIDGGNETVAAICIAATGRVAHIDMEDGLGEMESTTTSF NETATIIGVKALPPTFARGRRTTCVVMFPLCANGASTVTULPPTYSLIK PDSLIDGGNETVAAICIAATGRVAHIDMEDGLGEMESTTTSF NETATIIGVKALPPTFAFRGRRTTCVVMFPATSRCDLATEP KIA PSPLSTLYATITYDPSLYTYPLPATHYSUVICKVTNNSGSKEVTQX VMPTTCDDSSLYTYPLPALAQFONASSTATATSRDLATEP KIA PSPLSTLYATITYDPSLYTYPLTPDMVGCGGCOGGCUNAVNCC CYRRRYTFRGDYFANNYLPFDMVGCGFOUGCOGGCUNVYNC KKENNFPUNDLIERGGRAFGFOUNDELDRAFG	1			
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NETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDI QYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDG QWPDGLLASDNTLHFVHPLTFNYSGVYICKVT\NSPGSKEVTQK VHPTFQDPSLPTYPPLPALQFQWASPSTA*TSRD\LATEP*KIA PSPLSTL\ATIKGWTQLPTIIA*CSGVGALFIV\LVKCFGLGIF CYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDBLDPYPDSV KKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDL KMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV 5861 2051 1305 EVCACVQAFWLVASSGDDSQGDKCGCEVGSWVGSMRVVMARLL SEGEQGIPTACAAFAQQPAG/BPRRGLAGVGEGGPQCSWVNYRC TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML*DVHRRVI				
QYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDG QWPDGLLASDNTLHFVHPLTFNYSGVYICKVT\NSPGSKEVTQK VHPTFQDPSLPTYPPLPALQFQWASPSTA*TSRD\LATEP*KIA PSPLSTL\ATIKGWTQLPTIIA*CSGVGALFIV\LVKCFGLGIF CYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDELDPYPDSV KKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDL KMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV 5861 2051 1305 EVCACVQAFWLVASSGDDSQGGDKCGCEVGSWVGSMRVVMARLL SEGEQGIPTACAAFAQQPAG/BPRRGLAGVGEGGPQCSWVNYRC TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML*DVHRRVI	1			
QWPDGLLASDNTLHFVHPLTFNYSGVYICKVT\NSPGSKEVTQK VHPTFQDPSLPTYPPLPALQFQWASPSTA*TSRD\LATEP*KIA PSPLSTL\ATIKGWTQLPTIIA*CSGVGALFIV\LVKCFGLGIF CYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDBLDPYPDSV KKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDL KMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV 5861 2051 1305 EVCACYQAFWLVASSGDDSQGGKCGCEVGSWVGSMRVVMARLL SEGEQGIPTACAAFAQQPAG/BPRRGLAGVGEGGPQCSWVNYRC TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML*DVHRRVI	1			
VHPTFQDPSLPTYPPLPALQFQWASPSTA+TSRD\LATEP+KIA PSPLSTL\ATIKGWTQLPTIIA+CSGVGALFIV\LVKCFGLGIF CYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDELDPYPDSV KKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDL KMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV 5861 2051 1305 EVCACVGAFWLVASSGDDSQGGKCGCEVGSWVGSMRVVMARLL SEGEQGIPTACAAFAQQPAG/BPRRGLAGVGEGGPQCSWVNYRC TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML+DVHRRVI				~
PSPLSTL\ATIKGWTQLPTIIA+CSGVGALFIV\LVKCFGLGIF CYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDBLDPYPDSV KKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDL KMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV 5861 2051 1305 EVCACVQAFWLVASSGDDSQGDKCGCEVGSWVGSMRVVMARLL SEGEQGIPTACAAFAQQPAG/EPRRGLAGVGEGGPQCSWVNYRC TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML+DVHRRVI	1			1 -
CYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDBLDPYPDSV KKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDL KMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV 5861 2051 1305 EVCACVQAFWLVASSGDDSQGDKCGCEVGSWVGSMRVVMARLL SEGEQGIPTACAAFAQQPAG/EPRRGLAGVGEGGPQCSWVNYRC TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML*DVHRRVI	1		1	1
KKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDL KMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV 5861 2051 1305 EVCACVQAFWLVASSGDDSQGDKCGCEVGSWVGSMRVVMARLL SEGEQGIPTACAAFAQQPAG/EPRRGLAGVGEGGPQCSWVNYRC TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML*DVHRRVI	1	1		1
KMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV 5861 2051 1305 EVCACVQAFWLVASSGDDSQGGDKCGCEVGSWVGSMRVVMARLL SEGEQGIPTACAAFAQQPAG/BPRRGLAGVGEGGPQCSWVNYRC TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML*DVHRRVI	1			
5861 2051 1305 EVCACVQAFWLVASSGDDSQGGDKCGCEVGSWVGSMRVVMARLL SEGEQGIPTACAAFAQQPAG/BPRRGLAGVGEGGPQCSWVNYRC TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML*DVHRRVI	1	1		KKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDL
5861 2051 1305 EVCACVQAFWLVASSGDDSQGGDKCGCEVGSWVGSMRVVMARLL SEGEQGIPTACAAFAQQPAG/BPRRGLAGVGEGGPQCSWVNYRC TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML*DVHRRVI				KMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV
SEGEOGIPTACAAFAQQPAG/BPRRGLAGVGEGGPQCSWVNYRC TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML*DVHRRVI	5861	2051	1305	
TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML*DVHRRVI				
	1			
LE*KMINSGSPAKUNAPSQKFCTMLSEGLKFGISPSWKEALYGCH	Į.			1 - 1
	L	<u> </u>	L	DE-KENNOGSPAKUNAPSQKFCINLSEGLKFGISPSWKBALYGCH

0770	Dona dd abad	Predicted end	I have a gold assessed containing signal montion
SEQ	Predicted		Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł		Bequence	
	sequence	·	\=possible nucleotide insertion)
			A .
5862	1556	483	PPFQLIMGEIKVSPDYNWFRGTVPLKKIIVDDDDSKIWSLYDAG
1	1		PRSIRCPLIFLPPVSGTADVFFRQILALTGWGYRVIALQYPVYW
	1		= ::
			DHLEFCDGFRKLLDHLQLDKVHLFGASLGGFLAQKFAEYTHKSP
1	}	į	RVHSLILCNSFSDTSIFNQTWTANSFWLMPAFMLKKIVLGNFSS
			GPVDPMMADAIDFMVDRLESLGQSELASRLTLNCQNSYVEPHKI
1			RDIPVTIMDVFDQSALSTEAKEEMYKLYPNARRAHLKTGGNFPY
1	l .		·
	1	i	LCRSAEVNLYVQIHL/R/RNSMEPNTRPLTHQWSVPRSLRCRKA
			ALASARRSSSVSLAVNDELTRCVLV*SVASAPVSRPFPSGSSGS
1	1		PVLTVSGK
5863	2714	249	PFPSRGSLPLAAPREDTMGPLMVLFCLLFLYPGLADSAPSCPON
		1	VNISGGTFTLSHGWAPGSLLTYSCPQGLYPSPASRLCKSSGQWQ
-			
1	1		TPGATRSLSKAVCKPVRCPAPVSFENGIYTPRLGSYPVGGNVSF
1			ECEDGFI\LRGSPVRQCRPNGMWDGETAVCDNGAGHCPNPGISL
1	1		GP\VRTGFRFGHGDKVRYRCSSNLVLTGSSERECQGNGVWSGTE
J	}		PICROPYSYDFPEDVAPALGTSFSHMLGATNPTOKTKESLGRKI
			QIQRSGHLNLYLLLDCSQSVSENDFLIFKESASLMVDRIFSFEI
1	I		1
1			NVSVAIITFASEPKVLMSVLNDNSRDMTEVISSLENANYKDHEN
			GTGTNTYAALNSVYLMMNNQMRLLGMETMAW\QEIRHAIILL\T
	i		DGK\SHMGGSPKTAVDHIREILNINQKRNDYLDIYAIGVGKLDV
			DWRELNELGSKKDGERHAFILODTKALHOVFEHMLDVSKLTDTI
		i	CGVGNMSANASDQERTPWHVTIKPKSQET\C\RGALISDQWVLT
		1	
			AAHCFRDGNDHSLWRVNVGDPKSQWGKEFLIEKAVISPGFDVFA
1			KKNQGIL\EFYGD\DIALL\KLAQKVKM\STHCQGPSCLP\CTM
			\EANLGFLRETFKGSTCR\DHENEL/VWNKQSV\PAHF\VAL\N
			GSKLEHLTLRMGVEWTSCCRGLSPKKKTM\FPNLT\DVRE\VVT
ł	ŀ	İ	D\QFL\CS\GPQEDESP\CK*E\SGGA\VFLERRFRLSAGGVWC
1			SWGL\YNP\CLGSA\DKNSPKKGPSVAKVPPPTR/DFHIN\LFP
1	1		Q*SPWLRQHPGGMS*IFLPLLANGHLSPFACPARICRPLHFLPS
1			EWATLRTL
5864	173	1013	PLISVPQSLISLPQPLLCFPGGQEPSAPSPCLYSFLWACSFTMG
3004	1/3	1 1013	
			KLPPSIPPSSPLACVLKNLKPLQLTPDLKPKCLIFFCNTAWPQY
	1]	KLDNDSK*PENGTFEFSILQVLDNSCHKMGKWSEVPDVQAFF\S
	1		HWSLPSLCSQC/GLIPNLSSFSPFCSFG/PPPQVPSP/TESFFS
1			MDSSDLPPSPQAAPRQAEPGPNSHLASAPPPYNPFITSPPHTWS
		i	
1			SLQFHSVTSPPPPAQQFTLKKVAGAKGIVKVSAPFSLSQIR*RL
			GSFSSNIKIQPSSWLIWQQP
5865	568	1684	CLPGPRWGEGWRAGHTIVGCIFFKTAIISHFKGGMYLCVCMCTC
			LSVCVCVQVGSWICV/CVSMCACVSLCTC\ICRCISMYTREHAC
1		{	ACTRV*VYMCMS/VCTCVSTCIDVRVCAHVCVYMCLCLGYA*AC
			TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI
			/CVYVCVLCVWACMRMSTCVWLVYG*ACTCVWMHM/CSCTCR/C
1			VHVCCMSMHACECLCVYLHICGCAGTRRWWAGSARGSRSCSRLP
1		Į.	CWAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW
		1	GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC
			GGRGWVCAPPLNGPOCCCFSIKPELKAKKKK
F 2 5 5	 		
5866	98	3197	ARPEVPAPPAWLSRRGAAKMGDKKDDKDSPKKNKGKERRDLDDL
	1		KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA
1	1	1	LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED
İ			DPSGDNLYLGIVLAAVVIITGCFSYYOEAKSSKIMESFKNMVPO
1	1		1
			QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC
	1		KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA
			RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIBHFIQLITGV
1	· ·	1	AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV
1	1	!	CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM
			_ 1
1]	J	TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF+H/LLGFC
			NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE
			RNKKVAEIPFNSTNKYOLSIHETEDPNDNRYLLVMKGAPERILD
1			RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL
			-
1		[PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG
		L	KCRSAGIKVIMVTGDHPITAKAIAKGVGIIFEGNETVEDIAARL
			

SEQ	Predicted	Predicted end	Amino and assent contribution
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	
-	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of		S=Serine, T=Threonine, V=Valine,
1		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			NIPVSQVNPRDAKACVIHGTDLKDFTSEQIDEILQNHTEIVPAR
			TSPQQKLIIVEGCQRQGAIVAVTGDGVNDSPALKKADIGVAMGI
			AGSDVSKQAADMILLDDNFASIVTGVBEGRLIFDNLKKSIAYTL
			TSNIPEITPFLLFIMANIPLPLGTITILCIDLGTDMVPAISLAY
]			EAAESDIMKRQPRNPRTDKLVNERLISMAYGQIGMIQALGGPFS
	ł		YFVILAENGFLPGNLVGIRLNWDDRTVNDLEDSYGQQWTYEORK
			VVEFTCHTAFFVSIVVVQWADLIICKTRRNSVFQQGMKNKILIF
			GLFEETALAAFLSYCPGMDVALRMYPLKPSWWFCAFPYSFLIFV
			YDEIRKLILRRNPGGWVEKETYY
5867	3	1485	LPGRRARGGRGLGWPPAQALDGSRMGKAKVPASKRAPSSPVAKP
			GPVKTLTRKKNKKKKRFWKSKAREVSKKPASGPGAVVRPPKAPE
		1	DFSQNWKALQEWLLKQKSQAPEKPLVISQMGSKKKPKIIQQNKK
	[ETSPQVKGEEMPAGKDQEASRGSVPSGSKMDRRAPVPRTKASGT
			EHNKKGTKERTNGDIVPERGDIEHKKRKAK\GQPQPHPPR/IDI
		ĺ	WFDDVDPADIEAAIGPEAAKIARKQLGQSEGSVSLSLVKEQAFG
İ	ì	Í	GLTRALALDCEMVGVGPKGEESMAARVSIVNQYGKCVYDKYVKP
1			TEPVTDYRTAVSGIRPENLKQGEELEVVQKEVAEMLKGRILVGH
			ALHNDLKVLFLDHPKKKIRDTQKYKPFKSQVKSGRPSLRLLSEK
			ILGLQVQQAEHCSIQDAQAAMRLYVMVKKEWESMARDRRPLLTA
			PDHCSDDA+QSCPAAAAAPLQRQCDQSQGQITSPQSGNSGETFS
			ESWQRGVAWCY
5868	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
			AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
			TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA
1			LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH
	!		IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
1			CCLPVCAVNFKCLHELVKHEENGLVFEDSBELAAQLQMLFSNFP
			DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5869	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
			AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
			TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA
			LESRV+T\MTLDGHNLPSLVCVITGKGPLRBYYSRLIHQKHFOH
İ			IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
Ì	ĺ		CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP
			DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5870	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
			AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
1			TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA
1			LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH
!			IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
			CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5871	3	3465	
1 30.1		2403	FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS
1			VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP
			LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT
			CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI
			KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS
1	l		YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF
			CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ
]	ļ J		L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR
1]		SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR
]		FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG
			VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE
			KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI
			DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV
			FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR
1			PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID
			DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA
			LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTBELPEFKS
			FEELEPPKHSKVKRQSSTPSAPELGQQPDVNISEWKDKPTHEIL
			QKLNDCSCLASQAILLGILLKREGPNFITKEGTVSDHIERVYRR
	<u></u>		*

Deginning nucleotide location corresponding to first smin acid residue of residue of sain acid sequence	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No: mucleotide location corresponding to first amino acid tresidue of amino acid residue of amino acid residue of amino acid residue of amino acid sequence "Peroline, O-Giutanine, R-Argaine, Peroline, amino acid sequence "Peroline, O-Giutanine, R-Argaine, Peroline, amino acid sequence "Peroline, O-Giutanine, R-Argaine, Peroline, amino acid sequence "Peroline, O-Giutanine, R-Argaine, Peroline, Alphanour, Peroline, Alphanour, Peroline, Alphanour, Peroline, Alphanour, Peroline, Alphanour, Peroline, Alphanour, Peroline, Alphanour, Peroline, Alphanour, Peroline, Alphanour, Peroline, Alphanour, Peroline, Alphanour, Peroline, Alphanour, Peroline, Alphanour, Peroline, Alphanour, Peroline, Alphanour, Peroline, Peroline, Alphanour, Peroline, Pero	_			And actu segment containing signal peptide
corresponding to first anino acid anino acid residue of anino acid anino ac		-		Glutamic Acid F-Phonylalanina C Clusica
to first amino acid residue of amino acid sequence 8-Serine, T-Threonine, V-Valine, w-Trytpohan, Y-Tyrosine, X-Unknown, **Stop Codon, /*spossible nucleotide deletion, V-possible nucleotide	No.			H-Mighidine I-Isolausine V-Isolausine
to first amino acid residue of amino acid am	1			Hantstidine, Taisofeddine, Kabysine,
mino acid residue of mino acid sequence describe of codon, /=possible nucleotide deletion, /=				
residue of amino acid sequence (Codon, /=possible nuclectice deletion, /=possible nuclectice d	}		1	
amino acid sequence Codon, /=possible nucleotide insertion) AGSOKIANSVWRANSILSKVUPSILDRSTYNUVCKKVUTLARC HEEVISMPLSPRVIOLITYSCHTORERSVUQGELVITARGE HEEVISMPLSPRVIOLITYSCHTORERSVUQGELVITARGE HEEVISMPLSPRVIOLITYSCHTORERSVUQGELVITARGE SEVAGLIBLDIAPOGROCHERREDICESUKTPTPOFTROKEN BEVAGUELDIAPOGROCHERREDICESUKTPTPOFTROKEN BEVAGUELDIAPOGROCHERREDICESUKTPTPOFTROKEN BOSRIKKIEKODMTSTYNTPPLGRRGTCSYLTKAWGHLLEG EVPRINDIPCLIS S872 68 665 VOGYWYRVIKINSCYSEKTSICERIDRCTGELDATOPPPTPUVF NIALDSSSIGCI\SPKLDAKV\SPKRHYPLLINTGEKYNTLLING GPCPTRIIPO\LOCGODPTHHORITGKSLISSEPDOENFI\LEH TAROVLSTANADPTTROSPFICTARTVHYLLINTGEKYNKYDGMS IVEALERSOSRINGTSKKITANATOGOL SREPESSGGGRTRAREPIPPSILDLILSWANGFENNASSE HHGLIASARQPSVCHYGTKIACCYGGRRRKSWCCATCEPOCKF GECVGPNRCCEPPSTYGENCESPOWTCGMPROCKTPCTYGERYCTSCHTORECKE SGGKLABARGENCEPPSTATGTSCSGWITCSCHTORECKTPCTPGCKF GECVGPNRCCEPPSTATGTSCSGWITCSCHTORECKTPCTPGCKF GECVGPNRCCEPPSTATGTSCSGWITCSCHTORECKTPCTPGCKF GECVGPNRCCEPPSTATGTSCSGWITCSCHTORECKTPCTPGCKF GECVGPNRCCEPPSTATGTSCSGWITCSCHTORECKTPCTPGCKF GECVGPNRCCEPPSTATGTSCSGWITCSCHTORECKTPCTPGCKF GECVGPNRCCEPPSTATGTSCSGWITCSCHTORECKTPCTPGCKF GECVGPNRCCEPPSTATGTSCSGWITCSCHTORECKTPTGSTYCK KOOYKGNURCSAT PERSKENCESPTGSTATGTSCHTORECKTPCTPGCKF GECVGPNNCLIPPTRIATGTSCHTORECTTGSTTCSTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	i			
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VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIBGSLSPKBRTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMIYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDMGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGGEBAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL\ALGAPALFTGLLQVTCFPFG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDPAQQKL\TDK\NLGFQ\MLQKMGKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF 5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEBQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVAFFRWEBLGEGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				
QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFIR APGLKHHGRQAPGLS\QAKFSLPDRND\AAKD\CPLDPV\GPSP QPPSLEASGFSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEEDEDDDGGEBAPA\PGRG GPSLEGSTPADGLPPEA\AEDDL/ALGAPALFTGLLQVTCFPFG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKKPKDLDPAQQKL\TDK\NLGFO\MLQKMGWKEGHGLGSLGK GIR\SRSACTOQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF 5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLPPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEBQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVAFFRWEELGEGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				
SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLPLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTTSSPCPSADIDMKDNGRTTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGGEBAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPFG RGFSSKSLKVGMIPAPKRVCLIQEFKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF 5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLPPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEBQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEBLGEGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS		1		
RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QPESLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGGBEAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL\ALGAPALFTGLLQVTCFPFG RGPSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEBQRPVFKQHIPANTKVMLISDIDGGCREL VVGYTDRVVRAFRWEELGEGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS	1			-
APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QPPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQGSSPVDLME GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGGBEAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL\ALGAPALFTGLLQVTCFPFG RGPSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLPPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEBQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGEGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS	1	1	1	
QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESSVDLME GEAEFEDEPPPREAELESPEVMPEEEDDEDGEGEBAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL\ALGAPALFTGLLQVTCFPFG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF 5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGEGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS	1			
KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEEDEDDEGGEEAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPFG RGPSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKKPKDLDPAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF 5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEBQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGEGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS	1			
FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGGBEAPA\PGRG GPSLEGSTPADCLPGEA\AEDDL/ALGAPALFTGLLQVTCFPFG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDPFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF 5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLPPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEBQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVYAFRWEELGEGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS	1		}	l
GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGGEBAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPFG RGPSSKSLKVGMIPAPKRVCLIQEFKVHEPVRIAYDRPRGRPMS KKKKKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF 5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLPPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEBQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVVAFRWEBLGEGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				
GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPFG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAMGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHSTLIGEBQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEBLGEGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				
RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEBQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWERLGEGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS	1			
KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF 5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEBQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGEGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS	I	Į.		
KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF 5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEBQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGEGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS			}	
GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF 5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEBQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEBLGEGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS	l			
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5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGEGPEHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS	1			
LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGEGPEHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS	5875	296	1848	
WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGEGPEHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS		1	1 20.0	1
VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGEGPEHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS	1			
VVGYTDRVVRAFRWEELGEGPEHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS	1			
VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS	1	1		
	1			
/SGDPSCPRRGAAPDIWPYPQQECLHSPNWQHQT\SHGTESSGS	1		1	
	İ	1	L	/SGDPSCPRRGAAPDIWPYPQQECLHSPNWQHQT\SHGTESSGS

6776			
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	seguence	_	\=possible nucleotide insertion)
			GLFALCTLDGTLKLMEEMEEADKLLWSVQVDHQLFALEKLDVTG
			NGHEEVVACAWDGQTYIIDHNRTVVRFQVDENIRAFCAGLYACK
	1		BGRNSPCLVYVTFNQKIYVYWEVQLERMESTNLVKLLETKP\ST
		İ	TACCRSWAWILTTSL*LVPCFTKRSTIQTSHHSVLPQASRIPPS
			WTCLIAGEGFF*TPTLPPKGVFGSHCAAAGSITKO
5876	1122	224	
3878	1122	224	HLPLGVPSKVAGAAAMEPQEERETQVAAWLKKIFGDHPIPQYBV
1	1		NPRTTEILHHLSERNRVRDRDVYLVIEDLKQKASEYESEAKYLQ
ĺ			DLLMESVNFSPANLSSTGSRYLNALVDSAVALETKDTSLASFIP
1	}		AVNDLTSDLFRTKSKSEEIKIBLEKLEKNLTATLVLEKCLQEDV
			KKAELHLSTER\AKVDNRRQNM\DFLKAKSEEFRFGIQAAGEQL
			SARGQ\DAFSVPIQSLVALIRENWPRLKQQTIPLK\KKLESYLD
1			LMP\NPSHCSK*RIEBAK\RELA\SIEABLTRRVS\MMEL
5877	2030	1907	GTLGKMAASSSGEKEKERLGGGLGVAGGNSTRERLLSALEDLEV
			LSRELIEMLAISRNQKLLQAGEENQVLELLIHRDGEFQELMKLA
			LNQGKIHHEMQVLEKEVEKRDSDIQQLQKQLKEAEQILATAVYQ
i	<u> </u>		AKEKLKSIEKARKGAISSEEIIKYAHRISASNAVCAPLTWVPGD
			PRRPYPTDLEMRSGLLGQMNNPSTNGVNGHLPGDALA/RRKIAR
			CPCSTVS/NGSQMTCR*INIILILQKSVCEL
5878	950	2113	GLWKCMQLQGPHTHRVQP*PTPRQQGPQ\VPVAVIAGNRPNYLY
1			RMLRSLLSAQGVSPQMITVFIDGYYEEPMDVVALFGLRGIQHTP
			ISIKNARVSQHYKASLTATFNLFPEAKFAVVLEEDLDIAVDFFS
			FLSQSIHLLEEDDSLYCISAWNDQGYEHTAEDPALLYRVETMPG
1			LGWVLRRSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECII
			PDVSRSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDSL
			KKEAYEVEVHRLLSEAEVLDHSKNPCEDSFLPDTEGHTYVAFIR
			MEKDDDFTTWTQLAKCLHIWDLDVRGNHRGLWRLFRKKNHFLVV
			GVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT
5879	3	981	RLTEAAAAGSGSRAAGWAGSPPTLLPLSPTSPRCAATMASSDED
			GTNGGASEAGEDREAPGKRRRLGFLATAWLTFYDIAMTAGWLVL
1 1			AIAMVRFYMEKGTHRGLYKSIQKTLKFFQTFALLEIVHCLIGIV
-			PTSVIVTGVQVSSRIFMVWLITHSIKPIQNEESVVLFLVAWTVT
			EITRYSFYTFSLLDHLPYFIKWARYNFFIILYPVGVAGELLTIY
			AALPHVKKTGMFSIRLPNKYNVSFDYYYFLLITMASYIPLFPQL
ł			YFHMLRQRRKVLHG\G*L*KRMIK*SLQTRCFFQNNQDYLSPSF
			NNKNKQLCEISWIVWFLKI
5880	1138	1324	SLWCLVAGGLGLGPSSQNPLQRAGILARPREARGTFSALTACSA
			SVTSKGKSSSGMWPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD
]]			*KKKRGRCSS/WLSQPQHEREKEVVLLRRSMAEGERARAASDVL
			CRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRNVGERSP
	1		DQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKWQRYN
	1	•	ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNROLEEKINDC
			AEVKQBLAASRTARDAALBRVQMLEQQILAYKDDFMSERADRER
	į		AUCELUEINERAJETTHONGREUDGEBEDDYGETTHYGGGERADKEK
			AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA
			ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH
5003	26		CLQCFSDEQGEELLRHVABCCQ
5881	26	441	GGIHPSPTEAPRAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG
	-		SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE+MGPFD
ĺ	-		LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV
			HHCATDTV
5882	2407	2216	SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE
		Ì	RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR
ľ			HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER
			MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG
			ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREOE
ļ			ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ
1	1		IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR
1			SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF
			TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL
		i	LDNSCREYLFICEFFVVSGPAAHDLFHAVMGRTLSMTLKHLDSY
			LADCYDAIAVFLCIHIVLRFRNIAAKRDVPALDRYWEQVLALLW
			T DOI WILLY DOLLAR TANKEN Y PADDKING V DADLW

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0,	location	corresponding	Giddanic Acid, rememylatanine, Geglycine,
}			H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence	_	\=possible nucleotide insertion)
	<u> </u>	 	PRFELILEMNVQSVRSTDPQRLGGLDTRPHYITRYAEFSSALV
1	ì	i	SINQTIPNERTMQLLGQLQVEVENFVLRVAABFSSRKEQLVFLI
ĺ	1		ABIVONMI CUI MA E-EDA A DOCUMENTO DOCUMENTO DE COMPANI
ļ	1	1	NNYDMMLGVLM\E*ERAADDSKEVESFQQLLNARTQEFIEELLS
1	1		PPFGGLVAFVKEAEALIBRGQAERLRGEEARVTQLIRGFGSSWK
}	1	J	SSVESLSQDVMRSFTNFRNGTSIIQGALTQLIQ\LYHRFHRV\L
	1	1	SQPQLRALPARAELINIHHLMVELKKHKPNF
5883	2	1374	EFPGRRFRAVMEAGAGAGAGAGWSCPGPGPTVTTLGSYBASEG
			CERKKGQRWGSLERRGMQAMEGEVLLPALYEEEEEEEEEEEVE
	1	1	EEEEQVQKGGSVGSLSVNKHRGLSLTETELEELRAQVLQLVAEL
1	1	1	FETDEL ACOUEDDS! ELOCI I EDEDI A CARCADITATION CARCA
	1	ĺ	EETRELAGQHEDDSLELQGLLEDERLASAQQAEVFTKQIQQLQG
			ELRSLREEISLLEHEKESELKEIEQELHLAQAEIQSLRQAAEDS
ł	į		ATEHESDIASLQEDLCRMQNELEDMERIRGDYEMEIASLRAEME
i	į		MKSSEPSGSLGLSDYSGLQEELQELRERYHFLNBEYRALQESNS
1			SLTGQLADLESERTQRATERWLQSQTLSMTSAESQTSEMDFLEP
1			DPEMQLLRQQLRDAEEQMHGMKNKCQELCCELEKLQHHRQVSEE
1			EQRRLQRELKCAQNEVLRFQTSHS\SPSHPLPPIPPSSPCLL+A
Ī	1	1	LVVISALLWCWWAETSS
5884	4261	2522	GVLARASARLRVPLTGVRACAEPEVGAEPAKVAGAAEPDEDGGR
1 3001	1	1.	
1			SRLRDCGDYTPSERLGPKGAMLWFQGAIPAAIATAKRSGAVFVV
	1		FVAGDDBQSTQMAASWEDDKVTEASSNSFVAIKIDTKSEACLQF
	l		SQIYPVVCVPSSFFIGDSGIPLEVIAGSVSADELVTRIHKVRQM
			HLLKSETSVANGSQSESSVSTPSASFEPNNTCENSQSRNAELCE
1	Į.	1	IPSTSDTKSDTATGGESAGHATSSQEPSGCSDQRPAEDLNIRVE
1		!	RLTKKLEERREEKRKEEEQREIKKEIERRKTGKEMLDYKRKQEE
1	1	1	ELTKRMLEERNREKAEDRAARERIKQQIALDRAERAARFAKTKE
	l		EVEAAKAAALLAKQAEMEVKRESYARERSTVARIQFRLPDGSSF
1)	1	TNQFPSDAPLEEARQFAAQTVGNTYGNFSLATMFPRREFTKEDY
	ľ	!	KKKLLDLELAPSASVVLLP/ALFINF*AGRPTASIVHSSSGDIW
ł	ļ	ł	TLLGTVLYPFLAIWRLISNFLFSNPPPTQTSVRVTSSEPPNPAS
		ļ	SSKSEKREPVRKRVLEKRGDDFKKEGKIYRLRTQDDGEDENNTW
			NGNSTQQM
5885	900	467	AAGGGRRSRLSRSWPTGPSKSPSGVRCCG\RR\AWEDKDEFLDV
1		i	IYWFRQIIAVVLGVIWGVLPLRGFLGIAGFCLINAGVLYLYFSN
1	}	ì	YLQIDEEEYGGTWELTKEGFMTSFA/IVHGHLDHLLHCHPL*LM
i			VYSSQVLPIQSKGPS
5886			
3000	86	1341	PFRGRALTLKKQPRPGVAPPSLGTCHKSDPGRPAAQSQPPSPGS
Į.		1	GTFGLLSFRMVRTKTWTLKKHFVGYPTNSDFELKTSELPPLKNG
1		1	EVLLEALFLTVDPYMRVAAKRLKEGDTMMGQQVAKVVESKNVAL
		1	PKGTIVLASPGWTTHSISDGKDLEKLLTEWPDTIPLSLALGTVG
1		1	MPGLTAYFGLLEICGVKGGETVMVNAAAGAVGSVVGQIAKLKGC
1			KVVGAVGSDEKVAYLQKLGFDVVFNYKTVESLBETLKKASPDGY
1		ł	DCYFDNVGGEFSNTVIGQMKKFGRIAICGAISTYNRTGPLPPGP
			PPEIGIYQELRMEAFVVYRWQGDARQKALKDLLKWVLELPYFVI
1			
1			D*LQANTLVYKSMKSAKPSLEYISEKLVSG\KIQYKEYIIEGFE
FOCO	1535		NMPAAFMGMLKGDNLGKTIVKA
5887	1937	104	APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLLGLRE
			RPDRCHPGGDDRGPQLHRGSPG/SPSELSRRPGPPGLPGLQGPP
			PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS
			ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI
			FCIHITN*NLHYPLLIQKYL/NENNFDTLMKTSDGFTLNABSY
1		1	VSETTKI DI DTA KVEVCUDI OTCOCCI DEDCAT MOAT OTCOC
			VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNP
1			AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPBILRVPDSRK
		1	KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV
	1		LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ
			ENTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIOTTNRYGOLTI
1			LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ
]	1		KVKSLLWGQGFPDYVAPFGNSQGP/ADMLDWVPIHFITQSFNRK
1	l		
I	1		DSCQLPGALVIEVKWTKYGSLLNPQAKIVNVTANLISSSFPEAN
I			SGNERTILISTAVTFVDVSAPAEAGFRAPPAINARLPFNFFFPF
L			V

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide		Cluberia haid B Phone 2 1
NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ì	ſ	sequence	
	sequence		\=possible nucleotide insertion)
5888	375	2302	LLCRTPGVAMQRADSEQPSKRPRCDDSPRTPSNTPSAEADWSPG
1	1		LELHPDYKTWGPEQVCSFLRRGGFEEPVLLKNIRENEITGALLP
1	}		CLDESRFENLGVSSLGERKKLLSYIQRLVQIHVDTMKVINDPIH
	1		GHIELHPLLVRIIDTPQFQRLRYIKQLGGGYYVFPGASHNRFEH
		}	SLGVGYLAGCLVHALGEKQPELQISERDVLCVQIAGLCHDLGHG
1	ĺ	}	PFSHMFDGRFIPLARPEVKWTHEQGSVMMFEHLINSNGIKPVME
	Į.	1	
			QYGLIPEEDICFIKEQIVGPLESPVEDSLWPYKGRPENKSFLYE
į.		1	IVSNKRNGIDVDKWDYFARDCHHLGIQNNFDYKRFIKFARVCEV
		1	DNELRICARDKEVGNLYDMFHTRNSLHRRAYQHKVGNIIDTMIT
1	1	Į.	DAFLKADDYIEITGAGGKKYRISTAIDDMEAYTKLTDNIFLEIL
1			YSTDPKLKDAREILKQIEYRNLFKYVGETQPTGQIKIKREDYES
1			LPKEVASAKPKVLLDVKLKAEDFIVDVINMDYGMQEKNPIDHVS
1		ļ	
	Ì	ì	FYCKTAPNRAIRITKNQVSQLLP\EKFAEQ\LIRVYCKKVDRKS
			LYA\ARQYFVQW\CADR\NFT\KPQDGRCY*PPTP*HPQKKGW\
L	<u> </u>		NDSTFSPKIPTRLPRRLPKSRV\QLFKDDPM
5889	1831	731	LPAACGRPVTARPRQAPEGRSGRPRDLDPYPPQVFPPRPDRVAI
1			VTGGTDGIGYSTAKHLARLGMHVIIAGNNDSKAKQVVSKIKEET
1			LNDKET*VLLCCPGWLCLWNSSDPPTSASRGAGTTGVHHHFLLK
		1	FGIFIL\DLASMTSIRQFVQKFKMKKIPLHVLINNAGVMMVPQR
			KTRDGFEEHFGLNYLGHFLLTNLLLDTLKESGSPGHSARVVTVS
i]	1	
ł	i	İ	SATHYVAELNMDDLQSSACYSPHAAYAQSKLALVLFTYHLQRLL
1	ļ	1	AAEGSHVTANVVDPGVVNTDLYKHVFWATRLAKKLLGWLLFKTP
ļ		!	DEGAWTSIYAAVTPELEGVGGRYLYNKKETKSLHVTYNQKLQQQ
1			LWSKSCEMTGVLDVTL
5890	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS
}	}	1	GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP
1		ļ	LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV
{		i	
	i		ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD
			PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR
			RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI
			KQKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI
			AYPHEVVRTRLREEGTKYRSFFQTLSLLVQEEGYGSLYRGLTTH
	1		LVRQIP\NTAIMMATYELVVYLLNG
5891	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS
			GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP
	į.		
			LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV
		Ì	ILEKBGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD
1			PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR
Į			RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI
l	ľ	ľ	KQKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI
1	1		AYPHEVVRTRLREEGTKYRSFFQTLSLLVQEEGYGSLYRGLTTH
l			LVRQIP\NTAIMMATYELVVYLLNG
5892	1764	379	VVLRVCGRLSVNSAVSSRTGGWSAGLTCAMQRLQVVLGHLRGPA
~~~~		],,,	
	[		DSGWMPQAAPCLSGAPHASAADVVVVHGRRTAICRAGRGGFKDT
1	İ		TPDELLSAVMTAVLKDVNLRPEQLGDICVGNVLQPGAGAIMARI
1			AQFLSDIPETVPLSTVNRQCSSGLQAVASIAGGIRNGSYDIGMA
	1		CGVESMSLADRGNPGNITSRLMEKEKARDCLIPMGITSENVAER
	1		FGISREKQDTFALASQQKAARAQSKGCFQAEIVPVTTTVHDDKG
	•		TKRSITVTQDEGIRPSTTMEGLAKLKPAFKKDGSTTAGNSSQVS
1	-	1	DGAAAILLARRSKAEELGLPILGVLRSYAVVGVPPDIMGIGPAY
1	1	}	AIPVALQKAGLTVSDVDIFEINE\AFASQAAYCVEKLRLPP*EG
1			l ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' '
			*TPLGGASGP*GHPLGLHWGHVQVITLAQ*S*SARGKRAYRSGC
			PCAIGSWNGSPLPVFEYPWGT
5893	3	1653	ILSKRRCQKAKTKELMAKKVAVIGAGVSGLISLKCCVDEGLEPT
I		,	CFERTEDIGGVWRFKENVEDGRASIYQSVVTNTSKEMSCFSDFP
I			MPEDFPNFLHNSKLLEYFRIFAKKFDLLKYIOFOTTVLSVRKCP
l	<b>{</b>		DFSSSGQWKVVTQSNGKEQSAVFDAVMVCSGHHILPHIPLKSFP
	1		
i			GMERFKGQYFHSRQYKHPDGFEGKRILVIGMGNLGSDIAVELSK
1			NAAQVFISTRHGTWVMSRISEDGYPWDSVFHTRFRSMLRNVLPR
1			TAVKWMIBQQMNRWFNHENYGLEPQNKYIMKEPVLNDDVPSRLL
i			CGAIKVKSTVKELTETSAIFEDGTVEENIDVIIFATGYSFSFPF
	·		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ſ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid		
		residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	'		LEDSLVKVENNMVSLYKYIFPAHLDKSTLACIGLIQPLGSIFPT
			AELQARWVTRVFKGLCSLPSERTMMMDIIKRNEKRIDLFGESQS
Ì	ľ		QTLQTNYVDYLDELALEIGAKPDFCSLLFKDPKLAVRLYFGPCN
			SY*YRLVGPGQWEGARNAIFTQKQRILKPLKTRALKDSSNFSVS
			FLLKILGLLAVVVAFF\CQLQWS
5894	174	1673	RYSPKKVLQNKESSLKLGMATALVSAHSLAPLNLKKEGLRVVRE
			DHYSTWEQGFKLQGNSKGLGQEPLCKQFRQLRYEETTGPREALS
			RLRELCQQWLQPETHTKEHILELLVLEQFLIILPKBLQARVQEH
1		į	HPESREDVVVVLEDLQLDLGETGQQVDPDQPKKQKILVEEMAPL
1			KGVQEQQVRHECEVTKPEKEKGEETRIENGKLIVVTDSCGRVES
ł			SGKISEPMEAHNEGSNLERHQAKPKEKIBYKCSEREQRFIOHLD
			LIEHASTHTGKKLCESDVCQSSSLTGHKKVLS*ERKVIQC\HGV
			LGKAFQRSSHLVRHQKIHLGEKPYQCNECGKVFSQNAGLLEHLR
1			IHTGEKPYLCIHCGKNFRRSSHLNRHQRIHSQEEPCECKECGKT
1			FSQALLTHHQRIHSHSKSHQCNECGKAFSLTSDLIRHHRIHTG
1			EKPFKCNICQKAFRLNSHLAQHVRIHNEEKPYQCSECGEAFRQR
			SGLFQHQRYHHKDKLA
5895	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGB
			MRLFVSDGVPGCLFVLAAAGRARGRAEVLISTVGPEDCVVPFLT
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW
			EATELOPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
			RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW
			FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
			EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPOO
1			NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
1			RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA
1			DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
1			TVEQLRCEHCARF\LADRF4EGVCPFCGYBEARGDQCDKCGKLI
١,			NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL
			PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E
			GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPBQVDLYQ
1	}		
			FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG
			K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
			FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
İ			LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
			GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
			QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP
1			LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA
			LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG
			KPPEAPKGKKKK
5896	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE
1	1		MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW
			EATELOPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
1			RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW
1	İ		FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
1	1		EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPOO
			NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
			RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA
			DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLOD
			TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI
			NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL
			PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E
			GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ
	l		
			FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG
			K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
			FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
			LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
			GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
1	}	•	QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP
L	L		LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
			P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG
			KPPEAPKGKKKK
5897	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE
1			MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
1			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW
			EATELOPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
			RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW
1			FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
1			EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ
ŀ			NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
1			RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA
1			DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
1			TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI
1			NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL
			PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E
1			GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ
			FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG
1			K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
			FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
i			LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
			GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
	•		QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP
			LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA
		•	LMDEVTKQGNIVRELKAQKADKNEVAABVAKLLDLKKQLAVAEG
1			KPPEAPKGKKKK
5898	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE
			MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW
			EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
			RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW
			FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
1 :			EGKGLSPIEPEEEBLATLSEEBIAMAVTAWEKGLESLPPLRPQQ
			NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
]			RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA
į		•	DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
			TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI
1			NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL
1			PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E
			GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ
}			FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG
			K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
			FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
1			LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
1			GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
			ODAWALI /AATEL /VETVOREWRYKARIA CALLATION DE CALCALINA
		1	QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP
		}	LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA
[			LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG
5899	326	1000	KPPEAPKGKKKK
ا لادود	326	1078	NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ
[			EANEKAEBIDAKAEBEFNIEKGRLVQTQRLKIMEYYEKKEKQIE
] ]			QQKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDP
į l			EVYQGLLDKLVLQGLLRLLEPVMIVRCRP\QDLLLVEAAVQKAI
			PEYMTISQKHVEV\QIDKEA*LAVECSWEVWEVYSGNQRIKVSN
لحييا			TLESRLDLSAKQKMPEIRMALFGANTNRKFFI
5900	64	1409	KAASRDSPCLEFCPLCGVSSHDLQHRMWYHRLSHLHSRLQDLLK
	1	1	GGVIYPALPQPNFKSLLPLAVHWHHTASKSLTCAWQQHEDHFEL
		ļ	KYANTVMRFDYVWLRDHCRSASCYNSKTHQRSLDTASVDLCIKP
[			KTIRLDETTLFFTWPDGHVTKYDLNWLVKNSYEGQKQKVIQPRI
	1		LWNAEIYQQAQVPSVDCQSFLETNEGLKKFLQNFLLYGIAFVEN
i			VPPTQEHTEKLAERISLIRETIYGRMWYFTSDFSRGDTAYTKLA
1	ļ		LDRHTDTTYFQEPCGIQVFHCLKHEGTGGRTLLVDGFYAAEQVL
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REKHCVPETKTPROGTNOASEQVQKEEVELQTLLITNSQSSINSH DGSSEDVITSERPHYGCDICGAATTHETILGNIQLABENTRPOES AIVEKKARLIKGNYKKONCSRTFFSENGLESHROTHIGDVEKTYM CPICGERPPSLLTLTEHKVTHSKSLDTGNORT-WIGGSEEFI EHCQM:PPLINSITGFRCVVCMQTVTSTLELKHGTFHMQKTGN GSAVOTTGRGGHVQKLYKCASCLKSFRSKQDLVKLDINGLFVGL CAGCVALEKSASPGINVPEDTKREFRSKQDLVKLDINGLFVGL KTRCS-LATFKF-VLKVELPEPPRFPHROVSREDSSTTCLKTP QVSSMPRTISPSGDEKKTYQCIKCQMFYTMENDIQVSIVANIMH)D EGINHBCKLCSQTFDSPAKLQCHLSHSFEGMGGTFRCVCFTV FVQANKLQMIFFSAHGQBEKLTVCTQCQVFFFQTELQMHTMTQ EGINHBCKLCSQTFDSPAKLQCHLSHSFEGMGGTFRCVCFTV FVQANKLQMIFFSAHGQBEKLTVCTQCQVFFFQTELQMHTMTQ FPLXPRQNSEVENTOCTQCQVFFFQTELQMHTMTQ FPLXPRYNFTHSAHGQBEKLTVCTQCQVFFFQTELQMHTMTQ HSS  5902 712 209 LKRRRSRSSIRGSISTSVSRMLTSLFTYLDHTADVOTV-REP IPLKPRQ FD-MTQSHLHAWGDTLEEAFBCCMMAMFGYMTDGT VEPLQTVVEVETCOGDOLGGLLPH-LDHLLLYLTDHOTQT-V-REP IPLKPRQ FD-MTQSHLHAWGDTLERAFBCCMMAMFGYMTDGT VEPLQTVVEVETCOGDOLGGLLPH-LDHLLLYLTDHOTQT-V-REP PALPALSAVVFGODDGOLGLEH-LDHLLHLULTDFRCAB- GLSTCKTIDMBLVKRRTEAIRGQLLSKLELASPPSGCSPPGD- PALPALSAVVFGODSSHANGHLAWGDTLEEAFBCCMMAMFGYMTDGT VEPLQTVEVETCOGDOLGGLLPHLDHLHLULTDFRCAB- GLSTCKTIDMSLVERKREAIRGQLLSKLELASPPSGCSPPGD- LPEVALALVASTRDRVAGESSABPEPEPEAPYLLSRAELLLRI- KLKVEQHUELVGYSYMSNEKTURNILABPSDFBLLSFDVTGVV RQMLSRGGEIGFFLSAKCSCOSENDATLQVDINGFTTGR-KGDL ATIHGMNPPFLILLMAPDLERAGNLGS\STRIAGALDTATKSVTRAMMTC\L GDCPYIWSLDTAVSKVLALVNQ\HKPG\ASAAP\CCVPALEP\ LPIVYY\QNRFNVEGLSMHIVRSCKCS  S904 3 1126 MMESISNAINTFREEGRIFYEBLIKEKTINNELSAISRKIDTW ALGNSTEKAFRAISSKVPVDKVTPSTLEPEVLDERKPQOTGA RQGMDDYHGNVVXVRNSHKKGPFTPEEVLEHLEGKTDDEVQ HEKKYQKILALBERKKESIGIMTKKXQARSEIFFLLKEKDDATP VLFHNQEDNOKQKERGRKXQKLAVEAARKQKSIFMSMKCASOL KEEEEKEKKHQKERGFFVKLUBURSGCCSPELLYLEKTI RENABRAEKRENNADBISRPCBEDLYNTTQRIAGRTNQKTRAL ATSTYPT*GYSNLETRITEKSMR  ASSPPRANGCRRVKLVBARDGCLQMFLLHGTKNVTNSSELRLP RENABRAEKRENNADBISRPCGCQMFLLHGTKNVTNSSELRLP RENABRAEKRENNADBISRPCGFTLIVETRIN-TYNSSELRP RENABRAEKRENADBISRPCGCQMFLLHGTKNVTNSSELRP GSSPAMSGGRRVKLVBARDGSVERGSSVERGSKCVIKHH RFRRGOODLLLALATIONSGRK LKHUDVTNSLLLLUNDHTGVVRDL TFAPDGSLLLVASSRBKTLRWDDINDMKVLLERGGNWYY\ SCAFSPDSSMCKGCKGCNATALATURV				
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ATVEKRABLIKGNYKKNYCSRTFFSEGIGLERHOTHLIGSEERFI CPHIOGREPPSILITICHENYTHKSIDTMORGICHAPHOSEERFI EHCOMIPDLRNSLITGFROUWONTVISTLELKIHGTFHMAKTGN GSAVGTTGROGHVOKLYKCASCIKEFRSKODLVKIDINGLPVGL CAGCVALSKASSIGINVPPGTNRFGLGORSHISATEKKKNYGGI KTRGS-LATFKF-VILKVELEPEPIPSUPPHROVSREDSSTYCKTP OVSSMPRTISSPSGDEKKTYGCIKCOMFYTHENDIQVIVANHHID EGINHBECKLCSQTFDSPAKLQCHLEBISFEGMGSTFKCFVCFTV PVQANKLQHIFPSAHGQDENIYDTCOTQCOPFPFOTELQHITHTO HSS  5902 712 209 LKNRRSRPSIRGIGSTSVSRWLTSLFTYLDHTADVQ-V-REP IPLKPRO-ED-MTGSGHLAWGDTLEERAPECCAMAMGGYMTDGTG VEPLQTVVEVETOGDLOSLLPHILDBHLYKERDEPIP VGGGE EFSLSHHPQGTEVKATTYSAMQVYNEENPEVPVILDI  5903 2106 735 DTPOFBLISTTATPSSLRELSFPSRSPSYLLFGDPPQLAGGGLPTT PALPALSAVPGGASSMPPSGERLLPLLIPLLUNLTGRPAA GLSTCKTIDMSLVKRKRIBAIRGQLISKIKLASPPSGGEVPPG- LPPENVLALVINSTRORVAGESSBEPEPEADYLAKSVTRVLMVET HNEIYDKFKQSTISIIMFFRTSELREAVPEPVLLSRAERLERL KLKVEGNVELVGYSMNSMRYLSINLLABPSBLSFDTOTVVV RQMLSRGGEIEGFRLSAKICSGDSRDNTLQVDINGFTTGR KGDL ATHGMNRPPLLLMAPPLERRACHLOS\S\RTGALFACTUTAKSVTRVLMVET HNEIYDKFKQSTISIIMFFRTSELREAVPEPVLLSRAERLERL KLKVEGNVELVGYSMNSMRYLSINLLABPSBLSFDTOTVV RQMLSRGGEIEGFRLSAKICSGDSRDNTLQVDINGFTTGR KGDL ATHGMNRPPLLLMAPPLERRACHLOS\S\RTGALFSTFTDTAKSVTRVLMVET HNEIYDKFKQSTISIIMFFRTSELREAVPEPVLLSRAERLERL LGPLYVYVVGRKPKVEQLSMMIVRSCKCS SQRAMDAVHGNVKKRNIKGRPTFMEEVLERLBGKTODEVQ HEKMYGKFLALBERKESSIOMKVTPSTLDEEVLIDFEKFLOTOG RQGAMDDYHGNVKKRNKKGRPTFMEEVLERLBGKTODEVQ HEKMYGKFLALBERKKESIOMKTKKOQNESEIFIGLEETI REALEKAEKRNAADBISRFOERDHJKLELKLDSNTOQKESPLRLEETI REALEKAEKREKNAADBISRFOERDHJKLELKLIDRORKDERSQ KGREAKLEKEVENNSDDPSBLYJNTHQRLGRTNNCKTBAP DASSPPANGGGRTVKUPBNSQCLQMFLHCHTRNYTNSSELRLP RASSPPSNCKEGVANALDISRFOERSPLYJNTHQRLGRTNNCKTBAP DASSPPANGGGRTVKUPBNSQCLQMFLHCHTRNYTNSSELRLP REALEKAEKREKNAADBISRFOERDHJKNEKKHURDARBDRYYN SCAFSPDSSMLCSVGRSGVKKLAVEARKKGSEFRIEKEST REALEKAEKREKNAADBISRFOERDHJKNEKKHHTGATMVLS NAEVNSLLATGLAFTTIG-SNLAFVLJOGVLVVHRCKSMSTCF SPPLFFFKYLTLATGLATGANSKT KLIDDYTTGKTHTGVTSTMIM-SI MLSMGFSVLFFGILLSGRDDLTARLFYTFNILMVTNNSSELRLPS LLIFRI-LTFRALLISS LLIFRIS-LUFPATHM-LISHLTJFFKLLITFRALLISS LLIFRI-LTFRALTISS LLIFRIS-LUFPATHM-LISHLT		<b>!</b>	[	
CPIGGRPPSILITIPHKYTISKSLDTGKCRICKMPLOSEEFIL BHCCMMPDIANSILGRPCVCMCQTYSTISKHGTFHMOKTGM GSAVQTTGRGQHVQKLYKCASCLKEFRS KQDLVKLDIMGLPYGL CAGCVWLSKSASPGINVPGTYRRGLGQMENISAIEGKGKVGGL KTRGS-LAFREY-VLKVELBPEHNKPFHRSVSRPDSNSTQLKTP QVSPMPRISPSGSBEKKTYQCIKCOMVFYNEMDIQVHVANHMID BGLNHECKLGSQTDSPSALQCHLI BHSPEGMGGTFKCFVCPTV PVQANKLQQHIPSAHGQEKIYDCTQCPQKFFFQTELQMHTMTQ HSS  5902 712 209 LKNRRRSRPSIRQSIGSTSVSRWLTSLFTYLDHTADUVV-NER IPLEYPON-SD MPGOSMLHAMGDTTERSPFCOMAMPGYMTDTGT VEPLQTVEVETQDDLQSLPHFLDEWLYKFSADEPPIP\GWGE BFSLSKHPQGTEVKALTYSAMQVYNEENPEVPVIIOT TO PALPALSAVPGGAASPMPPSGLRLLPLLLPLLWLLVLTBGRPAA GLSTCKTIDMELVRRKRISEFPSRFSYLLFGFFQPPLQGRGUPTT PALPALSAVPGGAASPMPPSGLRLLPLLLPLLWLLVLTBGRPAA GLSTCKTIDMELVRRKRISEFPSRFSYLLSFGFFQFVLGRRUPTT HNEITYDKFKQSTHSIYMFMTSELRRAVPULSRAELRLLRL KLKVEGHVELVGYKVSNNSKRYLSNRLLAPSDSPBKLSPDVTGVV RQMLRAKKROSTHSITMFTSELRRAVPULSRAELRLLRL KLKVEGHVELVGYKVSNNSKRYLSNRLLAPSDSPBKLSPDVTGVV RQMLRAGKLGC/VHC-HLIFRKDL\GWG\KWALNEINFOTGTRGK\RGDL ATHGMNRPFLLLMATPLERRACHQS\SHRADALCTUN\CPSF HGGRNCLRG-/VHC-HLIFRKDL\GWG\KWALNEINFOTGTRGK\RGDL ATHGMNRPFLLLMATPLERRACHQS\SHRADALCTUN\CPSF HGGRNCLRG-/VHC-HLIFRKDL\GWG\KWALNEINFOTGTRGK-RGDL ATHGMNRPFLLLMATPLERRACHG\S\SHRADALCTUN\CPSF HGGRNCLRG-/VHC-HLIFRKDL\GWG\KWALNEIN-RCALEPPLQGTGG RQGAMDDYHOPWVRWNHKGKPTMEWELPHLOGKTGDEVQ HEKWYQKFLALEERKKES IQIHKTKXQQKREBIFKLKEKADMTP VLFHINKGBINGXOKREQRKKQKLAVZAMKKQKI BERKLEKEL REKAEKAEKRKNADADEISFPGENDIHKLEKHLDGKTGDEVQ HEKWYQKFLALEERKKES IQIHKTXXQQKREBIFKLKEKADMTP VLFHINKGBINGXOKREQRKKQKLAVZAMKKQKI BERKLEKEL REKAEKAEKRKNADADEISFPGENDIHKLEKHLINUDHTGVVRDL TFAPDGSLLIVASASRIKTHUVTGKLLILMI.VDHTGVVRDL TFAPDGSLLIVASASRIKTHUVTGKLLILMI.VDHTGVVRDL TFAPDGSLLIVASASRIKTHUVTGKLLILMI.VDHTGVVRDL TFAPDGSLLIVASASRIKTHUVTGKLLILMI.VDHTGVVRDL TFAPDGSLLIVASASRIKTHUVTGKLLILMI.VDHTGVVRDL TFAPDGSLLIVASASRIKTHUVTGKLLILMI.VDHTGVVRDL TFAPDGSLLIVASASRIKTHUVTGKLLILMI.VDHTGVVRDL TFAPDGSLLIVASASRIKTHUVTGKLLILMI.VDHTGVVRDL TFAPDGSLLIVASASRIKTHUVTGKLLILMI.VDHTGVVRDL TFAPDGSLLIVASASRIKTHUVTGKKKMAKF*TIEM **ULYMRIK***INTOKASLITASSRIKTHUVTGKKKMAKF*TIEM***INLSSPKKGKOMNNLLILTRLSVFFKN				DGSEEDVDTSEPMYGCDICGAAYTMETLLQNHQLRDHNIRPGES
BHCQM:PDLRNSLIGFRCVVCMQTVTSTLELKHIGTFHMCKTGN GSAVOTTGRGQHVQKLYKCASCLKEPRSQLYKIGHLOFHMCKTGN GSAVOTTGRGQHVQKLYKCASCLKEPRSQLYKIGHCUNVLDINGLPYGL CAGCVHLKSKAS-FGINVPGTTNRPGLQMENLSAIEGKGKVGGL KTRCS-LATFKF-VLKVELPEPHPKPFHRGVSRPDSBTQLKTP QVSHMPKIS-PSQSDEKKTYCCTQCKQVMFYNSMDIQVHVANIMID EGLNHBCKLCSGTDSPAKLQCHLIEHSFEGMGSTFKFPVCFTV FVQANKLQQHIFSAHGQEBKIYDCTQCPQKFFPQTELQMHTMTQ HSS  5902  712  209  LKNRRSRSPSIRGSIGSTSVSRWLTSLFTYLDHTADUQ-V*-REF IPLKPRQ-ED-MFQSWLHAWGDTLEEAPGCAMAMFGYMTDTGT VEPLQTVRVETQGDDLQSLLHFHJDEWLYKFSADEPIP\GWG EFSLSKHIPQGTEVXAITTSAMQVVNEENPSPVVIIDI  5903  2106  735  DTGPPSLFSTTAPPSLRSLSPPSRPSVLLFGGPQPLQGRUPTT VEPLQTVRVETQGDDLQSLLHFHJDEWLYKFSADEPIP\GWG EFSLSKHIPQAFGASAMPPSGIRLIPLLILLULUTTGRPAA GLSTCKTIDMELVKRKRIEAIRGGLSKPLKLASPPSGEVPGP LPEAVLALYNSTRDRVAGESABPEPEPEADYXHCEVTRUMGET RNEIYDKFRQSTHSITMFFNTSELRRAVPEPVLLSRAELRLLRL KLKVEQHVELVQKYSNNSNRVLSNRLLAFSDSFEWLSPDVTSVV RQWLSRGGEIGEFLSAHGCDSRDMTLQVDINOFTTGR\RQDL ATHGMNRPFLLLAATPLERQCHLQS\SHRRQAL\DTNV\CFSF HGGRNCLRG-VHC-HLIFRENQLHQS\SHRRQAL\DTNV\CFSF HGGRNCLRG-VHC-HLIFRENQLHQS\SHRRQAL\DTNV\CFSF HGGRNCLRG-VHC-HLIFRENQLHQS\SHRRQAL\DTNV\CFSF HGGRNCLRG-VHC-HLIFRENQLHQS\SHRRQAL\DTNV\CFSF HGGRNCLRG-VHC-HLIFRENQLHQS\SHRRQALDTNV\CFSF HGGRNCLRG-VHC-HLIFRENQLHQS\SHRRQALDTDNV\CFSF HGGRNCLRG-VHC-HLIFRENQLHQS\SHRRQALDTDNV\CFSF HGGRNCLRG-VHC-HLIFRENQLHQS\SHRRQALDTDNV\CFSF HGGRNCLRG-VHC-HLIFRENQLHQS\SHRRQALDTDNV\CFSF HGGRNCLRG-VHC-HLIFRENQLHQS\SHRRQALDTDNV\CFSF HGGRNCLRG-VHC-HLIFRENQHLQS\SHRRQALDTDNV\CFSF HGGRNCLRG-VHC-HLIFRENQHLQS\SHRRQALDTDNV\CFSF HGGRNCLRG-VHC-HLIFRENQHLQS\SHRRQALDTDNV\CFSF HGGRNCLRG-VHC-HLIFRENGHTANGKSTTHEREF ALGMRNTHANGKSTTHEREVLJEFHQTGG RGGAMDDYHOPKVVRNHKGKSTTMESVLEHLPGKTQDEVQ HEKWYQKFLALEERKKESIQIWKTKKQQKREEIFKLEKENDTTP VLFHINGEDNOKQKEERGEKKGKLAVARBUKSLEMMCASOL KEEEKKKHQKERGNOKQKERGHTYLLEGTNATUNGKSLTHLAR ATSTYPT-GYSNLETRITKKSMR  DGSTFANSGGNT-WKLUPHSQCLONFILLHGTNNUTNSSLRLPR DGSTFANSGGNT-WKLUPHSQCLONFILLHGTNNUTNSSLRLPR HLIFFNCHLIFFSVYFFSUSPTWALHAUNGKKTHERENGNSTTCF SPFLFFFFKVLIFFNLWVSKK NARSPPRINGENGHTWKLUPHSGVLYFOTWNILHFACSICFSS-N USARSPPDSSMLCSGRSKAVVAAL				AIVKKKAELIKGNYKCNVCSRTFFSENGLREHMQTHLGPVKHYM
GSAVOTTGRGGHVOKLYKCASCLKEFRSKODLVKLDINGLPYGL CAGCVNLSKSASPGINNPOTTRPBIGGBRUSAIBEKKKVGGL KTRCS-LATFKF+VLKVELPEPHPKPFHRGVSRPDSNSTQLKTP QVSPMPRISPSGSBEKTYQCIKCOMPYNNENDIQVIVANHMID EGLNHEKKLGSQTDEPSHALQCHLIEHSFEGMGGTFKCPVCFTV FVQANKLQQHIFSAHGGEKIYDCTQCPQKFFFQTELQMHTMTQ HSS  5902  712  209  LKNRRSRPSIRGIGSTSVSRWLTSLFTYLDHTADUQ+V*REF IPLKPRQ*ED*MPGSHLHAWDTLEBAFPQCAMAMFGYMTDTGT VEPLQTYEVETGGDLQSLLEHFLDEWILKFSADBFFIP\GWGE EFSLSKHPQGTEVKAITYSAMQVYNERNPEVPVIIDI 5903  2106  735  DFPOPSLSFTTAPPSIRSISFPSRPSYLLEMGPOPPLOGRGLPTT PALPALSAVPGGAASPMPPSGLRLLPLLLPLLHILLVLTGRRAA GLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSGGEVPPGP LPPAVLALVTNSTRDRVAGGSAEPPSPEADLYAKEVIRVINGT HNEIYDKFKGSTHSITMFFNTSELREAVPEPVLIGATER, KKYEQHVELVGYKSNNSKYLSNELLABSDFSRWLSFDVTGVV RQWLSRGGEIEGFFLSAHGCGDSRDNTLQVDINGFTTGR\RGDL ATHGMNRSPFLLMAMTLERRAQHLOS\SARALLALRLL KLKYEQHVELVGYKSNNSKYLSNELLABSDSPBWLSFDVTGVV RQWLSRGGEIEGFFLSAHGCGDSRDNTLQVDINGFTTGR\RGDL ATHGMNRSPFLLMAMTLERRAQHLOS\SARALLALRLL KLKYEQHVELVGYKSNNSKYLSNELLABSDSPBWLSFDVTGVV RQWLSRGGEIEGFFLSAHGCGDSRDNTLQVDINGFTTGR\RGDL ATHGMNRSPFLLMAMTLERRAQHLOS\SARALLALRLLRL KLKYEQHVELVGYKSNNSKYLSNELLABSDSPBWLSFDVTGVV RQWLSRGGEIEGFFLLSAHGCGDSRDNTLQVDINGFTTGR\RGDL ATHGMNRSPFLLMAMTLERRAQHLOS\SARALLALRLLRL KLKYEQHVELVGYKSNNSKYLSNELLABSDSPBWLSFDVTGVV RQWLSRGGEIEGFFLLSAHGCGDSRDNTLQVDINGFTTGR\RGDL ATHGMNRSPFLLMAMTLERRAQHLOS\SARALLALBALRLLRL KLKYEQHVELVGYKSNNSKYLSNELLABSDSPBWLSFDVTGVV RQWLSRGGENTVSCLDSHTTARVDLENDGRALD\TGR\RGDANDYCSPB LGGAMDDYHDNFVKVRNHKKSKFTMEEVLEHLDFREPLQOTGG RGGAMDDYHDNFVKVRNHKKSKFTMEEVLEHLDFREPLQOTGG RGGAMDDYHDNFVKVRNHKKSKFTMEEVLEHLDFREPLDOTSRLD HERWYQKFLALLEERKKRSIQIKINGCHENGTDEVQD HERWYQKFLALLEERKKRSIQIKTWLNDFROGLONFLLLKERSIND VLFHNXGBDNQKKERGRFKKKRLALESSTYCRKKGSEERKMADDELSP REKAEKAERKRNAADELSFPQERDLHALLELDROARBDKSO KQRRLLALKEKVENNVSRDPSRLV/NTHQRLGRTNVANDRAD DGSSTGAKKRYREHLIDCDTUVMLAPRSSVEEKGSNCVILEHH RFRFGQDQLLLATGLISNGRIKTWADLRDGAM,MKVTLRGHGNWYY SCAFSPDSMLCSVGASKAVVAATLV*LLRLCHHISHTGATMVLS WABRVASLATIGDERSSTYRENGTHTIG*SNLFAVULQUTYNKLLFACSICFSS*A VGGPSLLVTSPTVKHCHOTTSRLIFACSICFSS*A VGGPSLLVTSPTVKHCHOTTSRLIFA	1			CPICGERFPSLLTLTEHKVTHSKSLDTGNCRICKMPLQSEEEFL
CAGCVALSKSASPGINVPPGTNRPGLGQNENLSAIEKGKVGGL KTRCS-LAFFKFV-LUKUPLEPBHYKPHENPENPENPENPENDENSTOLKTP QVSPMPRISPSQSDEKKTYQCICKCQMVFYNENDIQVHVANHMID EGLNHRCKLCSQT7D5PAKLQCHLIEHSFEGMGTFKCPVCFTV FVQANKLQQH1FSAHGQEBKIYDCTQCPQKFFFQTBLQNHTMTQ HSS  5902  712  209  LKNRRRSRFSIRQSIGSTSVSRWLTSLFTYLDHTADVQ*V*REF IPLKPRQ*ED*MFQSMLAHAWGDTLEEAPFDCCAMMRCYMTDTGT VEPPLQTVEVETGQDDLQSLEPHFLDEWLKKFSADEPFIP\GWG EPSLSKHPQGTEVKAITYSAMQVYNEENPEVFVIIDI  5903  2106  735  DTFGPBSLPSTTAPPSLRSLSFPSREPSVLLPGDPQPLQGRUPTT PALPALSAVPQGAASYMPPSGIRLIPLLLPLLULLVLTPGRPAA GLSTCKTIDMELVRKRIEAIRGGISKKRLASPPSQGSVPFGF LPPAVLALNNSTRDRVAGSASPPPPBEDAPLLPLMILLVLTPGRPAA GLSTCKTIDMELVRKRIEAIRGGISKKRLASPPSQEVPGF LPPAVLALNNSTRDRVAGSASPPPPBEDAPLLSKRALRLURL KLKVEQHVELVQKYSNISWRYLSNRLLAPSDS PBRLSFPDVTLWGET HNEITYDKFRQSTHSITMFFNTSELREAVPEPVLLSRAELRLURL KLKVEQHVELVQKYSNISWRYLSNRLLAPSDS PBRLSFPDVTLWGET HNEITYDKFRQSTHSITMFFNTSELREAVPEPVLLSRAELRLURL KLKVEQHVELVQKYSNISWRYLSNRLLAPSDS PBRLSFPDVTLY RQMLSRGSEIEGFFLSSAHGSCDSRDMTLQVDINOFTTGR\RDDL ATHGMRRFPLLIAATPLERQCHLQG\SARAP\CCVPQALEP\ LPIVYY\CVRPKVEQLSMATVRSCKCS  GGGNDLYMCHWENTENDLAWGS\SHRRQAL\DTN\CFSF HGGRCLRC,VHC*HLIFEKDL\GW\KRPG\ABAAP\CCVPQALEP\ LPIVYY\CVRPKVEQLSMATVRSCKCS  GGGNDDYBHONFVKVRNCHKGKETFMEULDEKPLQOTOG RQGMDDYBHONFVKVRNCHKGKETFMEULDEKPLQOTOG RQGMDDYBHONFVKVRNCHKGKETFMEULDEKPLQOTOG RQGMDDYBHONFVKVRNCHKGKETFMEULDEKPLQOTOG RQGMDDYBHONFVKVRNCHKGKETFMEULDEKPLQOTOG RQGMDDYBHONFVKVRNCHKGKETFMEULDEKPLQOTOG RQGMDDYBHONFVKVRNCHKGKETFMEULDEKPLQOTOG RQGMDDYBHONFVKVRNCHKGKETFMEULDEKPLQOTOG RQGMDDYBHONFVKVRNCHKGKETFMEULDERGKTQDEVQ HEKMYQKFLALEERKKESIQIMKTKKQQKRESIFKLEKEANNTE  VLFHNKGEDNOXQKEBGRKKGKLAVERAMKQKSIEMSMKCASOL KEEEKKEKHOKERGRFKLILLESTTQKKEGEEFLLEKERI  PERAEKAEKREKRNADBISRFOPRILHLEILDROAKBDEKSO KQRRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETHTTISKEM  SGGSGKKKKRFREHILDCDLTWSLLARGSVPERGSVENUSHH RFRGQODLLLATGISNGRIYMFTGELLAPAAPFDKKCGRENWTVAFAP DGSYFAMSCGHTVKLVPMSQCLONFLLIHTGTNTKMSM  SCAFSPDSSMLCSGASKAVVAAILV*LRCCHHHSHTGVHSFYLM*S  WLSNGFSVLFFGILLSSSRDLLRE-FNLKFVULIFF*CK-CUSVOK KKKPRRTALLOERSS-TVALIFASCHYNTLI			1	EHCQMHPDLRNSLTGFRCVVCMQTVTSTLELKIHGTFHMQKTGN
KTRCS+LATPKF*VLKVELEPPPPKPFRRGVSRPDSTOLCHVANNIMID  QVSMPRISPSGSDEKKTYQCIKCOMYSRDIOLQVHVANNIMID  EGLNHECKLCSQTFDSPAKLQCHLIEHSFEGMGGTFKCPVCFTV  FVQANKLQQHIFSAHGQEDKIYDCTQCPQKFFFQTELQMTHTTQ  HSS  5902  712  209  LKNRRRSPSIRQSIGSTSVSRWLTSLFTYLDHTADVG*V-FR  IPLKRRGV, 5D*MFQSWLAMAGGTLERAFPGCCAMAMGYMTDTGT  VEPLQTVEVETQGDDLQSLLPHFLDEWLYKFSADEPFIP\GWGE  EFSLSKHPQGTEVKAITYSAMQYVRERPEVFYILDI  5903  2106  735  DTPOPSLEPSTAPPSLESLESPSRFSYLFGDPQFLQGRGLPTT  PALFALSAVPGGAASPMPPSGLRLLPLLIPLLHULTUTGRPAA  GLSTCKTIMELVVRK KIERIRGGILSKLRLASPSSQCEVPGF  PALFALSAVPGGAASPMPPSGLRLLPLLIPLLHULTUTGRPAA  GLSTCKTIMELVVRK KIERIRGGILSKLRLASPSSQCEVPGF  LPEAVLALYNSTRDRVAGESABPEPSPEADYYAKEVTRVLMVET  HNEITYMFKQSTHSIYMFFNTSELREAPPEDYVLLSRAELRLLL  KLKVEQHVELYQKVSNNSWRYLSNRLLAPSDSPEMLSPOVTGVV  RQMLSRGGEIEGFRLSAHCSCOSENNTLQVDINGFTGR\RGDL  ATHIGMMSPFLLLAATPLERACHLQS\SRHRQAL\STRY\CFSF  HGGRNCLRC/VUC*HLIFRRDL\GW\SRHRQAL\STRY\CFSF  HGGRNCLRC/VUC*HLIFRRDL\GW\SRHRQAL\STRY\CFSF  HGGRNCLRC/VUC*HLIFRRDL\GW\SRHRQAL\STRY\CFSF  HGGRNCLRC/VUC*HLIFRRDL\GW\SRHRQAL\STRY\CFSF  HGGRNCLRC/VUC*HLIFRRDL\GW\SRHRQAL\STRY\CFSF  HGGRNCLRC/VUC*HLIFRRDL\GW\SRHRQAL\STRY\CFSF  HGGRNCLRC/VUC*HLIFRRDL\GW\SRHRQAL\STRY\CFSF  HGGRNCLRC/VUC*HLIFRRDL\GW\SRHRQAL\STRY\CFSF  HGGRNCLRC/VUC*HLIFRRDL\GW\SRHRQAL\STRY\CFSF  HGGRNCLRC/VUC*HLIFRRDL\GW\SRHRQAL\STRY\CFSF  HGGRNCLRC/VUC*HLIFRRDL\GW\SRHRQAL\STRY\CFSF  HGGRNCLRC/VUC*HLIFRRDL\GW\SRHRQAL\STRY\CFSF  HGGRNCLRC/VUC*HLIFRRDL\GW\SRHRQAL\STRY\CFSF  HGGRNCLRC/VUC*HLIFRRDL\GW\SRHRQAL\STRY\CFSF  HGGRNCLRC/VUC*HLIFRRDL\GW\SRHRQAL\STRY\CFSF  HGGRNCLRC/VUC*HLIFRRDL\GW\SRHRQALP\CFSP  LPIVY\VURRPKVEQLSMNIVRSCCS  NORMADDYDHONFVKVNNKIKGRPTFMEEVLEHLPGKYDDEVQ  HEKWYQKFLALEERKKSI GINMKTKGREIFKLEKEXANNTP  VLFHNKQEDNQXQKEEQRKXQKLAVEAWKQKSIEMSKANGKCASQL  KEEBEKKKHAADEISRRGETGREDLHKLEKLIDROAKKCASQL  KEEBEKKKHAADEISRRGETGREDLHKLEKLIDROAKKCASQL  KEEBEKKEKKHAADEISRRGETGREDLHKLEKLIDROAKKCASQL  KEEREKARKAADISRRGETGREDLHKEEN  DGSTFANSGGRHTVKLVPBSQCLQNFLLHENTKAVTNSSLLLPR  QNSDGGRKNFREHITOGTIWSSTRTEKSM  AFRYTO-SYSLLETRITEKSM  NASSTPPT-FYSSLINGHWWYN-SLEKLIFFYSTILFT**C			ļ	GSAVQTTGRGQHVQKLYKCASCLKEFRSKQDLVKLDINGLPYGL
OVSMMPRISPSGSDEKKTYQCI KCOMVFYNENDIQUHUANIMMID EGLNHECKLCSQTFDSPAKLQCHLI EHSFEGMGSTFKCPVCFTV FVQANKLQQHIFSAHGQEDKI YDCTQCPQKFFFQTELQMHTMTQ HSS  5902 712 209 LKNRRRSRFSIRGSIGSTSVSRWLTSLFTYLDHTADVQ*V*REF IPLKPRQ*ED*MFQSWLHAWGDTLEEAFEQCAMAMGCYMTDTGT VEPLQTVEWETQGDLQSLLFHFLDEWLYKFSADEPFIP QGGE EFSLSKHPQGTEVKAITYSAMQVYMERNEVEYVIIDI  5903 2106 735 DTPGPSLPSTTAPFSLRSLSPFSRPSYLLPGDPQPLQGRGLPTT PALPALSALVPGAASPMPPSGLRLLJPLLLMLLVTIFGRPAA GLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPSSGVPPGP LPPAVLALVNSTRRVAGESABPEPEPEAPYLKAEVTRVLWVET HNEIYDKFKQSTHSI YMFFNTSSLRAAVPEVALSAELRLLRL KLKVEQHVELYQKYSNNSNRYLSNRLLAPSDSFBLSFDVTGVV RQMLSRGGEIEGFGLSAHCSCOSENDTLQVDINGFTTGR RGDL ATHGMRPPLLLMATPLERACHLOS\SRHRQAL\DTNY\CFSF HGGRNCLRC/VHC*HLIFRKDL\GW\KWI\HE\PKGYHANFC\L GPCPYIMSLDTYSSKVLALVNO\HKPG\ASAAP\CCVPQALEP\ LPIVYY\VGRKPKVEQLSNNIVESCKCS  MMESIENALNTFKERGENIYEELIKEETITNNELSAISRKIDTW ALGNSETEKAFRAISSKVPUMVTPSTLPEBVLLDFEKPLQOTGG RQGANDDYYDHONFFVVRNNIKKKPTFMEEVLEHLEGKTQDEVQ HEKHYQKFLALEERKESIGINKTKLQQKRESIFKLEKEI RGGANDDYYDHONFFVVRNIKKKRPTFMEEVLEHLEGKTQDEVQ HEKHYQKFLALEERKKSIGINKTKLQQKRESIFKLEKEI REKAEKAEKKKHQDERGOFKIKLLLESYOKKROESIFKLEKEI REKAEKAEKKRHAADBISRTGERDLHKLEKLILDGAKSDEKSQ KQRHALKLEVENNVSRPSPSRLY\NTHQKRCASGLEY KGEREKKKHQDERGOFKIKLLLESYOKKROESIFKLEKEI REKAEKAEKKRNAADBISRTGERDLHKLEKLILDGAKSDEKSQ KQRHALKLEVENNVSRPSPSRLY\NTHQKRCHTRUM ATSTYPT*GYSNLETRRTEKSMR  5905 287 2912 MASSFPREVNEKSIUZERTIGELLAPAAPFDKKGGRENTVAFAA DGSYFAANSGGRTVKVLDWSQCLQMYHRCMSNSTFCF SFFLFFFFKVISPTVKYH*LLSKLIFQFYGGSLTSETNLM*SI GNSGGGQKNKPREHIIDCGDIVWSLAPGSSVPEKQSRCVNIEWH RFRGQDQLLLATGINSGRIKHDVTTGKLJTHLSVSSLRLPR VSCHRAHLQEERLS*PKPSSHLLY*DRLCHWHSNTGATHVLS WAREVASLATGLAGFTTG'SNLATHLY*LRCUCHHSNTGATHVLS WAREVASLATGLAGFTTG'SNLATHLY*LRCUCHHSNTGATHVLS WAREVASLATGLAGFTTG'SNLATHLY*LRCUCHHSNTGATHVLS WAREVASLATGLAGFTTG'SNLATHLY*TRCUCHHSNTGATHVLS WAREVASLATGLAGFTTG'SNLATHLY*TRCUCHHSNTGATHVLS WAREVASLATGLAGFTTG'SNLATHLY*TRCUCHHSNTGATHVLS WAREVASLATGLAGFTTG'SNLATHLY*TRCUCHHSNTGATHVLS WAREVASLATGLAGFTTG'SNLATHLY*TRCUCHHSNTGATHVLS WAREVASLATGLAGFTTG'SNTAVHIFTCSCTFS*A QVGDPSLL*TSDYLKGRCOWNN	1		1	CAGCVNLSKSASPGINVPPGTNRPGLGQNENLSAIEGKGKVGGL
### FIGURIER KILCSGTFDS PARKLOCHLI EHS PERMEGTEKCP VCFTV PVQANKLQHIPSAHQQEDKIYDCTQCPQKFFPQTELQNHTMTO HSS    100	1		1	KTRCS*LATFKF*VLKVELPEPHPKPFHRGVSRPDSNSTQLKTP
FVQANKLQQHIFSAHGQEDKIYDCTQCPQKFFFQTELQNHTMTQ HSS  5902  712  209  LKNRRRSRPSIRQSIGSTSVSRWLTSLFTYLDHTADVQ*V*REF IPLKPRQ*SD*MFQSWLHAWGDTLEEAFEQCAMAMFGYMTDTGT VEPLQTVEWTGTQBDLQSLLPHIGULYKFSADBPFIP\GWGE EPSLSKHPQGTBVKALTYSAMQVYNEENPEVPVIDI  5903  2106  735  DTPGPSLPSTTAPFSLRSLSPPSRPSYLLPGDPQPLQGRGLPTT PALFALSAVPGGAASPMPSGLRLPLLLDLLWLULTPGRPAA GLSTCKTIDMELVKRRIEAIGGLLSKLKLASPPSQGEVPPGP LPPAVLALMYNSTRDAVAGGSASPPDEPEADYYAKEVTRVLMVET HNEIYDKFKQSTHSIYMFFNTSELREAVPEPVVLSRAELRLLRL KLKVEGNVELYGXYSNNSWRVLSNRLLASPBSBFWLSPDYTGVV RQWLSRGGEIEGFRISAHCSCDSENDTLQVDINGFTTGR\RGDL ATTHGMRRPFLLMATPLERAQHLQS\SRHRQAL\DTMY\CPSF HGGRNCLRCV/NC+HLIFRKDL\GWAYLNYE HVANTAVCL GPCPYIWSLDTQYSKVLALYNQ\HKPG\ASAAP\CCVPQALEP\ LPIVYY\VGKKFKVEOLSNMTVRSCKCS  MMESI ENALNTFKEEGRILYEELIKEKETTNEELSAISRKIDTW ALGNSTEKAFRAISSKVPUKVTPSTLPBEVLDFEKFLQQTGG RQGAMDDYDHQNFVKVRNKHGKFUTYGVLKGESEFLELKEKI REKHYQKFLALEERKKESIQIWKTKKQQKREBIFKLKEKADNTP VLPHNKQEDNQKKEEQRKKQKLAVEAWKKQKSIEMSMKCASQL KEEEKKEKKHQKERQRFKKLLLSTQQKKEGEEFLELKERI REKAEKAEKKRNADDISRFQERDLHKLELKILDRQAKEDEKSQ KQRRLAKLKEKVENNVSRDPSRLY\NTHQRLGRTNQKKDTNRLM ATSTYPT*GYSNLETRNTEKSMR  5905  287  2912  MASFPPRWNKEIVELRTIGELLAPAAPFEKKGRENMTVAFAP ONSDGGQKNKPRHIIDCGDIVMELLHGTNNVTNSSSLELPR ONSDGGQKNKPRHIIDCGDIVMELLHGTNNVTNSSSLELPR ONSDGGQKNKPRHIIDCGDIVMELLHGTNNVTNSSSLELPR ONSDGGKNKPRHIIDCGDIVMELLHGTNNVTNSSSLELPR ONSDGGKNKPRHIIDCGDIVMELLAFGSSVPKKGRGNNVTV SCAFSPDSMLCSVGASKAVVAAILV*LRCHCHHSHTGATNVLS WAERVASLATGLGAFTIG*SNAFTTG*CNLTUCGVLYVHRCMSMSTFCF SFFLFFFFKVISPTVKYH*LLSKLIFPFV*CIVSVQK KKKPRRTALLGERRLS*DKPRSGHILT*CHGVHTSHTSLTFFKKFILM*SI WLSNGFSVLFFGILDSSBULRI-*FNLKVLUGGHVYMKMSFFIEM *LYYFHKIAFSFCUNV*+PCLLFFFV*KFGLIFFF*K*CIVSVQK KKKPRRTALLGERRLS*DKPRSHLITQGVTVKHLELLIFFF*K*CIVSVQK KKKPRRTALLGERRLS*DKPRSHLITQGVTVKHLELLUFFF*K*CIVSVQK KKKPRRTALLGERRLS*DKPSELTHTVTLIFFKKLLIINNA*L *LUFIT*NCI-*TTS*1TDFFTJQMTYDGSFGRKMVKF*FIEM *LYYFHYLAFSFCUNV*+PCLLFFKLHTJFSVYFFKNLUVSGKK REGGL*VLTLTFISVYFS*LVFGIMSGQYSVKLHCLUFFMRIL *LYTHRNI*NRI*ONGALINLETFLUTTHLSIFFKKLLIIINNA*				QVSPMPRISPSQSDEKKTYQCIKCQMVFYNEWDIQVHVANHMID
HSS	}			EGLNHECKLCSQTFDSPAKLQCHLIEHSFEGMGGTFKCPVCFTV
S902   T12   S09				FVQANKLQQHIFSAHGQEDKIYDCTQCPQKFFFQTELQNHTMTQ
IPLKPRQ*ED*MFQSWLHAWGDTLEEAPEQCAMAMFGYMTDTGT  VEPLQTVEVETQGDDLQSLLPHFLDEWLYKFSADEPFIP\GWGE EFSLSKHPQGTEVKATTYSAMQYMEEMPEVPVIIDI  5903  2106  735  DTPGGSLPSTTAPPSLBSLSPPSRPSYLLPGDPQDLQGRGLPTT PALFALSAVPGAASPMPPSGLRLPLLLPLLWLLVLTPGRPAA GLSTCKTIDMELVKRKRIEAIRGQTLSKLRALSPPSGGEVPPGF LPEAVLALYNSTRDRVAGESABPEPEPBEADYYAKEVTRVLMVET HNEITYDKFKGSTISISIMFPNTSELREAVPEVPLLGRAELRLLRL KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSPDVTGVV RQWLSRGGEIEGFRLSAHGSCDSRDNTLQUINGFTTGR\RGGL ATHGMREPFLLMATPLERACHLQS\SHRHQAL\DTNY\GFSF HGGRNCLRC/VHC*HLIFRCDL\GW\KWT\HE\PKGYMANFC\L GPCPYIWSLDTQYSKVLALYNQ\HKPG\ASAAP\CCVPQALEP\ LPIVYY\VGRKPKVEGLSMMIVSCKCS  MMESIENAINIFKEEGRLIYEELIKEEKTINDEJSAISKIDTW ALGMSETKAAFRAISSKVPVMYSTPLEEVLDPEKFLQQTGG RQGAWDDYDHQNFVKVRNKHKGKPTFMEEVLEHLDFEKFLQDTGG RQGAWDDYDHQNFVKVRNKHKGKPTFMEEVLEHLDFEKFLQDTGG RQGAWDDYDHQNFVKVRNKHKGKPTFMEEVLEHLDFEKFLQDTGG RQGAWDDYDHQNFVKVRNKHKGKPTFMEEVLEHLDFEKFLQDTGG RQGAWDCKERGRKKGKLAVEAWKKKSIEMSMKKCASQL KEEBEKEKKHQKERGRGFKLKLLLESYTQOKKEGEEFIRLEKEI REKAEKAEKRNAADBISRFQERDLKKLELKILDROAKEBEKSG KQRRLAKLKEKVENNVSRDPSRLY\NTHQRJGRTNQKRTRILW ATSTTYPT*GYSNLETRNTEKSMR  5905  287  2912  MASSPPRWREET UTLRTTGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGGKNKPREHIIDCGDIWWSLAPGSSVERGSRCVNIEMH FRFRGDQDLLLATGLANSGRIKTUVTFTGLLINDTHTGVVRDL TFAPGGSLILVSASRDKTLRVWDLRDDGN\MKVLRGHQNWY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRCHMHSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCMSMSTFCF SFFLFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDILLV*PRILEVHHSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCMSMSTFCF SFFLFFFFKVISPTVKYH*LLSKLIFQFYGGSLTSSTNLM*SI WLSNGFSVLFFGILSDSRDILLV*PRILEVHHSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLGGVLYVHRCMSMSTFCF SFFLFFFKVISPTVKYH*LLSKLIFQFYGGSSTSS*A QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLLVVSQKK REGGL*VITTUFSSLYGFLVFFVGTCHTCFGSTS*A QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLLVVSGKK REGGL*VITTUFSSLYFFLVFTTGLTTTLSSFFVKLHLLYFFKLLIVTNA*				HSS
IPLKPRG*ED*MPGOSILLAWGDTLEEAPBOCAMAMFGYMTDTGT VPPLQTVPVETQGDDLQSLLPHFLDEWLYKFSADEPFIP\GWGE EFSLSKHPQGTEVKAITYSAMQVYMEEMPEVPVIIDI  5903 2106 735 DTPGGSLPSTTAPPSLRSLSPPSRPSYLLPGDPQPLQGRGLPT PALPALSAVPGGASMPMPPSGERLPLLLPLLHULUTPGRPAA GLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGVPPGP LPEAVLALYNSTRDRVAGESABPEPEPBEADYYAKEVTRVLMVET HNEITYDKFKQSTISI'STMFMTTSELRSAVPEPVLLSRAELRLLRL KLKVEQHVELVQKYSNNSWRYLSNRLLAPSDSPEMLSFDVTGVV RQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFTTGR RGDL ATIHGMMRPPLLLMATPLERAQHLQS\SHRQAL\DTNY\CFSF HGGRNCLRC/VHC*HLIFRRDL\GM\KMY\HE\PKGYMANPC\L GPCPYINSLDTQVSKVLALYNQ\KKG\SSHRQAL\DTNY\CFSF HGGRNCLRC/VHC*HLIFRRDL\GM\KMY\HE\PKGYMANPC\L GPCPYINSLDTQVSKVLALYNQ\KKG\SPAPACCVPQALEP\ LPIVYY\VGRKPKVEQLSNMIVRSCKCS MMESIENAINTFKEEGRLIYEELIKEEKTINNESAISKIDTW ALGNSETEKAPRAISSKVPVMLYPSTLJEEVLDFEKFLQQTGG RQGANDDYDHQNFVKVRNKHKGKPTFMEEVLBHLBGKTQDEVQQ HEKHYQKFLALEERKKESIQINKTKKQKREEIFKLLKEKADNTP VLFHNKQEDMQKQKERGRKGKLAVEAWKKQKSIEMSMKKASQL KEEEEKEKKHQKERGRGKKLAVEAWKKQKSIEMSMKKASQL KGRRLAKLKEKVENNVSRDPSRLY\NTHGRIGGTNQKDRTNRLW ATSTTYF*GYSNLETRNTEKSMR  5905 287 2912 MASSPPRVNREETURLTTGELLLAPAAPFDKKGGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIWWSLAPGSSVEKQSRCNNIEMH FRFRGODOLLLARGHNSGHIKUVYTGKLLLINDTHGVVYDL TFAPGGSLLVSASRDKTLRVMDLRDDGN\MKVLRGHQNWY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRCHMHSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCMSMSTFCF SFFLFFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLPFGILSSRDILLTFRAILWS*LLLIFFR*LSVLYFKKLUVSVQK KKKPRIALLQEERLS*DKPPSSHLI*QTEVNIRILFFRAILHS* LLIFRI*NCI*TTS*IIDPFYQMTYDGR*FGKKMMVKF*FIEM VLYTHKLTFISSYTES*LUFGKTGGCPKKHLAVNILIFCRSS*CFS*A QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLLVVSKK REGGL**VITLTFISSYTES*LVFFINGNGPQYSFVVLHCLYFFKKLLIVSFK PLATTHKNI*NINGSALINLKTDEPLYTTTLTSTFKLLIYFFKLLIVYNGKK REGGL**TITLFISSYTES*LVFTINGTGFTYSFVVLHCLYFFFKLLIVINA*	5902	712	209	LKNRRRSRPSIROSIGSTSVSRWLTSLFTYLDHTADVQ*V*REF
VEPLOTTEVETCGDDLOSLLPHFLDEMLYKFSADEPF1P\GWGE  EFSLSKHPQGTEVKAITYSAMQVYNEENPEVFVIIDI  5903  2106  735  DTPGPSLPSTTAPPSLRSLSFPSRPSYLLPGDPQFLQGRGLPTT PALPALSAVPGGAASPMPPSGLRLLPLLLPLLWLLVLTPGRPAA GLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGP LPEAVLALYNSTRDRVAGESARPEPEPEADYYAKEVTRVLMVET KLKVEQHVELYOKYSNNSWRYLSNRLLAPSDPSPEADYTAKEVTRVLMVET KLKVEQHVELYOKYSNNSWRYLSNRLLAPSDPSPEADSPORTGVV RQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFTTGR\RGDL ATHGMMRPFLLLMATPLERAGHLQS\SHRQAL\DTNY\CFSF HGGRNCLRC\MC\MC\HIFFROL\GW\KMT\KE\PKGPLAYV\CFSF HGGRNCLRC\MC\MC\HIFFROL\GW\KMT\KE\PKGPANAPC\L GPCPYIWSLDTQYSKVLALYNQ\HKPG\ASAAP\CCVPQALEP\ LPIVYY\QRKPRVEQLSMNIVRSCKCS GPCPYIWSLDTQYSKVLALYNQ\HKPG\ASAAP\CCVPQALEP\ LPIVYY\QRKPRVEQLSMNIVRSCKCS RQGADDYDHQNFVKVRNCHKKRYFTMEEUSAISRKIDTW ALGNSETEKAFRAISSKVPVDKVTPSTLPBEVLDFEKFLQOTGG RQGADDYDHQNFVKVRNCHKKRYFTMEEUSAISRKIDTW VLFHNKGBDNQKOKEBGRKKQKLAVEAMKKQSI EMSMKCASOL HEKWYQKFLALEERKKESIQIHMITKKKQOKREEI FKLKEKADNTF VLFHNKGBDNQKOKEBGRKKQKLAVEAMKKQSI EMSMKCASOL KEEBEKEKKHQKERQROFKKKLLVEAMKKQSI EMSMKCASOL KEEBEKEKKHQKERQROFKKKLLLESTYQKKEQSEFLRLEKEI REKAEKAEKERNAADEISRFQERDLHKLELKILDRQAKEDEKSO KQRRLAKLKEVENNYSDPSRLY\NTHQRIGRTNQKDRTNRLM ATSTYPT*GYSNLETRNTEKSMR SHYPT*GYSNLETRNTEKSMR ONSDGQKNKPREHIIDCGDIVWSLAFGSSVERKGRCVNIEHH RFRRGQDQLLLATGLASGRIKWDVYTGKLLINLVDHTGVVRDL TFAPDGSILVSASRDKTLRVMDLRDDON\MKVLRGRQNNYY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCHWHSHTGATMVLS SCAFSPDSSMLCSVGASKAVVAAILV*LRLCHWHSHTGATMVLS SCAFSPDSSMLCSVGASKAVVAAILV*LRLCHWHSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF SFPLFFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI ULSNGFSVLPFGILSOSDGILL*NHLSHTGATMVLS KKKPRIALLQEERLS*DKPPSSHLI*QTEVGNYOKKFFILM *LYYTYHXIARSFGILSOSDGILK*PNLEVPLIFF**C*CIVSVQK KKKPRIALLQEERLS*DKPPSSHLI*QTEVNILFFASILHS* LLIFRI*NCI*TYS*IIDPFYLOMYTORG*FGKKKMWKFFILM *LYYTHKNIFNITMS*LVMSGLVYFKKLLVYFFKKLLVYSKK REGGL*YLTLTFISVYFS*LVFGINGSPQYSFVVKLHCLYFFMFRLI *LYYTHKNIFNITMS*LVMSALINLKTDFNLTTMTLSIFFKLLIIVNA*	3302	,	1	IPLKPRO*ED*MFOSWLHAWGDTLEEAFEOCAMAMFGYMTDTGT
EPSLSKHPQGTEVKALTYSAMQVYNEENPEVFVIIDI  5903  2106  735  DTPGPSLPSTTAPFSLERSLSPPSRESYLPGPDQPLQGRGLPTT PALFALSAVPGGASSMPPBSGLRLIPLLIPLIMLLUTTPGRPAA GLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGP LPEAVLALYNSTRDRVAGESABPEEPBEADYYAKEVTRVLMVET HNEITYDKFKQSTIESITMFINTSELRSAVPEPVLLGRAELRILRIL KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVV RQWLSRGGEIEGFRLSAHGSCDSRDNTLQVINGFTTRR\RGDL ATHGMREPFLLMATPLERACPLQS\SHRQAL\DTMY\GFSF HGGRNCLRC/VHC+HLIFRKDL\GW\KWI\HE\PKGAL\DTMY\GFSF HGGRNCLRC/VHC+HLIFRKDL\GW\KWI\HE\PKGANAPC\L GPCPYIMSLDTQYSKVLALYNO\HKPG\ASAAP\CCVPQALEP\ LPIVYY\GKRKPKVEQLSMWINSCKCS  5904  3  1126  MMEBIENAINTFKEEQRLIYEELIKEEKTINBELSAISRKIDTM ALGNSETEKAFRAISSKVPURKVTPSTLEPEVLDPEKPLQOTGG RQGAMDDYHGDNFVKVNNHKKKGKPTFMEEVLEHLPGKTQDEVQQ HEKWYQKFLALEERKKESIQIWKTKKQOKRESIFKLEKKADNTP VLFHNKQEDNGKQKERQRKKQKLAVEAWKKQKSIEMSMKCASQL KEEBEKEKKHQKERQROFKIKLLLESYTQQKKEGEFIRLEKEI REKAEKAEKKRNAADBISRPQERDLHKLELKILDRQAKEDEKSQ KQRRLAKLIKEKVENNVSRDGRLYNTHQKDRTNRLW ATSTYPT*GYSNLETINTEKSMR  5905  287  2912  MASPPPRWEKEIVRLTIGELLAPAPPBKKGGRENWTVAFAP DGSYFAWSGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR RFRFGQDQLLLATGINSGRIKIMDVYTGKLLINLVDHTGVVRDL TFAPDGSLILVSASRDKTLRVDLDEDDN\MMKVLRGHQNWVY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCCHHISHTGVTNVLS WAERVASLATGLGATFTIG*SVLAFVGLOGLVVHRCWMSSTFCF SFFLFFFFKVISPTVKYH*LLSKLIFGFYGIGSLTSETNLM*SI WILSNGFSVLFFGILSDSRDILRL*PNLKEVLIFF*K*CIUSVQK KKKPRIALLQEERLG*DKPPSSHLI*QTEVATRLFFSLYFFRILMS* LLIFRI*NCI*TY*S'IDPFYIQMTYDRG*FGKNKWKF*FIEM WILSNGFSVLFFGILSDSRDILRL*PNLKFVLIFF*K*CIUSVQK KKKPRIALLQEERLG*DKPPSSHLI*QTEVATRLFFAILHS* LLIFRI*NCI*TY*S'IDPFYIQMTYDRG*FGKNKWKF*FIEM *LYYTHKIARSFCNVV*HPCCLPKFHLAVNILFACSICTSS*A QVGDPSLL*TATDYLKGRCQWSNNILTLRFLSVYFFKNLUVVSGK REGGL*YLTLFISVYFFS*LVFGINNGFQYSFVVKLHCLYFFMFRLI FKLIFTNRI*NITMSICMSALINLKTDEPNITMTLSIFFKLLIIVNA*				
2106  735  DTPGPSLPSTTAPPSLRSLSPPSRPSYLLPGDPQPLQGRGLPTT PALFALSAVPGGASSPMPPSGLRLLIPLLIPLLIMILUTTPGRPAA GLSTCKTIDMELVYRKRIEJARGGILSKURLASSPSQGEVPPGF LPEAVLALYNSTRDRVAGESABPBEPBEADYYAKEVTRVLMVET HNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL KLKVEQHVELLYGKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVV RQWLSRGGEIBGFELSAHCSGDSRDNTLQVDINGFTTGR\RGDL ATHGMRRPFLLLMATPLERAQHLQS\SRHRQAL\DTNY\CFSF HGGRNCLRC\VHC+HLIFRKDL\GW\KWI\HE\PKGYHAMFC\L GPCPYIMSLDTQYSKVLALYNQ\KKPG\ASAAP\CCVPQALEP\ LPIVYY\GRKPKVEQLSNNTVRSCKCS  5904  3 1126  MMEBIENAINTFKEEQRLIYEELIKEEKTTNNELSAISRKIDTW ALGNSETEKAFRAISSKVPVDKVTPSTLPEEVLDFEKFLQQTTGG RQGANDDYDHONFVVRNKHKGKPFTMEEVLEHLDGKTDQDFVQQ HEKWYQKFLALERKKESIQIWKTKKQQKREEIFKLKEKADNTP VLFHNKQBDNQXQKEBGRKXQKLAVEAWKKQKSIEMSMKCASQL KEEBEKEKKHOKERGOPGKKXQKLAVEAWKKQKSIEMSMKCASQL KEEBEKEKKHOKERGOPGKKXQKLAVEAWKKQKSGEMSMKCASQL ATSTYPT*GYSNLETNTRLEKLLESYTYOKKGGEEIFKLEKEI REKAEKAEKRNAADEISRFQERDLHKLLEKILDROAKEDEKSQ KQRRLAKLKEEVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETNTRLEKLLESYTYOKKGGEEFLEKEI REKAEKAEKRKNAADEISRFQERDLHKLEKILDROAKEDEKSQ KQRRLAKLKEEVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETNTRLEKLLESYTYOKKGGEGEFLKGKLINLVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDDGN\MKVLRGHQNWVY\ SCAF\$PDSSMLGVSASKAVVAAILV*LRCCWHISHTGATTNVLS WAERVASLATGLGAFFTIG*SNLAFVLQGULYVHRCMSMSTFCF SFFLFFFFKVISPTVKYH*LLSKLIFFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSGBGILRL*FNLLFFYLIFF*K*CIVSVQK KKKPKRIALLQEERLS*DKPPSSHLI*QTEUNGRYFURF*KEILWSVQK KKKPKRIALLQEERLS*DKPPSSHLI*QTEUNGRYFKFLIHS* LLIFRI*NCI*TYS-1LDFFYIQMTYDRG*FGKNKMVKF*FIEM *LYYYTHKIAFSFCNV*HPCCLPKKFHLAVNILFFACICTSS*A QVGDPSLL*TSDYLKGRQOWSNNLLTLEFLSVYFFKNLVVSGKK REGGL*YLTLPISVYFS*LVFGINGPQYSFVVKLHCLYFMFRLI FKLTTNRNI**RKICMSALINLKTDFNLTMTLISIFFKLLITYNA*				
PALFALSAVPGGAASPMPPSGLRLLPLLLPLLWLLVLTPGRPAA GLSTCKTIDMSLVKRKRIEAIRGGILSKKRLASPPSGGEVPPGF LPEAVLALYNSTRDRVAGESABP EPEADYYAKEVTRVLWVET HNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL KLKVEQHVELVQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVV RQWLSRGGEIEGFELSAHCSCDSRDNTLQVDINGFTTGR\RGDL ATIHGMNRPFLLLMATPLERAQHLQS\SRHRQAL\DTNY\CFSF HGGRNCLRC/VHC*HLIFRKDL\GW\KNI\HE\PKGYHAMFC\L GPCPYIMSLDTQYSKVLALVNQ\KKPG\ABAAP\CCVPQALEP\ LPIVYY\VGRKPKVEQLSNMIVRSCKCS  5904 3 1126 MMEBIENAINTFKEEGRLIYEELIKEEKTINNELSAISRKIDTW ALGNSETKAFRAISSKVPUDKVTPSTLPEEVLDFEKPLQOTGG RQGAWDDYDHQNFVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ HEKWYQKFLALEERKESIGIWKTKAQOKREEIFKLÆKADNTP VLFHNKQBDNQKKEEGRKKKALAVEAWKKQKSIEMMKCASOL KEEEKEKKHQXERQRGFKLKLLLESYTQKKKEGEEFIRLEKEI REKAEKAEKRRNAADBISRTQERDLHKLELKILDRQAKBDEKSG KQRRLAKLKEKVENNVSRDBSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR  5905 287 2912 MASFPPRVNEKEIVULRTIGGLLAPAAFFDKKCGRENWTVAFAP DGSYFAMSGGRTVKLVPWSCLOPHLHGTKNVTNSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPEKQSRCVNIEWH RFRFGODCLLLATGLNSGRIKIWDVYTGKLLLLNLVDHTGVVRDL TFAPDGSLLLVSASRDKTLRVWDLRDDGN\MKVKLRGHQNWY\ SCAFSPDSSMLCSVGASKAVVAAILV-LRICWHHSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLLGVLYVHRCWSMSTFCF SFFLFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLPFGILSDSRDILRL*FNLKFVLIFF*K*CINSVQK KKKPRRIALLQEERLS*DKPPSSHLI*OTEVNIRILFFAILHS* LLIFRI*NCI*TYS*IIDFFYIQMTYDRG*FGKNKMVKF*FIEM *LYYFHKIAFSFCNV*HPCCLPKKFHLAVNILFACSICFSS*A QVGDPSLL*TSDYLKGRQOWSNNLLTLEFLSVYFFKNLVVSGKK KREGGL*YLTLPISVYFS*LVFGINGPQYSFVVKLHCLYFMFRLI FKLTFNRNI*NRICMSALINLKTDFNLTMTLSIFFKLLIYINA*	5002	2106	725	
GLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGF LPEAVLALYNSTRDKAGESABPESPEADYYAKEVTRUMVET HNEITYDKRKQSTHS IYMFRITSELRSAVPSPVLLSRAELELLRL KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVV RQWLSRGGEIEGFRLASAHGSCDSRDNTLQVDINGFTTGR\RGDL ATIHGMNEPFLLHAMTPLERACHLQS\SKHRQAL\DTNY\CFSF HGGRNCLRC\VHC*HLIFRKDL\GW\KW\HE\PKGYHANFC\L GPCPYIWSLDTQYSKVLALYNQ\HKPG\ASAAP\CCVPQALEP\ LPIVYY\VGRKPKVEQLSMMIVRSCKCS  MMESIENAINTFKEEQRLIYEELIKEEKTINNELSAISRKIDTW ALGNSETEKAFRAISSKVPVDKVTPSTLPEEVLDFERPLQDTGG RQGAWDDYDHQNFVKNRNKKKKPTFMEEVLEHLPGKTQDEVQQ HEKWYQKFLALEERKKESIQIWKTKKQQKREBIFKLKEKADNTP VLFHNKQEDNQXQKEBQRKKQKLAVEAWKKQKSIEMSMKCASQL KEEBEKEKKHQKERGRQFKLKLLLBSYTQQKKKQEEFLRLEKEI REKABKABKRKNAADBISSFQERDLHKLEKILDROAKBDEKSG KQRRLAKLKEKVENNVSRDPSRLY\NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR  5905 287 2912 MASPPRVNEKEIVRLRTIGELLAPAAPFDKKGGRENWTVAFAP DGSYFAMSGGHRTVKLVPWSQCLQWFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIDCGDIVWSLAFGSSVPBKQSRCVNIEWH RFRFGQDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL TFAPDGSLILVSASRDKTLRVMDLRDDGN\MMKVLRGHQNWYY SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS WAERVASLATGLGAFTTIG*SNLAFVLQGVLYVHRCWSMSTFCF SFFLFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDILRL*PNLKFVLIFF*K*CIVSVQK KKKPKRIALLQEERLS*DXPPSSHLI*QTYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDILRL*PNLKFVLIFF*K*CIVSVQK KKKPKRIALLQEERLS*DXPPSSHLI*QTFGGFGNKMVKF*FIEM *LYYFHKLAFFSFCNVV*HCCLPKKFHLAVNILFACSICFSS*A QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLLVYSGKK REGGL*YLTLPISVYFFS*LVFGINGPQYSFVVKLHCLYFMFRLI FKLTTNRNI*NRICKSALINLKTDERLITMILSIFFKLLIIYNA*	5903	2106	/33	1-
LPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVET HNEITYDKFKGSTHSIYMFFNTSELERAVEPPVLLSRAELRLLRL KLKVEQHVELYGKYSMNSWRYLSNRLLAPSDSPEWLSFDVTGVV RQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFTTGR\RGDL ATHGMNEPFLLLMATPLERAGHLQS\SRHRQAL\TITY\CFSF HGGRNCLBC\VHC*HLIFRKDL\GW\KWI\HE\PKGPLAMFC\L GPCPYIWSLDTQYSKVLALYNQ\HKPG\ASAAP\CCVPQALEP\ LPIVYY\GREPKVEQLSNMTVRSCKCS  MMEBIENAINTFKEEGRLIYBELIKEEKTTNNELSAISRKIDTW ALGNSETEKAFRAISSKVPVDKVTPSTLPEEVLDFEKPLQQTGG RQGAMDDVDHONFVKVRNCHKGKPTFMEEVLEHLPGKTQDEVQQ HEKWYQKFLALEERKKESIQIWKTKKQQKREBIFKLKEKADNTP VLFHNKQBDNQXKEEQRKKQKLAVEAWKKQKSIEMSMKCASQL KEEBEKEKKHQKERGRQFKLKLLLESYTQQKKRQEEFLRLEKEI REKAEKAEKRKNAADEISRFQERDLHKLELKILDRQAKEDEKSQ KQRLAKLKEKVENNVSRDPSLIY\NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR  S905  287  2912  MASFPPRVNEKEIVRLRTIGELLAPAAPFDKKCGRENWTVAFAP DGSYFAMSGGHRTVKLVDPSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQRNKPREHIDCGDIVWSLAFGSSVPEKQSRCVMIEWH RFRFGQDQLLLATGLNSGRIKIWDYTGKLLHUVDHTGVVRDL TFAPGSLILVSASROKTLRVNDLRDDGN\MMKVLRSHGNWVY SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCMSMSTFCF SFPLFFFKVISPTVKYH*LLSKLIFGFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDILRL*FNLKFVLIFF*K*CIVSVQK KKKPRRIALLQEERLS*DKPPSSHLI*QTEVGIGSTETSTNLM*SI WLSNGFSVLFFGILSDSRDILRL*FNLKFVLIFF*K*CIVSVQK KKKPRRIALLQEERLS*DKPPSSHLI*QTEVGHFFAILHS* LLIFRI*NCI*TYS*IDPPSYLMTROF*GRNKWVKF*FIEM *LYYFHKLAFSFCNVV*HPCCLPKKHLAVNILFACSICFSS*A QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLLVSGKK REGGL*YLTLPSISVYFFS*LVFGINGPQYSFVVKLHCLYFMFRLI FKLTTNRNI*NNICNSALINLKTDFRLITMTLSIFFKLLIIYNA*		ì		
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WLSNGFSVLFFGILSDSRDILRL*FNLKFVLIFF*K*CIVSVQK KKKPKRIALLQEERLS*DKPPSSHLI*QTEVNIRILFRAILHS* LLIFRI*NCI*TYS*IIDPFYIQMTYDRG*FGKNKMVKF*FIEM *LYYFHKIAFSFCNVV*HPCCLPKKFHLAVNILFACSICFSS*A QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLVVSGKK REGGL*YLTLFISVYFS*LVFGINGPQYSFVVKLHCLYFMFRLI FKLTFNRNI*NRICMSALINLKTDFNLTMTLSIFFKLLIIYNA*	1		1	
KKKPKRIALLQEERLS*DKPPSSHLI*QTEVNIRILFRAILHS* LLIFRI*NCI*TYS*IIDPFYIQMTYDRG*FGKNKMVKF*FIEM *LYYFHKIAFSFCNV*HPCCLPKKFHLAVNILFACSICFSS*A QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLVVSGKK REGGL*YLTLFISVYFS*LVFGINGFQYSFVVKLHCLYFMFRLI FKLTFNRNI*NRICMSALINLKTDFNLTMTLSIFFKLLIIYNA*			1	
LLIFRI*NCI*TYS*IIDFFYIQMTYDRG*FGKNKMVKF*FIEM  *LYYFHKIAFSFCNVV*HPCCLPKKFHLAVNILFACSICFSS*A QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLVVSGKK REGGL*YLTLFISVYFS*LVFGINGPQYSFVVKLHCLYFMFRLI FKLTFNRNI*NRICMSALINLKTDFNLTMTLSIFFKLLIIYNA*				
*LYYFHKIAFSFCNVV*HPCCLPKKFHLAVNILFACSICFSS*A QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLVVSGKK REGGL*YLTLFISVYFS*LVFGINGPQYSFVVKLHCLYFMFRLI FKLTFNRNI*NRICMSALINLKTDFNLTMTLSIFFKLLIIYNA*			ł	
QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLVVSGKK REGGL*YLTLF1SVYFS*LVFGINGPQYSFVVKLHCLYFMFRLI FKLTFNRNI*NRICMSALINLKTDFNLTMTLSIFFKLLIIYNA*				
REGGL*YLTLFISVYFS*LVFGINGFQYSFVVKLHCLYFMFRLI FKLTFNRNI*NRICMSALINLKTDFNLTMTLSIFFKLLIIYNA*			1	
FKLTFNRNI*NRICMSALINLKTDFNLTMTLSIFFKLLIIYNA*				
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<u></u>			1	INDN-1-QF-YKMCHFVLCMSE-SYNICLFIAGF (LWNMDKYTM

SEQ	Predicted	Predicted end	I Smiles and A
ID	beginning	nucleotide	
NO:	nucleotide	location	Interest to the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr
	location	l .	Grucamic Acid, F=Phenvlalaning C_Cluster
	corresponding	corresponding	H=H1stidine, I=Isoleucine V_I;
1	to first	to first	L=Leucine, M=Methionine N=Asparacine
	amino acid	amino acid	Parcoline, OaGlutamine, Ranginine
	residue of	residue of	S=Serine, T=Threonine, V=Valine
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown t-Cha-
		sequence	Codon, /=possible nucleatide deletion
ļ	sequence		( \=possible nucleotide insertion)
			IRKLEGHHHDVVACDFSPDGALLATASVDTBVVTkDDVXCDTV
			EFGHLFPPPTPIFAGGANDRWVRSVSFSHDGLUVAGI ADDVAUD
		i	FWRIDEDYPVQVAPLSNGLCCAFSTDGSVLAAGTHDGSVYFWAT
			PRQVPSLQHLCRMSIRRVMPTQEVQELPIPSKLLEFLSYRI
5906	146	2038	REGAGSGRMASGA\YNPYIEIIEQPRQRGMRFRYKCEGRSAGSI
1			PGEHSTDNNRTYPSIQIMNYYGKGKV\RITLVTK\NDPYKPHPH
1			DLVGKDCRD\GYYEAEFGQE\RRP\LFFQN\LGIRCVKKKEVKE
			A/IITR/IKAGINDEDVD+VOLVETER CON/LGIRCVKKKEVKE
ì	}		A\IITR\IKAGINPFDVP*KQLNDIEDCDLDVVRLWFRVFLPDG
	1		HGNL\TTALPPV\VSSPIYDNRAPNTAELRVCRVNKNCGSVRGG
			DEIFLLCDKVQKDDIEVRFVLNDWEAKGIFSQADVHRQVAIVPK
			TPPYCKAITEPVTVKMQLRRPSDQEVSESMDFRYLPDEKDTYGN
1			KAKKQKTTLLFQKLCQDHVETGFRHVDQDGLELLTSGDPPTLAS
			QSAGITVNFPERPRPGLLGSIGEGRYFKKEPNLFSHDAVVREMP
			TGVSSQAESYYPSPGPISSGLSHHASMAPLPSSSWSSVAHPTPR
			SGNTNPLSSFSTRTLPSNSOGIPPFIRIPVGNDLNACNACNACNAC
			ADDIVGMEASSMPSADLYGISDPNMISNCSVMMMTERSPRAGER
i i			DNPRLLSMNLENPSCNSVLDPRDLROLHOMSSSSMSDCANSMITT
İ			VI VSQSDAFEGSDFSCADNSMINESGPSNSTNDNSUVPVODGOV
5907	99	1070	SGIGSMONEQLSDSFPYEFFOV
	,,,	1873	TYLLSSWSS**NLDTKIKSQVKV/RKGHKKISWPYPQPAKQNGK
1 1			LATSKYPSAPHFVHPNDHANREAEI.KKKWUPEMPEVOORARDON
1 1			ROWERTIES Y CODVLEROEEFEHKEEUT OF IMMEDIA DOES MOVED
			ATTREFREDVELEVLDARDPLGCRCFOMFFAUT BACCOUR
			KLATATUKIDLA SKEAA EKAP TATA KA SLOROVANI
1			NKCSVPVDQASESLLKSKACFGARNIMRVIGNVCBLCBURGHTER
1 1			VGVVGLPNVGKSSLINSLKRSRACSVGAVPGTTKEMOEUVI DVB
1	i		TRULDAPGIVPGPNSEVGTILRNCVHVOKLADDVTDVTTTI ODG
	]		NLBEISNYYGVSGFOTTEHFLTAVAHRIGKKKKCGLVCOROARK
1 1	1		AVLADWVSGKISFYIPPPATHTLPTHISAETVKEMTEVEDIEDE
1	ĺ		EQANEDTMECLATGESDELLGDTDPLEMETELLUCDMEET ADDAT
			ENKTIVYKIGDLTGYCTNPNRHOMGWAKPMUDUPPVENGATOVA
1	ł		SVDRRSVLQRIMETDPLOOGOALASALKNKKKMOKPADVIACVI
- 5000			SDSMMSALDLSGNADDGVGD
5908	247	975	HCGIKKRGEGSGSPSPASGGFQLGCQIPEPSLPSEEETHPHTRA
1 1			HTRTLRATLTRRPPRSHSTRLRFPMPLDGDGGLASWK/PMRER*
1 1			GWRRPAKAAGASLGVAATGKRGCRMSKRYLQKATKGKLLIIIFI
1 1			VTLWGKVVSSANHKAHHVKTGTCEVVALHRCCNKNKIEERSQT
1 1			VKCSCFPGQVAGTTRAAPSCVDASTVEOKWWCHMODGLEGERGK
H			VLPDRKGWSCSSGNKVKTTRVTH
5909	1	5002	PAIPGSTIIWAPGSHSAARADGRHGSLPSQSQAPGALCGARAPP
1 1			SSNLRADRSMICAQARAGKNLYHNRFLGLAAMAFPSRNSQSLRR
1 1		Ĭ	CKEPIRYSYNPDQFHNMDLRGGPHDGVTIPRSTSDTDLVTSDSR
1 1	1		STLMGRSSYYSIGHSQDLVIHWDIKEEVDAGDWIGMYLIDEVLS
1 1		1	ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEPETKICFKYYHGV
1 1			SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS
1			DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPALPHHGQERRSK
1			IIGNTVNPIWQAEQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL
l i			GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFRFEI
1			TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE
1	1	}	SSESWKPFOLGECCUPDED DONOG TEL CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTRO
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		1	VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGREASALLLE
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	[		IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV
			AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT
			HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS
1		İ	SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD
1			EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER
İ	ļ	1	SPEGLESPVAGPSNRREGECPILHNSOPVSOLPSI.PPFHULLVDT
1	į	i i	IDEPLIPENWEARIDSHGRVFYVDHVNRTTTWORPTAAATDDCMD
			RSGSIQQMEQLNRRYQNIQRTIATERSEEDSGSQSCEQAPAGGG
			300

		T = - 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence ·	•	\=possible nucleotide insertion)
		<del> </del>	GGGGSDSEABSSQSSLDLRREGSLSPVNSQKITLLLOSPAVKFI
ļ			TNPEFFTVLHANYSAYRVFTSSTCLKHMILKVRRDARNFERYOH
1	1		NRDLVNFINMFADTRLELPRGWEIKTDOOGKSFFVDHNSRATTF
		ļ	IDPRIPLONGRLPNHLTHROHLORLRSYSAGEASEVSRNRGASL
l		1	LARPGHSLVAAIRSQHQHESLPLAYNDKIVAFLRQPNIFEMLQE
ļ			RQPSLARNHTLREKIHYIRTEGNHGLEKLSCDADLVILLSLFEE
1		1	EIMSYVPLQAAFHPGYSFSPRCSPCSSPQNSPGLQRASARAPSP
ľ	l .		YRRDFEAKLRNFYRKLEAKGFGQGPGKIKLIIRRDHLLEGTFNQ
ļ			VMAYSRKELQRNKLYVTFVGEEGLDYSGPSREFFFLLSQELFNP
	İ	Į.	YYGLFEYSANDTYTVQISPMSAFVENHLEWPRFSGRILG\LALI
ł	1		HQYLLDAFFT\RPFYKALL\RLPC\D\LSDLEYLDEEFHQSLQW
		l	MKDNNITDILDLTFTVNBEVFGQVTERELKSGGANTQVTEKNKK
1	-		EYIERMVKWRVERGVVQQTEALVRGFYEVVDSRLVSVFDARELE
1	Í		LVIAGTAEIDLNDWRNNTEYRGGYHDGHLVIRWFWAAVERFNNE
1	ì		ORLRLLOFVTGTSSVPYEGFAAPPWEPMGLRRPLP*KKWGKITS
		1	
	1		LPPRG\HTCLQPDWDLPTVSPRTPMLYEK\LLTA\VEETSTFGT
5910	1526	446	VAEFAAMEPGRTQIKLDPRYTADLLBVLKTNYGIPSACFSQPPT
			AAQLLRALGPVELALTSILTLLALGSIAIFLEDAVYLYKNTLCP
		1	IKRRTLLWKSSAPTVVSVLCCFGLWIPRSLVLVEMTITSFYAVC
1	i	i	FYLLMLVMVEGFGGKEAVLRTLRDTPMMVHTGPCCCCCPCCPRL
		1	LLTRKKLQ\R*CWALSNTPS*R*R*PWWACFSSPTASMTQQTFL
1	}	!	RGAQLYGSTLSSA/CSTLLALWTLGIISRQARLHLGEQNMGAKF
1	ì	i	ALFQVLLILTALQPSIFSVLANGGQIACSPPYSSKTRSQVMNCH
1			LLILETFLMTVLTRMYYRRKDHKVGYETFSSPDLDLNLKALRWM
i	1	{	AWTMKGCCTH
5911	109	595	QLPLAPCIQGKGLEMRSPKPQSFIIRSSHSGAGLLVKNPSTPVF
			CGHRRGGAAFKYKPTPVVGPEQRPTGQKHMRGGVSLLSPRLECS
1			GTISAHCNLRLPSSSNSPAPAS*LAGITGVCHHAOLIFVFLVET
ì	t		GFHHVGQAGLELL/NVVIHLPRPPKVLGLQA
F03.3	024	277	
5912	924	2//	MILNKALMLGALALTTVMSPCGGEDIVADHVASYGVNLYQSYGP
	1		SGQYSHEFDGDEEFYVDLERKETVWQLPLFRRFRRFDPQFALTN
		1	IAVLKHNLNIVIKRSNSTAATNEVPEVTVFSKSPVTLGQPNTLI
İ	1		CLVDNIFPPVVNITWLSNGHSVTEGVSETRPSSPKSDHFLLQDQ
		ĺ	VTSPSFPFE**DL*TAKVEQLGAWFEPLLKHWGABIPTTL
5913	46	1198	QLRMAGAEGAAGRQSELEPVVSLVDVLEEDEELENEACAVLGGS
			DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYECHGS
1			HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN
		ļ	FFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE
i	1		SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM
1	1	1 .	E*/DDQEVIKPENGBHQDSTLKEDVPEQGKDDVREVKVEQNSEP
	1 .		CAGSSSESDLOTVFKNESLNAESKSGCKLOELKAKOLIKKDTAT
			YWPLNWRSKLCTCODCMKMYGDLDVLFLTDEYDTVLAYENKGKI
		i	
	<del> </del>	<del> </del>	AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED
5914	960	124	NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN
		1	ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG
		1	GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS
		1	IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE
		1	SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP
1	1	1	KAIAGGSACFIAP+SLGQRTRKRKAKARGTRTGASDPSCASWDH
		1	PHRHLPGLCRPAATS
5915	1604	703	FPGRPTRPLKLGRRRKRARI IQAPHCHSPRPRTCPPGALQAPEA
		1	PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT
		1	POEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS
		1	
		1	KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS
1		1	PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS
		<u> </u>	PVLQELPGPAGGEFPEGL**AAGPAAH
5916	256	633	SPRMWEIWGPWHRWESPSLEGEWPSRIPEPSPDSTKGTSGKGCR
			TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH
			PTRLILQ*NQATADKNN*TTALLQPHQRL\VSPRMAEA
5917	1343	827	AHQILTYLEP/ICLVVNYNKILTVFLTKSVLBI*KFIHTPQTYR
	<del></del>	<del></del>	.1

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	1 were bediment containing elemal mamel 3
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
)	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
i i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
] [	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
] ]			F*NDFFGIKEVYVSRRLRKTSF/RLAVTFLEQAVVSKECVPVDC
1 1			FMEHLLPSLLSLASDPVPNVRVLLAKALROMITERA VEDNACATE
5918			HLEVIETTLALQSDRDQDVSFFAALEPKRRNTIDTAVIERON
2318	13	1247	EGAQVARRESRROWRAGRCGRGRGGRRAERTGGRGPPGPDDDL
1			PGPARKGRRRMETPFYGDEALSGLGGGASGSGGTFASDCDL PDC
			APPTAAAGSMMKKDALTLSLSEOVAAALKPAPAPACYPDA\ADG
			APSAAPPOGLLASPOLGLLKLASPELERIJIOSNGI.VTTTDTGG
			QFLYPKVAASEEQEFAEGFVKALEDLHKONOLGAGDAAAAAAA
·			AGGPSGTATGSAPPGELAPAAAAPEAPVVA\NT.GGV\AGGCPGT
i 1		•	RGGAAT \VAFAAEPVPFPPPPPPPQALGPRRP /PLALOGPPPOTT
			PDVP\SFGESP\PLSPIET\DTPRRI\KAKRKRL\RNPQIRAPK
- 1	ľ		PASRKLGAQSRALERESEDPS*SPEHGSLASTASLLREQVAQLK QKVLSHVNSGCQLLPQHQVPAY
5919	1	4254	TSVOCDSOCTION CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL
	į		TSVQGDSQGTPTSSQGSINMEHWISQAIHGSTTSTTSSSSTQSG GSGAAHRLADVMAQTHIENHSAPPDVTTYTSEHSIQVERPQGST
			GSRTAPKYGNAELMETGDGVPVSSRVSAKIQQLVNTLKRPKRPP
			LREFFVDDFEELLEVQQPDPNQPKPEGAQMLAMRGEQLGVVTNW
i			PPSLEAALQRWGTISPKAPCLTTMDTNGKPLYILTYGKLWTRSM
-			KVAYSILHKLGTKQEPMVRPGDRVALVFPNNDPAAFMAAFYGCL
1	j		LAEVVPVPIEVPLTRKDAGSQQIGFLLGSCGVTVALTSDACHKG
[			LPKSPIGEIPQFKGWPKLLWFVTESKHT,SKPPPDWP\ DUTVDAN
ł			NDTAY I EYKTCK \ DGSVLGVTVTRTALLTHCOALTOACGVTEAE
į.	Ì		TIVNVLDFKKDVGLWHGILTSVMNMMHVISTPVSLMKVNDLEWT
	f		QKVCQYKAKVACVKSRDMHWALVAHRDORDINISSI.RMI.IVADG
			ANPWSISSCDAFLNVFOSKGLROEVICPCASSPEALTVAIDEDT
			DDSNQPPGRGVLSMHGLTYGVIRVDSEEKI,SVI,TVODVGLUMDG
	1		AIMCSVKPDGVPQLCRTDEIGELCVCAVATGTSVYGLSGMTVNT
1	j		FEVFAMTSSGAPISEYPFIRTGLLGFVGFGGLVFVVGKMDGLMV
			VSGRRHNADDIVATALAVEPMKFVYRGRIAVFSVTVLHDERIVI
	Į		VAEQRPDSTEEDSFQWMSRVLQAIDSIHQVGVYCLALVPANTLP
	j		KTPLGGIHLSETKQLFLEGSLHPCRVLMCPHTCVTNLPKPRQKQ PBIGPASVMVGNLVSGKRIAQASGRDLGQIEDNDQARKFLFLSE
Į	ľ		VLQWRAQTTPDHILYTLLNCRGAIANSLTCVQLHKRABKIAVML
	1		MERGHLQDGDHVALVYPPGIDLIAAFYGCLYAGCVPITVRPPHP
	1	i	QNIATTLPTVKMIVEVSRSACLMTTQLICKLLRSREAAAAVDVR
- 1			TWPLILDTDD*PKKRPAQICKPCNPDTLAYLDFSVSTTGMLAGV
ļ	j		KMSHAATSAFCRSIKLQCELYPSREVAICLDPYCGLGFVLWCLC
1			SVISGHQSILIPPSELETNPALWLLAVSOVKVRDTECGVCIMER
ŀ			CTRGLGSQTESLKARGLDLSRVRTCVVVAEERPRIALTOSESVI
i			FKDLGLHPRAVSTSFGCRVNLAICI.OGTSGPDPTTVVVDMBALD
İ			HDRVRLVERGSPHSLPLMESGKILPGVRIIIANPETKGBLGDGU
		-	LGEIWVHSAHNASGYFTIYGDESLOSDHFNSRLSFGDTOTTWAR
	1		TGYLGFLRRTELTDANGERHDALYVVGALDEAMELRGMRYHPID
			IETSVIRAHKSVTECAVFTWTNLLVVVVELDGSEQEALDLVPLV
1	1	1	TNVVLEEHYLIVGVVVVVDIGVIPINSRGEKQRMHLRDGFLADQ LDPIYVAYNM
5920	1381	1499	
			QLGAVAHAGVSRIPP*LFPPLHPTFLSLWCLHHKLP/HPPGASM VRPPVVPRRPPAHISSVRQASTQVPRTVPHTQRVANIGTQTTGP
	1		SGVGCCTPGRPLLPCKCSSAAHSTYRVQEPAVHIPGQEPLTASM
			LAAAPLHEQKQMIGERLYPLIHDVHTQLAGKITGMLLEIDNSEL
			LLMLESPESLHAKIDEAVAVLQAHQAMEQPKAYMH
5921	727	157	VCPGTGGE*GLWGQLGGLPKETPLKPMDAFTGSGLKRKFDDVDV
	1		GSSVSNSDDEISSSDSADSCDSLNPPTTASFTPTSILKRQKQLR
ł	}	1	KKNVRFDQVTVYYFARROGFTSVPSOGGSSLCMAORHNSUD CVT
ĺ			LCEFAQEQEVNHREILREHLKEEKLHAKKMKI.TKNGTVEGVEAR
		i '	GLTLDDVSDEDIDVENVEVDDYFFLOPLPTKRRRALLRASCIUR
ľ		i	1DAEEKQELRAIRLSREECGCDCRLYCDPEACACSOAGTECOUD
1		1.	KMSFPCGCSRDGCGNMAGRIEFNPIRVRTHYLHTIMKT.FI FCVD
		1.	O) CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CON
	ļ	1.	Q\GAAQQPQ*GALPDCQLQPDRSTGL*DPSWIGSKGI.SETGEG
5922	2475		Q\GAAQQPQ*GALPDCQLQPDRSTGL*DPSWIGSKGLSFTGKG AAATHLIILRVIENRGAEGKRK SYSNWGLPPSVFIQVPRSRTGNLKPIFLFYSYYE\CMETLKG\T

CEO	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning		
NO:	nucleotide	location	Glutamic Acid, FaPhenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Doquetion	\=possible nucleotide insertion)
	sequence	<u> </u>	CLYNATOYKVCSPRNDRPDACYNPSEPAATTVFEIRTGLLLGDT
			SKIITRTEEKEIPKQITLRFDACAAINSKKLEIGCGSLN*ERS*
Ì	1		RVENKYVCHESGVCKNCAYWPCVI*AT*KKNKNDSVYLQKGEAN
ļ	}		PSCAAGHCNPLELIITNPLDPHWKKGERVTLGINRTGLKPQVVI
ŀ		l .	LIKGEVHKCSPKPVFQTFYEELNLPAPELLKKTKNLFLQLAENV
			IFLLNGTSCYVRGGTTIGDRWPWEA*ELVPTDPAPDIIPI*KAE
			ASNF*VLKTSIIRQYCIAREGKDFIIPVGKPNCIGQKLYNSTTK
			TIT++DLNHTEKNPFSKFSKLKTA+AHAESH+DWTVPSGLY+IC
			RHRAYFRLPNKWADSCVIGTIKPSFFLLPIKMGELLGFSVYASR
1			EKKGIVIGNWKDNEWPRERIIQYYGPATWAQDGSWGYR/TP/VY
1			MLNWIIRLQAILEIISNETGRALTVLAWQETQMRNAIYQNRLAL
ļ			DYLLVAEGGVCRKFNLTNCCLQINDQGQVVKNIVRDMTKLAHVP
]			IQVWHKFDPESLFGKWFPAIGGFKTLIVGVLLVIRTCLLLPCVL
1			
1		İ	PLLFQMIKGIVATLVHQKTSAHVNYMNHYRSISQRDSKSEDESE
			NSH
5923	137	638	QLCGRRGQRFRTSIKRMHPI*RTCPNTNL/IILLSQENTQIRDL
			QQENRELWISLEEHQDALELIMSKYRKQMLQLMVAKKAVDAEPV
	1	1	LKAHQSHSAEIESQIDRICEMGEVMRKAVQVDDDQFCKIQEKLA
			QLELENKELRELLSISSESLQARKENSMDTASQAIK
5924	274	2146	EKGKVKDAGAEQWISLSLSCKGSWETQFSNHLNSLTPPTSVRRM
			PLITTVTLLKMVARHHMKLLCSKAFSTQLQQKIFLHSQMGIHHQ
i			SVCMKLKPNTSHIISILMGQPMALVQLETLAPLTIIIQKFQTQD
		1	HMKFWKNLPLHSHHLTPSVPQTVIPKKTGSPEIKLKITKTIQNG
1		1	RELFESSLCGDLLNEVQASE\Q*NQSIESRKEKRKKSNKHDSSR
			SEERKSHKIPKLEPEEQNRPNERVDTVSEKPREEPVLKEGSPSS
	1	ļ	ANTIFCSNNGSVHW\FKFQVGDLVWSKVGTYPWWPCMVSSDPQL
1	1		EVHTKINTRGAREYHVQFFSNQPERAWVHEKRVREYKGHKQYEE
1			LLAEATKQASNHSEKQKIRKPRPQRERAQWDIGIAHAEKALKMT
	}		REERIEQYTFIYIDKQPEEALSQAKKSVASKTEVKKTRRPRSVL
]			NTOPEOTNAGEVASSLSSTEIRRHSORRHTSAEEEEPPPVKIAW
			KTAAARKSLPASITMHKGSLDLQKCNMSPVVKIEQVFALQNATG
İ	1		DGKFIDQFVYSTKG1GNKTE1SVRGQDRL11STPNQRNEKPTQS
1	1	İ	VSSPEATSGSTGSVEKKQQRRSIRTRSESEKSTEVVPKKKIKKE
ł	i	1	OVGFLHVES
5925	216	1911	MMTAESREATGLSPQAAQEKDGIVIVKVEEEDEEDHMWGQDSTL
3323	1	1	QDTPPPDPEIFRQRFRRFCYQNTFGPREALSRLKELCHQWLRPE
	1		INTKEQILELLVLEQFLSILPKELQVWLQEYRPDSGEEAVTLLE
	1		DLELDLSGQQVPGQVHGPEMLARGMVPLDPVQESSSFDLHHBAT
	1	1	QSHFKHSSRKPRLLQSRALPAAHIPAPPHEGSPRDQAMASALFT
1			1
		1	ADSQAMVKIEDMAVSLILEEWGCQNLARRNLSRDNRQENYGSAF
		1	PQGGENRNENEESTSKAETSEDSASRGETTGRSQKEFGEKRDQE
1			GKTGERQQKNPEEKTRKEKRDSGPAIGKDKKTITGERGPREKGK
1	1		GLGRSFSLSSNFTTPEEVPTGTKSHRCDECGKCFTRSSSLIRHK
1			IIHTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHECNE
			CGKAFSHSSNLILHQRIHSGEXPYECNECGKAFSQSSD\LTKHQ
1			RIHTGEKPYECSECGKAFNRNSYLILHRRVHTREKPYKCTKCGK
<u></u>			\AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV
5926	2	233	DRCLMLKQGSQPGSPPAT/CEPPAPPVYQAPCQSCPBPPGAHEP
	1	1	SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS
5927	4146	1248	KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA
			YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR
	1		KRRLEFIEKEKKOKDOIISLMKAEOMKROBKERLERINRAREOG
		}	WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ
			MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR
			KREAMONKARAEGHMGILONLAAMYGGRPSSSRGKPRNKEEEV
			YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM
			RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV
			AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS
1			SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN
1		1	
			LSDTFEINVHEDAKEHBKEKSVSSDRKKWEAGGQLVIPLDELTL DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE
L		<u> </u>	DISESTIERNIVGEVIRLGPNGSPRRANGRSFIDSVERTIGERE

Decining nucleotide   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location	SEO	Predicted	Predicted end	
No: nucleotide location corresponding to first amino acid amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence se	_			Amino acid segment containing signal peptide
location   Corresponding   to first   amino acid   residue of   residue of   amino acid   residue of   amino acid   sequence   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Sec	4			A=Alanine, C=Cysteine, D=Aspartic Acid, B=
corresponding to first amino acid residue of residue of residue of amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence se	1			Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of residue of amino acid sequence    S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, T=Threonine, V=Valine,   S=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Serine, V=Seri				H=H1stidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid sequence  sequence  sequence  S=Serine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /-possible nucleotide deletion, \possible nucleotide insertion  LoLOTELLENTIRSEISPEGEKYRPITGEKKVQCISHEINPS ATVDSPVETKSPEPSEASPQMSLKLEGNLERPDOLETEILGEPS GTNNDe\SLPCTITUWWISEKERTKETGSADRITIGENSVEEDG VSSTVOLLSDHIBPGTNOSGHSKCOVDKOPSPPPHKVVHSE HLBILVPQVQSVQCSPESSFAFRSHSHLPPKNNNINSLIGLSTG LEPANNFKHARTGSLPPLSKLFPTLMDVSVPPPHRVVHSE HLBILVPQVQSVQCSPESSFAFRSHSHLPPKNNNINSLIGLSTG LEPANNFKHARTGSLPPLSKLFPTLMDVSVPPPHRVVHSE HLBILVPQVQSVQCSPESSFAFRSHSHLPPKNNNINSLIGLSTG LEPANNFKHARTGSLPPLSKLFPTLMDVSTVADDRODNELDEI EDENHIKGGSDSEDIVFESTDTDLGELQASMEQLLREQPGEEYS EBESSVLKNSDVEPTANGTDVADEDDNPSSESALNERHISDNSD GELASSCECDSVFNHLEELRILHEQEMFEKFFEVVEKIKAIHE DEDENHIECSKIVQNILGHEIQHLYAKILHLWMADGAYQENDDE HERSKSGALYQLKKPRSQONSISWMPAKTFPANKYGFPLA YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIEREKKXQKDQIISLMKABOMKRQEKERLERIHRAREGG WRNVLSAGGSGEVKAPFLOSGTIAPSSFSSRGGYENHALFDC MQOQRAEDNEAKMKRIYGGLPERGKGGLAVERAKQUEFFLQR KREAMONKARAGEMGHILJONLAMMYGGRFSSRGGKPENKEBEV YLARLRQIRLQNFNERQOTKAKKREIYGGLPERGKGGLAVERAKQUEFFLQR KREAMONKARAGEMGHILJONLAMMYGGRFSSSRGGVENKEBEV YLARLRQIRLQNFNERQOTKAKKREIYGGLAVERAKQUEFFLQR KREAMONKARAGEMGHILJONLAMMYGGRFSSSRGGVENKEBEV YLARLRQIRLQNFNERQOTKAKKREIYGGLAVERAKQUEFFLQR KREAMONKARAGEMGHILDNLAMYGGRFSSSRGGVENKEBEV YLARLRQIRLDNFNERQOTKAKKREIYGGLAVERAKQUEFFLQR KREAMONKARAGEMGHILDNLAMYGGRFSSSRGGVENKEBEV YLARLRQIRLDNFNERQOTKAKKENTSGSFSRGGVENKEBELL LOLOTELLENTITISSISTSERSKYRETITGKKVQCISHEINPS AIUDSVETKSPFSFSRAPQMSIKLLEGALERPDDLETEILOBPS GTNEMS (SLPCTTTOWN ISEKETKETGSKVQCISHEINPS AIUDSVETKSPFSFSRAPQMSIKLLEGALERPDDLETEILOBPS GTNEMS (SLPCTTTOWN ISEKETKETGSKVQCISHEINPS AIUDSVETKSPFSFSRAPGHIKLEGALERPDDLETTEILOBPS GTNEMSLSVYDTANGTUADEDNINSSSSALNEBHSINSG GELASCEGDSVNHHERLILLHLEGDEMFFRKYTVERDAITG LFDANNFRUSLYVLADHVVQDVQCSPEESFARSHEHPFRAVERSICHT LFDANNFRUSLYVLADHVVQDVQCSPEESFARSHEHPFRAVERGALLINN LTVSREBALALMNNKLDLLEGALTSADQGAHILVTPDAITG MNNNRDSLSYVLADHVVDTIVYPTRAMOVLPHLSAVFHSAMAMM RVMFNRDSLSYVL	1			L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence				P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence    Codon, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide insertion)   LoLOTELLENTTIRSEISFEREKYELTGEKKVGCISHEINPS     AlvospverksperseaspomsikkleckleppolletteILOEPS     CTNKDEN_SLDCTITOWISTSEKETKETGSADRITIQENEVSEDD     VSSTVDQLSDIHIEPCTNDSQHSKCUDVKSVQPEPPFHKVVHSE     LINLNEVOUSPUCSFEESFAFRSHSHLPPKNKNNSLLIGLSTE     LIPDANNEKMLRCSLPDLSKLPRITLMOPTGDVRGOVMEDIDE     LEDENIKEGFSDBEDIVFEETDTLOELOAMEQLLEEDGEEYS     EBESSVLKNSDVPEPTAMOTOVADEDDNSSESALMEEHHSDNSD     GELASCECCDSVPNHLEELRLHLEQEMGFEKFFEVYEKIKAHH     DEDENIEICSKIVQNILGMERGLKAKLLHLVWADGAVQEDNDE     EBESSVLKNSDVPEPTAMSTOVADEDDNSSESALMEEHHSDNSD     GELASCECCDSVPNHLEELRLHLEQEMGFEKFFEVYEKIKAHH     DEDENIEICSKIVQNILGMERGKLKELKIKAHARDAVQEDNDE     KRIFSKFOSQALVQLKFPSSQNSISTWPARQKIFFLARADGO     KRIFSKFOSQALVQLKFPSSQNSISTWPARQKIFFLARADGO     KRIFSKFOSQALVQLKFPSSQNSISTWPARQKIFFLARADGO     KRIFSKFOSQALVQLKFPSSQNSISTWPARQKIFFLARADGO     KRIFSKFOSQALVQLKFPSSQNSISTWPARQKIFFLARADGO     KRIFSKFOSQALVQLKFPSSQNSISTWPARQKIFFLARADGO     KRIFSKFOSQALVQLKFPSSQNSISTWPARQKIFFLARADGO     KRIFSKFOSQALVQLKFPSSQNSISTWPARQCEPKKJEFFLARADGO     KRIFSKFOSQALVQLKFPSSQNSISTWPARQCEPKLFRARADGO     KRIFSKFOSQALVQLKFPSSQNSISTWPARQCEPKLFRARADGO     KRIFSKFOSQALVQLKFPSSQNSISTWPARQCEPKLFRARADGO     KRIFSKFOSQALVQLKFPSSQNSISTWPARQCEPKLFRARADGO     KRIFSKFOSQALVQLKFPSSQNSISTWPARQCEPKLFRARADGO     KRIFSKFOSQALVQLKFPSSQNSISTWPARQCEPKLFRARADGO     KRIFSKFOSQALVQLKFPSSQNSISTWPARQCEPKLFRARADGO     KRIFSKFOSQALVQLKFPSSQNSISTWPARQCEPKLFRARADGO     KRIFSKFOSQALVQLKFPSSQNSISTWPARQCEPKSSQNSISTWPARQCEPKLFRARADGO     KLASALVQLASTADGO     KLASALVQLASTADGO     KLASALVQLASTADGO     KLASALVQLASTADGO     KLASALVQLASTADGO     KLASALVQLASTADGO     KLASALVQLASTADGO     KLASALVQLASTADGO     KLASALVQLASTADGO     KLASALVQLASTADGO     KLASALVQLASTADGO     KLASALVQLASTADGO     KLASALVQLASTADGO     KLASALVQLASTADG				S=Serine, T=Threonine, V=Valine,
Sequence    ence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence	1		!	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
JOLOTELLENTITIRSEISPEGEKYKPLITGEKKVQCISHEINPS ATVDSPVETKSEPPSEAPJOMSLKLEGNLEEPDDLETEILQEPS GTNKDE\SLPCTITOVWISEEKETKETGSADRITIGEREVSEDD VSSTVOQLSDIHIERGTINDSGHSKCDVDKSVQSEPPIKKVVHSE HINLIVPOVOSVQCSESEESFAFRSHSHEIPPKNKKNSLLIGISTG LFDANNFKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDMLEIDEI EDENIK KERSPSDESILVFFETTINDVPTVGDVRQDMLEIDEI EDENIK KERSPSDESILVFFETTINDVPTVGDVRQDMLEIDEI EDENIK KERSPSDESILVFFETTINDVPTVGDVRQDMLEIDEI EDENIK ISE STEUCKVONLIGNEHGHLIAKALHLIVPADGAVQCENDE FEESSVLKNSDVEPTANGTDVABEDDNSSESALAEBHNISNSD GELASECCDSVFNHLEELRILHLEGEMGFEKFFEVYEKIKAIHE PEDENIE ISICSKLVONLIGNEHGHLIAKALHLIVVADGAVQCENDE KHFSKFSSQALVOLKFRASGONSISVMPAGKITKFRAKYGIFLA YKKYGDKKLHEKKPLQHKKQAHOTPEKVYNTGERRKISEEAAR KRRLEFIEKEKKOKKDQIISLMKARGMKKGEKERLERINRAREGG WRAVUSAGGSGSVKAPFLOSGGTIAPSSFSSRGOVEHHALFOQ MQOQRABOMEANKREITYGRGIPERGKGGLAVERAKOVEFELOR KREAMONKARASGHGILONLAAMVGGRESSSEGKPENKEERV YLARLKGIRLONFERGOON KAKLGREKAGNLAVERAKOVEFELOR KREAMONKARASGHGILONLAAMVGGRESSSEGKPENKEERV YLARLKGIRLONFERGOON KAKLGREKANISEGGEGSEEADM RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKWEEHDU AKGVUSSDUSPPLOQHETGGSPSKQOMESVISVTSALKEVOVDS SLITTRETSEEMOKINNAISSKREILERINENKAQEDEKKKON LSDTFFINNHEDAKEHKKEKSVSSDRKKWERGGOLVIFLDELTI. DTSFSTTERHTVGEVILLGHONSDPRAKSPTDSULKILGEAE LQLQTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS AIVDSPVETKSPEPSRASPOMSIKLEGNLEEPDDLETEILQEBS GTNENGK\SIPCTITOVALESEKETKETGOSADRITTOREVSECO VSSTVOQLSDHIEPGTNDSOHSKCDUDKSVOPEPFFHKVVHGE HLANLVPOVOSVOCSPEESFAFRSISHLPNKNKSLILGISTG LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQNNLBIDEI EDENIKEGSSISPATSHSHLPNKNKSLILGISTG LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQNDLBIDEI EDENIKEGSSISPATSHSHLVLAWAGDAGVBONDB GELASSCCCDSVTHHLEERLRLILBGEMGFFKFFEVYEKIKAIHE EDEENIKEICSKIVONILGKHOHUTAUTHTFGASFGIFTCOPI LFPURNELASNIVANLTSVASHGATAROOTENTREPGGTTVORTUVFDBSGG KLVARYKRONLFMORTONVERSTENTTTTTTTGSSFTFTENTITTGTSFTFTCOPI LFPURNELASNINTYDSKMOTSGNAFFSTVFTDEETTVK LTDVSREBALAMNNLTPLKGABASTRAFEKTFTTDETFTVK LTDVSREBALALMNRHDLILGATSAADGGAHITVTE GRESTORTONTONTONTONTONTONTONTONTONTONTONTONTONT			sequence	Codon, /=possible nucleotide deletion,
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GTNKDE\SLPCTITOWHISERTKETCOSABIRTIQENEYSEDD VSSTVDQLSDHHEDTNDSQHSKCDVDKSVQDEPEPFHKVVHSE HLNLVPQVQSVQCSPESFAFRSHSHLPFKMKNKNSLLIGLSTG LFPANNFKMRRTCSLPDLSKLFRTLMDVPTYGDVRQDMLEIDEI EDENIKESPBDLSGLVFEETTDLQLQASMCQLLREDGGESYS ERESSVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD GELASECECDSVFNILLEELRIHLEQEMGFEKFFEYYERIKAHHE DEDENIBICSKTVQNILONERQHLYAKILHLWARGAYGENDEN 5928 4146 1248 KHFSKFGSQALYQLKRPASGONSISVWPAQKITKFPAAYGIPLA YKKYGDKKLHEKKPLQKKKAPAGTPEKKRVTGEBERKISEEAAR KRRLEFIEKKKKONQIISLMKAAQMTPEKKRVTGEBERKISEEAAR KRRLEFIEKKKKONQIISLMKAAQMTPEKKRVTGEBERKISEEAAR KRRLEFIEKKKKONQIISLMKAAQMTROCKEKRLERINRAREQG WRNVLSAGGSGEVKAPFLGSGGTIAPSSTSSGQVEHYHAIFDQ MQQORABDMANKKRIYGKGLPERQKGQLAVERAKQVEEFLQR KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPNKEEEV YLARIKQIIKLQNFNERQQIKKKLEKKEANISEGGGSEEADM RKKKISLSLARAMARAAVLKEQLEKKEANISEGGGSEEADM RKKKISLSLARAMARAAVLKEQLEKKEANISEGGGSEEADM RKKKISLSLARAMARAAVLKEQLEKKEAVERGEKKWEEHLV AKGYKSSDVSPPLGQHETGGSPSKQOMRSVISVTSALKEVGVDS SLTDTERTSBEMQKTNNAISSKREILRRLNENLKAQEDBKGKON LSDTFSINNHEDAKEHKEKSVSSDRKKWEAGGQLVIFLDELTL DTSSSTTERHTVGEVIKLGPNGSBRRAMGKSFTDSVLKILGERE LQLQTLZLLENTTIRSEISPBGGSVLLTGEKKVQCISHEINPS ATVDSPVETKSPEFSEASPQMSIKLEGNLEEPDDLETTILQBES GTNEDASLSPCTITOVMISEKETKETGSBADITIQENEVSERG VSSTVOLDEDHILEGETNDSQHSKCVDVKSVQPEPFFHKVVHSE HLNLVPQVGSVQCSPESSFARRSHSHLPPKNKNKNSLLIGLSTG LFDANNFKMLRTCSLPDLSKLFRTLMDVTQDVRQONLEIDEI EDENIKEGFSDSEDIVFERTDTDLGELQASMEQLLERQFGESSE EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD GELASECCDSVFNILEBELHLLEDERGFEKYFEVYEKKAHB DEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYGEDNDE EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD GELASECCDSVFNILEBELBLLEDEDERGFEKYFEVYEKKALHE DEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYGEDNDE EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD GELASECCDSVFNILEBELBLLEDEDERGFEKYFEVYEKKALHE DEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYGEDNDE KUPARSDLYPYLEDIPPEVMIPPENAYFRAYEHAMAMOM RVSFLASANTHYSKKMMGSGIVAPRASAFHYDMKTEEGKLLLS OLDSHFSHSAVVNWTSYASSIBALSSGNKEFKGTVFFDBEFTFUK LTGVAGNTTVQKDLCCHLSYKMSENINENEYHJAGAFGKLLLS OLDSHFSHSAVVNWTSYASSIBALSSGNKEFKGTVFFDBEFTEVK LTGVAGNTTVQKDLCCHLSYKMSENINENEYHJAG				AIVDSPVETKSPEFSEASPOMSLKLEGNLEEPDDLETEILOEPS
VSSTYDQLSDIHLERGTNDSQHSKCDUDKSVQPEPPFRKVVHSE HINLVPQVQSVQCSPESFAFRARSHLPPKNNKNSLLIGLSTG LFDANNPKMLRTCSLPDLSKLFRTLMDVFTVGDVRQDNLEIDEI EDENIKEGPSGSEDIVFEETDTDLQELQASMEQLLREQPGERYS ERESSVLKNSDVEPTANGTDVADEDDSSESALMERHISDNSD GEIASECECDSVENHLEELRHLEQEMGFEKFFEVYEKIKATHE DEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE  S928 4146 1248 KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAARVGIPLA KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAARVGIPLA YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEBRRKISEEAAR KRILEFIEKEKKQKDQLIISLMKARGKGEKERLERINRAREQG MRNVLSAGGGGEVKAPFLGSGGTIAPSSTSSRGQYEHYHAIFDQ MQOQRAEDMEAKNKREIYGRGLPERQKGQLAVERAKQVEEFLQR KREAMONKARASGHASILQNILAAMKGEKKEANHSEGCGSEEADM RKKYLSDLANDARAVLKEQLERKKREAYEREKKUMEEHLV AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEWGUDS SLITTTETSEEMQKTNNAISSKEILBRINBERGKQCLSKEEADM RKKYLSISLAHANARAAVLKEQLERKKREAYEREKKWEGHEHV AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEWGUDS SLITTTETSEEMQKTNNAISSKEILBRINBEKKQCISHEINSS AIVDSFVETKSPEFSEASPOMSLKLEGNLEERDDLETHLGEBE GTNKDE\SLPCTITOVMISEKETKETQSADRITIQENEWSEDG VSSTVODLGDHIH JEGTINDGOHSKVQCEPPFFKVVHSE HLNLVPQVQSVQCSPEESFARSHSHLPPKKNKNSLLIGLSETG LFDANNFRHLRTCSLPDLSKLENLEERDDLSTEILQEBS GELSSCULKHSSDVEPTANGTDVADEDDNPSSESALMEEMHSDNSD GELASFCECDSVFNHLEBLRHLDEQMEFFFEVFEKKKAHE DEDENIECSKIVONILGNEHDDLSTEPPLYTFNTTGORGFGFEXS EEEESVLKHSSDVEPTANGTDVADEDDNPSSESALMEEMHSDNSD GELASFCECCSVFNHLEBLRHLDEQMEFFFEVFEKKKAHE DEDENIECSKIVONILGNEHOHLVAKLLHLUMADGAYQEDNDE LDPSMTTQLPAVVALLFYVSRASCQDFFTAAVVEHAATIFNAT LTPVSREERALAIMMRILDILEGATADGGAHITYPEDALTYG MNFNRDSLYPVLEDIPDPEVNMIPCNNRNRFGQTPVQERLSCL\ AKNNSIYVVANIGKKRCOTSDPQCPPDGRYQNTDVVP\DSOG KLVARYHKQNLFMEGNGPNYPKEPFIVFFTNTTFGSFG1FTCFDI LFFDPAVTLVVANIGKKRCOTSDPQCPPDGRYNTDVVP\DSOG KLVARYHKQNLFMEGNGPNYPKEPFIVFTNTTFGSFG1FTCFDI LFFDPAVTLVVANIGKKRCOTSDPQCPPDGRYNTDVVP\DSOG KLVARYHKQNLFMEGNGPNYPKEPFIVFFTNTHSGFFTFUL LTGVAGNTTVVQNDLCCHLSYKMSENIINEGKLLISGTPGTOO GRYYLGICTLLKKVTTILNTCGGSAGATASTFFPMFSIAGRTPHTOM	ĺ		1	GTNKDE\SLPCTITDVWISEEKETKETQSADRITIOENEVSEDG
HINLYPOVGSVGCSPEESFAFRSHSHLIPKKNKNSLLIGLSTG LFDANNPKMLRTCLSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI LFDANNPKMLRTCLSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI EDENIKEGPSDSEDIVFEETDTDLGELGASMEGLLREGPEGEYS BEBESSULKNSDVEPTANGTDVADEDDNESSESALNEEWHSDNSD GEIASECECDSVFMHLEELRIHLEOGMGFEKYFEVYBRIKAIHE DEDENIBICSKIVONILGNEHOHLYAKILHLWMADGAYQEDNDE KHFSKFGSQALYQLKFPASGQNSISWPAGNITKFRAKYGIPLA KKFSKFGSQALYQLKFPASGQNSISWPAGNITKFRAKYGIPLA KKRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERIMRAREQG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSRGGYEHYHAIFOQ MCQORAEDNEAKMKREIYGRGJEPEROKGGLAVERAKQUEFFLQR KREAMONKARAECHMSILONLAAMYGGEPSSRGGKPRNEEEV YLARLRQIRLQNFMEQQIKAALRGGKERAHNSEQGESEADM RRKK\IESLKAHANARAAVLKEQLERKKKAMSEGGESEADM RRKK\IESLKAHANARAAVLKEQLERKKKAMSEREKKVMEEHLV AKGVKSSDVSPPLGGHETGGSPSKQOMSVISVTSALKKVGVDS SLTDTETSESMOKTNNAISSKREILRRLINEILAGDEBKGKON LSDTFEINWEDAKEHEKEKSVSSDRKKWEAGGQLVIFIDELIL DTSFSTTERHTVGEVIKLGPNSSPRRAMGKSPTDSVLKILGEAE LQLQTELLENTITIRSSISSEGEKYXPLITGEKKVQCISHEINPS AIVDSPVETKSPEFSEASPOMSLKLEGNLERPDDLETEILQEPS GTNKDE\SLPCTITDVWISEEKKTKETQSADRITIGENEVSEDG GTNKDE\SLPCTITDVWISEEKKTKETQSADRITIGENEVSEDG VSSTVOQLSDIHIEGGTDNSOKKCDVBKSVQDEPFPHKKVVIGE HLALLVQVQSVQCSPEESFAPRSHSHLPPRNKKNSILIGLSTG LFDANNPKMLRTCSLDDLSKLFINDVPTVGDVRQDNLEIDEI EDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEETS EEEESVLKNSDVEPPANGTDVADEDDNSSESALNEEMISDNSD GELASECCDSVFNHLEBLRILATUDVPTVGDVRQDNLEIDEI EDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEETS EEEESVLKNSDVEPPANGTDVADEDDNSSESALNEEMISDNSD GELASECCCSVFNHLEBLRILADEMGFKFFVVEKIKA HE DEDENIECSKIVQNILGMEHOHLVAKILHLVMADGAYQEDNDE LTPVSNEERALALMNNRILDILEGATISAADQGAHI IVTPEDAITG WNFNRDSLYPYLEDIPDPEVWIPCHARNFRQOTPVOERLSCL\ AKNNSTYVANIGDKKPCDTSDPQCPPDGRYQYNTDVVP\DSQ KLVARYHKONLFMGENGFNVFKEREFLIVTFNTTEGSFGIFTCFDI LFFHDPAVTLVKDFHVDTIVFTAMMVLUPHLSAVEPHSAMANGM RVFFLASNIHYPSKRMTGSGIFTAMSTEEMSVLLAGAFDGLHTVE LTGVAGNYTVCQKOLCCHLSYKMSENIPREVYALGAFDGLHTVE LTGVAGNYTVCQKOLCCHLSYKMSENIPREVYALGAFDGLHTVE GRYYLGICTLLKCKTTNLNTCGGSAETASTRFEMPSLGGFTGTO				VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVOPEPFFHKVVHSR
LEPANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI EDEN IKEGPSDSED IVFEETDTDLQELQASMEQLLREQPGEYS EEEESVLKNSDVEPTANGTDVADEDDNPSSESALMEEWHSDNSD GEIASECECDSVFNHLEELRLHLEQEMGFEKFFEVYRKIKAIHE DEDEN ISICSKLVONLLGMEHGHLYAKILHLUMADGAYQEDNDE SPERM 1248  KHFSKFGSQALYQLKFPASGQNS ISVMPAQKITKPAAKYGIPLA YKKYGDKKLHEKKPLQKHKQANGTPEKKRUTGERRKISEBAAR KRRLEFIEKEKKOKQDIISLMAEOMKRQEKKERLERINRAREQG MRIVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ MQOQRAEDNBAKNKRBIYGRGLPERQKGLAVERAKQUEFFLQR KREAMQNKARAEGHMGILQNLAMYGGRPSSRGGKPRNKEEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGGEGSEBAM RRKK\IESLKAHANARAAVLKSQLERKKEAKPEREKKWEEHLU AKGVKSSDVSPPLGQHETGGSFSKQQMESVISVTSALKEWGDHS SLTDTRETSBEMGKTNNAISSKREILRRLNENLKAQEDBKGKQN LSDTFEINVHEDAKEHEKKSVSSDRKWERAGGQLVIFLDELTL DTSFSTTERRIVGEVLKLGPNGSPRRAWGKSPTSALKEWGOS SLTDTRETSBEMGKTNNAISSKREILRRLNENLKAQEDBKGKQN LSDTFEINVHEDAKEHEKKSVSSDRKWERAGGQLVIFLDELTL DTSFSTTERRIVGEVLKLGPNGSPRRAWGKSPTDSVLKLIGEAE LQLQTELLENTTIRSSISPEGKYKPLITGEKKVQCISHEINPS AIVDSPVETKSPEFSEASPQMSLKLEGNLEEPDDLSTEILQBES GTNKDE\SLPCTITOWISEEKETGQSADRITIQENEWS BED VSSTVOQLSDIHIEPGTNDSQHSKCDVDKSVQPPPFPHKVVHSE HLNLVPQVQSVQCSPEESFAPRSHSHLPPKNKNKNSLLIGLSTG UFDANNFKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI EDENIKEGPBGEDIVFRETDTDLQEQASMEQLLREQPGEEYS EEEESVLKNSDUPPTANGTDVADEDDNPSSESALNEEMHSDINSD GELASECCDSVFNHLEBLRHLEQEMGFEKFFEVVEKKKAHE DEDENIEICSKIVQNILGNEHQHLYAKILHLIVADGAYQEDNDE LDFSMTTOLDAYVATLLFFYVERAGCOPPTRAVYYEKAATHPNAT LTPVSREEALALMNNNLDILEGATISAADQSAHIIVTPEDAITG WNFNRDSLYPYLEDIPPDLWHIPCNNRNFFGGTPYQCERLSCL\ AKNNSTLYVANIGDKKPCDTSDOPPDRSKSAHIIVTPDDAITG WNFNRDSLYPYLEDIPPDLWHIPCNNRNFFGGTPYQFRLSCL\ AKNNSTLYVANIGDKKPCDTSDOPPDRSVXNTDVVF\DSQ KLVARYHKONLFMGENGVPVFKEPEIVTFNTTTGSFGIFTCCDI LFFIDPAVTLVKDFHVDTIVFTAMMVVLPHLSAVEFHSAMAMGM WNFHASNIHYPSKKMTGSGIYAPNSRAPHYDMKTEBCKLLLS OLDSHSHSAVWWTSYASSIEALSSGNKEFKSTVFFDEFFTVK LTGVAGNYTVCQKDLCCHLSYKMSENIPREVYALGAFDGLHTVE GRYYLQICTLLKKKTNININGGSAETASTRFEMPSLGGTFGTO				HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG
EDENIKEGPSDEDIVFETTDTLUGELQASMEQILIREQPGEEYS EBESSVLKINDVEPTANGTDVADEDDNPSSEALNEEMHSDNSD GELASECECDSVFNHLEELRLHLEQEMSFEKFFEVYEKIKATHE DEDENIEICSKIVQNIIJGNEHQHLYARILHLWANDGAYQEDNDE YKRYGDKKLHEKKPLQKHKQAHGTPEKRVNTGEERRKISEEAAR KRREFTEKEKKQKQDIISLMKABOMKQEKELERINRAREGG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGGYEHYHAIFOO MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQUEEFLQR KREAMQNKARAEGHMGILQNLAMYGGGRPSSSRGGKPRKKEEBEV YLARLRQIRLQNFMERQQI KAKLRGEKKEANHSGGGGSEADM RKK\ ISSLKAHANARAAVLKEQLERKREAYEREKKVMEEHLV AKGVKSSDVSPPLGQHETGGSPSKQOMRVISVTSALKBYGUDS SLTDTRETSSEMQKTNNA 1SSKREILRRINENLKAQEDBKGKQN LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLUPPLDELITL DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE LQLQTELLENTITRSEISPEGEKYKPLITGEKKVQCISKEINPS AIVDSPVETKSPEFSSASPQMSIKLEGNLEEPDDLETEILQBPS GTNKDE\SLPCTITDWWISEKTKETQSADRITIQENEVSEDG VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVQFEPFFHKVVIISE HLAILVPQVGSVQCSPEESFAFRSHSHLPRINKNSHLIGLSTG UFDANNFKMLRTCSLEPLISKIPFILMDVPTVGDVRQDNLEIDEI EDENIERGPSDSEDIVFETDTDLQELQASMEQLLREQPGEEYS EEESSVLKNSDVEPTANGTDVADEDDNPSSESALMEEMHSDNNS GELASECCDSVRNHLEBELRHLBEQEMGFEKFFEYVEKKATHE DEDENIEIGSKIVQNILGMEHQHLYAKLIHLUWADGAYQEDNDE  SDEMTGLSSPTTQDAYAILLFYVSPASCQDTFTRAVYEHAATLIPNAT LTPVSREBALALMNRNLDILGGAITSAADQGAHIIVTEDAIYG WNFNRDSLYPYLEDIPDPSVNNIPCNRNRRFGQTPVQERLSCL\ AKNNSIYVVANILGKREQDTSDPQCPPDGRYGYYNTDVVV\DSQG KLVARYHKQNLFMGENQFNVVPREPEIVTFITTGSFGIFTCFDI LFIDDPAVTLVKDFHVDTIVFPTAMMNVLPHLSAVFFHSAMAMGM RVAFFLASNIHTYPSKKMTGSGI YANDSSRAFHDUMTEEGKLLLS OLDSHPSHSAVVNWTSYASSIEALSSGNKEPKGTVFFPSEPTYK LTGVAGNYTVCQKDLCCHLSYYMSSIENINEVYALGAFFGTTO				LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRODNLEIDEI
EEESSVLKNSDVEPTANGTDVADEDDNESSSALMEWHSDNSD GEIASECECDSVFNHLEELRLHLEQEMGFEKFFEVYEKIKATHE DEDENIBICSKIVONIJGNEGHLYAKILHLVMADGAYQEDNE SP28 4146 1248 KHFSKFGSQALYQLKFPASGONSISVMPAQKITKPAAKYGIPLA YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGERRKISEEAAR KRRLEFIEKEKKQKDQIISLMKAEQMKRQKKEKELERINRAREGG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSKGGYEHYHAIFDQ MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR KREAMQNKARAEGHMGILQNLAAMYGGRPSSSKGGKPRKEEEV YLARLRQIRLQNFMERQQIKAKLURGEKKENNESGGGGSEADM RKKK\IESLKAHANARAAVLKEQLERKKKEAYEEREKKVWEEHLV AKGVKSSDVSPPLGQHETGGSFSKQQMRSVISVTSALKEVGVDS SLTDTRETSSEMQKTNNAISSKREILBRLNBNLKAGDEKKGQN LSDTFEINVHEDAKEHBKEKSVSDRKKWEAGGQLVIPLDELTL DTSFSTTERHTVGEVIKLGFNGSPRRAWGKSPTDSVLKILGEAE LQLGTELLENTTIRSEISPBGEKYKPLITGEKKVQCISKEINPS ALVDSPVETKSPFSRASPGNSKLEGNLEEPDDLETEILQEPS GTNKDE\SLPCTITDVWISEEKETKETQSADRITIQENEVSEDG VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVIISE HLNLVPQVGSVCSPEESFAFRSHSHLPPKNKKNSLLIGLSTG LFDANNPKMLRTCSLPDLSKLFTILMDVPTVGDVRQDNLEIDEI EDENIKGFBDSEDIVFETTDTDLGELQASMEQLLREQPGEEYS EEESSVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD GELASECCCDSVFNHLEELRLHLEQEMGFEKFFEYEKKKAIHE DEDENIEIGSKIVQNILGMEHGHLVAKALLHLUMADGAYGEDNDE  SP29 3 1558 LDFSMTTQLFBYVAILLFYVSRASCQDFFFAAVYEHAATLPNAT LTPVSREEALALMNRNLDILEGAITSAADQGHIIVTEDAIYG WNNRNSLYPYVALDIPDPSVNNIPCCNDRNRFFQTFVQERLSCL\ AKNNSTYVVANIDAKPKCDTSPCCPPDGRYGYNTDVVP\DSQG KLVARYHKQNLFMGENQFNVPKEPEIVTFNTTFGSFGIFTCFDI LFHDPAVTLVKDPHVDTIVFPTAMMNVLPHLSAVFHSAMAMMG RVMFLASNIHTYPSKKNTGSGIYANSRRFHYDMTTEEGKLLLS QLDSHFSHSAVVNWTSYASSIEALSSGNKEPKGTVFFDEFTFVK LTGVARGNYTVCQKDLCCHLSYXMSENINEVYALGAFDGLHTVE GRYYLGICTLLKCKKTTNLNTCGDSAETASTRFFMSSLGGTFGTTO		ļ		EDENIKEGPSDSEDIVFEETDTDLOELOASMEOLLREOPGEEYS
GEIASECECDSVFNHLEELRLHLEQEMSFEKFFEVVBRIKAIHE DEDENIBICSKIVQNILGNEHQHLYAKILHUWADGAYQEDNDE 5928 4146 1248 KHFSKFGSQALYQUKRPASGONSISWPAQRITKPAAKYGIPLA YKKYGKKLHEKKELQKHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIEKEKKQKDQIISLMKAEQMRQEKERLERINRAREGG WRNVLSAGGSGEVWAPFLGSGGTIAPSSFSSRGGYBRYHAIFDQ MQQRAEDNEAKWREIYGRGLPERQKGQLAVERAKQVEEFLQR KREAMQNKARAEGHMGILQNLAMYGGRPSSSRGGKPRNKEEBEV YLARLRQIRLQNFMERQOIKAKLMGEKKEANHSEGQGESEEADM RRKK\IESLKAHANARAAVLKEQLERKKEAYEREKKWEEHLV AKGYKSSDVSPPLGQHETGGSPSKQOMRSVISVTSALKRWGUDS SLTDTRETSEEMGKTNNAISSKREILRRINBNLKAQEDBEKKGVON LSDTFEINVHEDAKEHEKEKSVSSDRKWEAGGQLVIFLDELTL DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE LQLCTELLENTITRSEISPEGBRYKVPLITGEKKVQCISHEINPS AIVDSPVETKSPEFSEASPQMSIKLEGNLEEPDDLETEILQEPS GTNKDE\SLFCTITDWISEEKETKETGSADRITIGENEVSBCG VSSTVDQLSDIHTEPGTNDSKKOVDKSVQPEPFFHKVVHGE HLNLVPQVQSVQCSPEESFAFRSHSHLPPRNKKNSLLIGLSTG LFDANNPKMLRTGSLEPDLSKLFRTIMDVPTVGDVRQDNLEIDEI EDENIKEGFSBSEDIVFEFTDTDLVELQASMEQLLREQPGEEYS EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEMHSDNSD GELASECCCSVSNHLEBELRLHLEQEMGFEKFFEVYEKKATHE DEDENIEICSKLVONILGNEHQHLYAKILHLVMADGAYQEDNDE  5929 3 1558 LDFSMTTQLPAYVAILLEFVSKASCCDTFTAAVYEHAALLENAT LTPVSREEGALALNNRNLDILEGAITSAADQGAHIIVTPEDAIYG WNFNRDSLYPYLEDIPDPEVNMIDCNNRNFGGTPVGERLSCL\ AKNNSIYVVANIGDKKPCTSSPQCCPPDGRYQYTNDVVF\DSOG KLVARYHKONLFMGENGFNVPKEPEIVTFNTTFGSFGIFTCFDI LFFDPAVTLVKDFHVDTIVFTTAMMNVLPHLSAVCFHSAMAMGM RVMFLASNIHYPSKKMTGSGIYAPNSSRAFHYDMKTEGSKLLLS QLDSHPSHSAVNWMTSYASSIEALSSGNKEPKGTVFFDEFTFVK LTGVARGNYTVCQKDLCCHLSYKMSENINEVYALGAFFGATF				EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNERWHSDNSD
DEDENIELCSKIVQNILGNEHQHLYAKILHLWAADGAYQEDNDE  WHYSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA YKKYGDKKLHEKKPLQHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIEKEKKQKDQIISLMKAEQMKQGEKERLERINRAREQG WRNVLSAGGSGEVKAPFLGSGTIAPSSFSSRGVGHYHALIPDQ MQQQRAEDNEAKWKEIJGRGLPEQKGGLAVERAKQVEEFLQR KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGGGSEEADM RRKK\IESLKAHANARAAVLKEQLERKKRKAYEREKKWWEEHLV AKGVKSSDVSPPLGGHETGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSEEMQKTNNAISSKREILRRLINELKAQEDKSKQN LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELIL DTSFSTTERHTVGEVIKLGPNGSPRRAMGKSPTDSVLKILGEAE LQLQTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS AIVDSPVETKSPEFSEASPQWSLKLEGRLEEPDDLEFILQBPS GTNKDE\SLPCTITOWISEEKETKETQSADRITIQENEVSEDG VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHISE HLALVPQVQSVQCSPESSFARSHSHLPPKNKNKSLIGLSTG LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI EDENIKEGPSDSEDIVFEETDDLQLQASMEQLLREQPGEEYS EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSINSD GETASECCDSVPNHLEELRLHLEQEMGFEKFFEVYEKIKAIHE DEDENIEICSKIVQNILGNEHQLIVAKILHLWMADGAVQEDNDE  5929 3 1558 LDFSMTTQLPAYVAILLFYVSRASCODTFTAVYEHAALIPNAT LTPVSREALALNNRNLDILEGATTSAADQGAHIIVTPEDAIYG WNFNRDSLYPYLEDIPDPEVNWIRGRGYNTDVVD\DSQG KLVARYHKQNLFMGENGFNVPKEPEIVTFNTTFGSFGIFTCFDI LFFUDPAVTLVKDFHVDTIVVFTAWNUPHLSAVEFHSANAMMGM RVMFLASNIHYPSKMTGSGIYAPNSSRAFHYDMKTESGKLLLS OLDSHFSHSAVVWITSVASSIEALSSGNKEFKGTVFFDEFTFVK LTGVAGNYTVCQKDLCCHLSYKMSENIPNEVYJLGAPPGLHTVVE GRYYLQICTLLKCKTTHAINTGGDSAETASTRFEMFSLEGTEGTO				GEIASECECDSVFNHLEELRLHLEOEMGREKEFEVVRKTKATUR
HISSEGGALYQUERPASGONSISYMPAQKITKPAAKYGIPLA YKKYGKKLHEKKPLQKHKQAHQTPEKRVNTGEBRRKISEEAAR KRRLEFIEKEKKQKQQIISLAMKAAHQTPEKRVNTGEBRRKISEEAAR KRRLEFIEKEKKQKQQIISLAMKAAHQTPEKRVNTGEBRRKISEEAAR WRNULSAGGSGEVRAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ MQQQRAEDNEAKMKREIYGRGLPEBQKGGLAVERAKQVEEFLQR KREAMQNKARAEGHMGILQNLAAMYGGRESSSRGGKPRIKEEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLEKKRKEAYEREKKWEEHLV AKGYKSSDVSPPLGQHETGGSPSKQOMRSVISVTSALKEVGVDS SLTDTRETSBEMQKTNNAISSKREILRRLINENLKAQEDBKGKQN LSDTFEINVEDAKEHEKKEKSVSSDKKWEAGGQLVIPLDELTIL DTSFSTTERHYVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE LQLQTELLENTTIRSEISPEGEKYKPLITGEKKVQCISEEINPS AIVDSPVETKSPEFSEASPQMSLKLEGNLEEPDDLETEILQEPS GTNKDE\SPVETKSPEFSEASPQMSLKLEGNLEEPDDLETEILQEPS GTNKDE\SPVETKSPEFSEASPQMSLKLEGNLEEPDDLETEILQEPS GTNKDE\SLPCTITDVWISEEKKTKETQSADRITIQEREVSBCG VSSTVDCLSDIHIEPGTNDSGHSKCDVDKSVQPEPFFHKVVIISE HLNLVPQVQSVQCSPEESFAPRSHSHLPPKNKNKNSLLIGLSTG LFDANNPKMLRTCSLPDLSKLFRTLMOVPTVGDVRQDNLEIDEI EDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREPGGEYS EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEMHSDNSD GEIABECECDSVTMLEELRLHLBQEMGFEKFFEVYEKIKAIHE DEDENIEICSKIVQNILGAMFOHLYAKAILHUMADGAVQEDNDE  DEDENIEICSKIVQNILGAMFOHLYAKAILHUMADGAVQEDNDE DEDENIEICSKIVQNILGAMFOHLYAKAILHUMADGAVQEDNDE TUPVSREEALALNNRNLDILEGATTSAADQGAHIIVTPEDAIYG WNFNRDSLYPYLBDIPPEVWHPPCNRNRPGQTPVQERLSCL\ AKNNSIYVVANIGDKRCDTSDPCPPDGRYQYNTDVVF\DSOG KLVARYHKQNLFMGENGFNVPKEPEIVFFNTTFGSFGIFTCFDI LFHDPAVTLVKDFHVDTIVFPTAMMNVLPHLSAVEFHSAMMMM RVNFLASNIHYPSKMTGSGIYAPNSSRAFHYDMKTESGKLLLS QLDSHFSHSAVVWHTSVASSIEALSGNKEPKGTVFFDEFTFVK LTGVAGNYTVCQKDLCCHLSYKMSENIPNEVYALGAPPGLHTVVE GRYYLQICTLLKCKTTIALNTCGDSAETASTRFEMFSLEGTGGTO			ļ	DEDENIEICSKIVONILGNEHOHI.YAKTI.HI.VMADGAYOFDNDE
YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREGG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ MQQQRAEDNEAWKREIYGRGLPERQKGQLAVERAKQVEEFLQR KREAMQNKARAEGHMSILQNLAAMYGGFPSSSRGGKPRNKEEEV YLAALROITLQNFINERQICKAKLIGEKKEANHSEGGEGSEADM RRKK\IESLKAHAMRAAVLKEQLERKRKAYBERKKWEEHLV AKGVKSSDVSPPLGQHETGGSFSKQOMRSVISVTSALKEVGVDS SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEBEKGKQN LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELTL DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE LQLQTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS AIVDSPVSTKSPEFFSEASPQMSLKLEGNLEEPDDLETEILQEPS GTNKDE\SLPCTITDVWISEEKETKETQSADRITIQENEVSEDG VSSTVDQLSDTHIEPGTNDSQHSKCDVDKSVQPEPFPHKVVHGE HLNLVPQVQSVQCSPESFARRSHSHLPPKNKNKNSLLIGLSTG LFPANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI EDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEEYS EEEESVLKNSDVEPTANGTDVAADEDDNPSSESALNEEMHSDNSD GELASECGCDSVFNHLEBURLHLEQEMGFFKFPEVYEKIKAIHE DEDENIEICSKIVQNILGNEHQHLVAKILHLWAADGAYQEDNDE EDENIEICSKIVQNILGNEHQHLVAKILHLWAADGAYQEDNDE SDEDENIEICSKIVQNILGNEHQHLVAKILHLWAADGAYQEDNDE LDFSMTTQLPAYVAILLFYVSRASCQDTFTAAVEHAAILPNAT LTPVSREEALALMNRNLDILEGRAITSAADQSAHIIVTPEDAIYG WNFNRDSLYPYLEDIPDEVNNIPGNNRFGGTPVQGRLSCL\ AKNNSIYVVANIGDKKPCDTSDPQCPPDGRYQYNTDVVF\DSQG KLVARYHKQNLFMGENGPNVPKEPETVTFNTTEGSFGIFTCFDI LFHDPAVTLVKDFHUDTUVPTAWMNVLPHLSAVEFHSAWAMGM RVNFLSSILYVANIGDKRPCCTTSPDQCPPDGRYQYNTDVVF\DSQG KLVARYHKQNLFMGENGPNVPKEPETVTFNTTEGSFGIFTCFDI LFHDPAVTLVKDFHUDTUVPTAWMNVLPHLSAVEFHSAWAMGM RVNFLSSILYPYLSGTYPDSSRAFHYDMKTEEGKLLLS QLDSHFSHSAVNNTSYASSIBALSSGNKEFKGTVFFDEPTFVK LTGVAGNYTVQQKDLCCHLSYKMSENIPNEVYALGAFDGLHTVE GRYYLQICTLLKCKTTNINTCGDSAETASTRFEMFSLSGTFGTO	5928	4146	1248	KHESKEGSOALYOLKEPASCONSTSUMPAOKITYPAAVVOIDE
KRRLEFIEKEKQKDQIIISIMKAPOMKRQEKERLERINRAREGG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHHAIFDQ MQORAEDNEAAWKREIYGRGLERGQKOGLAVERAKQVEEFLQR KREAMONKARAEGHMGILQNLAAMYGGRPSSSRGKPRNKEEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEAHHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLERKKKAPERKKWWEEHLV AKGVKSSDVSPPLGQHETGSPSKQOMRSVISVTSALKEVGVDS SLTDTRETSBEMQKTNNAISSKREILRRLHENLKAQEDBKGKQN LSDTFEINVHEDAKEHKKEKSVSSDRKKWEAGGQLVIPLDELTL DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE LQLQTELLENTTIRSEISPEGBKYKPLITGEKKVQCISHEINPS AIVDSPVETKSPEFSEASPOMSLKLEGNLEEPDDLETEILQEPS GTNKDE\SLPCTITDVWISEEKETKETQSADRITIGENEVSEDG VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVQPEPFFKKVVHSE HLNLVPQVQSVQCSFEESFAFRSHSHLPPKNKNKNSLLIGLSTG LFPANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI EDENIKEGPSDSEDIVFETDDLGLQASMEQLLRECPGEEYS EEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEMHSDNSD GELASECECDSVFNHLEBLRHLEQEMGFEKFFEVYEKIKAIHE DEDENIEICSKIVONILGNEHGHLVAKILHLVMADGAYQEDNDE LDFSMTTQLPAYVAILLFYVSRASCQDTFTAAVYEHAAILPNAT LTPVSREEALALMNRIDIILEGATISAADQGAHIIVTPEDAIYG WNFNRDSLYPYLEDIPDPEVNNIPCNNRRFGQTPVOGENLSCL\ AKNNSIYVVANIGDKKPCDTSDPQCPPDGRYQXNTDVVF\DSQG KLVARYHKQNLFMGENQTNVPKEPEIVTFNTTGSFGIFTCFDI LFFDPANTLVKDFHVDTIVFPTAWMNVLPHLSAVEFHSAWAMGM RVNFLASNIHYPSKKMTGSGIYAPMSSRAFHYDMKTEEGKLLLS QLDSHFSHSAVNNTSYASSIBALSSGNKEFKGTVFFDEFTFVK LTGVAGNYTVQQKDLCCHLZYKMSENIPNEVYALGAFDGLHTVE GRYYLQICTLLKCKTTNLINTCGDSAETASTRFEMFSLGGTGGTO				YKKYGDKKI HEKKPI OKHKOAHOTDEVPIAMTCEPPPY CETA AD
WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGGYEHHAIFDQ MQQQRAEDNEAKWKREIJYGRGLPERQKGGLAVERAKQUEEFLQW KREAMQNKARAEGHMGILQNLAAMYGGRESSRGGKPRNKEEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGGEGSEADM RRKK\IESLKAHANARAAVLKEQLERKRKEAYBREKKWEEHLV AKGVKSSDVSPPLGQHEFTGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSEEMQKTNNAISSKREILRRINENLKAQEDBKGKQN LSDTFEINTHGENKTNNAISSKREILRRINENLKAQEDBKGKQN LSDTFEINTHGEVIKLGGMGSPRRAWGKSPTDSVLKILGEAE LQLOTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS AIVDSPVETKSPEFSEASPQMSLKLEGNLEEPDDLETEILQEPS GTNKDE\SLPCTITDWISEEKETKETQSADRITIQENEVSEDG VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVQVEPFFHKVVHISE HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKNSLLIGLSTG LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI EDENIKEGPSDSEDIVFEETDTDLQELQASMEGLLREOPGEEYS EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD GELASECECDSVFNHLEERLHLEQEMGFEKFFEVVEKKAIHE DEDENIEICSKIVQNILGNEHQHLYAKILHLWADGAYQEDNDE  5929 3 1558 LDFSMTTQLPAYVAILLFYVSRASCQDTFTAAVYEHAAILPNAT LTPVSREEALALMNRNLDILEGAITSAADQGAHIIVTPEDAIYG WNFNRDSLYPYLEDIPDPEVNWIPCNNRNRFGQTPVQERLSCL\ AKNNSIYVVANIGDKKPCDTSDPQCPPDGRYQYNTDVVF\DSQG KLVARYHKQNLFMGENGFNVFREFEINFTITFGSFGIFTCFDI LFHDPAYTLVKDFHVDTIVYPTAMMNVLPHLSAVEPHSAWAMGM RVNFLASNIHYPSKKMTGSGIYAPNSSRAFHYDMKTEEGKLLLS QLDSHFSHSAVVNWTSYASSIEALSSGNKEFKGTVFFDEFTFVK LTGVAGNYTVCQKKDLCCHLSYKMSENIPNEVYALGAFDGLHTTVE GRYYLQICTLLKCKTTNLNTGGDSAETASTRFEMFSLSGTFGTTO	1	1	1	KRRIEFIEKEKKOKDOTISIMKAFOMEDOEKEDI EDINDADOG
MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGKPRNKEEEV YLARIRQIRLQNFNERQQIKAKURGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSBEMQKTNNAISSKREILRRLNEALKAQEDBKGKQN LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELTL DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSFTDSVLKILGEAE LQLQTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS AIVDSPVETKSPEFSEASPQMSLKLEGNLEEPDDLETEILQEPS GTNKDE\SLPCTITDVWISEEKETKETQSADRITIQENEVSEDG VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSE HLANLVPQVQSVQCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI EDENIKEGFSDSEDIVFBETDTDLQELQASMEQLLREQPGEEYS EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD GELASECECDSVPNHLEBLRLHLEQEMGFEKFFEVYEKIKAIHE DEDENIEICSKIVQNILGNEHHHLYAKILHLVMADGAYQEDNDE LDFSMTTQLPAYVAILLFYVSRASCQDTFTAAVYEHAATLPNAT LTPVSREEALALMNRNLDILEGAITSAADQGAHIIVTPEDAIYG WNFNRDSLYPYLEDIPDFEVNWIPCNNRNRFGQTPVQERLSCL\ AKNNSIYVVANIGDKRFCDTSDPQCPPDGRYQYNTDVF\DSQG KLVARYHKQNLFMGENQFNVPKEPEIVTFNTTFGSFGIFTCFDI LFHDPAVTLVKDFHVDTIVFPTAWMNVLPHLSAVEFHSAMAMGM RVNFLASNIHYPSKKMTGSGIYAPNSSRAFHYDMKTEEGKLLLS QLDSHFSHSAVVNWTSYASSIEALSSGNKEFKGTVFFDEFTFVK LTGVAGNYTVCQKDLCCHLSYKMSENIPNEVALGAFDGLHTVE GRYYLQICTLLKCKTINLNTCGDSAETASTRFEMFSLSGTFGTO				WRNVLSAGGSGEVKADELGSGGTTADGGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
KREAMONKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGGESEEADM RKKK\IESLKAHANARAAVLKEQLERKKKEAYHSEKKVWEEHLV AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSBEMQKTNNAISSKREILRRLNENLKAQEDBKGKQN LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELITL DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE LQLQTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS AIVDSPVETKSPEFSEASPQMSIKLEGNLEEPDDLETEILQEPS GTNKDE\SLPCTITDVWISEEKETKETQSADRITIGENEVSEDG VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVQPEPFHKVVHSE HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG LFDANNPKMLRTCSLPPLSKLFRTLMDVPTVGDVRQDNLEIDEI EDENIKEGPSDSEDIVFETTDTLQELQASMEQLERQPGEEYS EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD GELASECCCDSVFNHLEELRLHLEQEMGFEKFFEVYEKIKAIHE DBOENIELCSKIVQNIIGNEHHHLVAKILHLWAADGAYQEDNDE  5929 3 1558 LDFSMTTQLPAYVAILGYVSRASCQDTFTAAVYEHAAILPNAT LTPVSREEALALMNRNLDILEGAITSAADQGAHIIVTPEDAIYG WNFNRDSLYPYLEDIPDFEVNWIPCNNRNRFGQTPVQERLSCL\ AKNNSIYVVANIGDKRECDTSDPQCPPDGRYQYNTDVVF\DSQG KLVARYHKQNLFMGENQFNVPKEPEIVTFNTTFGSFGIFTCFDI LFHDPAVTLVKDFHVDTIVFPTAWMVLPHLSAVEFHSAAMAGM RVNFLASNIHYPSKKMTGSGIYAPNSSRAFHYDMKTEEGKLLLS QLDSHPSHSAVVNWTSYASSIEALSSGNKEFKGTVFFDEFTFVK LTGVAGNYTVCQKDLCCHLSYKMSENIPNEVALGAFDGLHTVE GRYYLQICTLLKCKTINLNTCGDSAETASTRFEWFSLSGTFGTTO				MOOORAEDNEAKWKRETYGRGI DEROVGOLAURDAVOLUBRI OR
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residue of amino acid dequence  whityptophan, Y-Tytosine, X-Unknown, *-Stop Codon, /-possible nucleotide deletion	ļ			P=Proline, Q=Glutamine, R=Arginine,
Codon, /-possible nucleotide deletion,				S=Serine, T=Threonine, V=Valine,
Codon, /-possible nucleotide deletion,	1	1		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
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KKKLKNDAFALSQRLEEKALAVINLEKTINRILOGELDILTVDLD HOROVASNLEKKO, KKPODLLAEKS IS ARYABERDRABARE KETTALSLARALEEALEAKEEFRONKOLRADMEDLMSS KDDVG KNVHELEKS KRALEQOV, EEMRTQLEELEBILQAFEDAFEDAKELEEV NMQAMRAQFERDLQTRDEONEEKRILIK KOVERLEBAELEDERKG RALAVASKKMEIDLKDLEAGIERAMRARDEVI KOLRKLOAOMK DYGRELEERARSRDEI FAGS KESEKLEBERI LOLGELELAS ERARRHASCERDELADE ITNSASGKSALLDEKRILBAR I JAQLEE ELEEEGSIMMELINDRIFKTITLQVOTLABELAAERSAAQKSDNAR OOLERONKELKARLOELEGAVKSKFKATISALEAKIGQLEEQLE QEAKERAAANKLVRITEKKILKEI FMOVEDERRHADOYKEGMEKA NAMMOLKROLERAEBEATRANASRRIKOELDDATEAKRANDKEGMEKA NAMMOLKROLERAEBEATRANASRRIKOELDDATEAKRANDKEGMEKA NAMMOLKROLEBRABEATRANASRRIKOELDDATEAKRANDKEGMEKA NAMMOLKROLEBRABEATRANASRRIKOELDDATEAKRANDKEGMEKA NAMMOLKROLEBRABEATRANASRRIKOELDDATEAKRANDKODIQ KAMPPKFSKVEDMAELTCLNEASULHALKDRYYSGLIVTTYSGLF CVVINFYNILBIVSENIIEMYNGKKRHEMPRIVATSESSAYRGM LOPREDOSILCTGESGAGKTENTKKVI JAHIVASSKKRODIN 1F08LLERQLLQANFILESFGNARTVONDNSSRFGKFIRINFDV TGYIVAMI ETYLLEKSRAVROANDERHIFYOLLGS, GAGEHL KSDLLLEGFNNYRPLSNGYIPI FOO\QDKOMPROPGEAMHING FSHEEILSMLKVVSSVLOFGNISFKKENTDJORGEAMHING FSHEEILSMLKVVSSVLOFGNISFKKENTDJORGEAMHING FSHEEILSMLKVVSSVLOFGNISFKKENTDJORGEAMHING FSHEEILSMLKVVSSVLOFGNISFKKENTDJORGEAMHING FSHEEILSMLKVVSSVLOFGNISFKKENTDIOAFEFFEIN VATURELFRIDVIRINKALDETKROGGSFIGITENGFPIDFOL DLOPCIDLIERPANPFGVLALLDEECKFFRADKTFUENGLO DLOPCIDLIERPANPFGVLALLDEECKFFRADKTFUENGLO DLOPCIDLIERPANPFGVLALLDEECKFFRADKTFUENGLO DLOPCIDLIERPANPFGVLALLDEECKFFRADKTFUENGLO DLOPCIDLIERPANPFGVLALLDEECKFFRADKTFUENGLO NVATLLHGSSDRFVABLINGVORT IVGLOVTGMTETAFGSAYKT KKGMFTVGQLYKESLITLUNATIRNTNMFVKCII INHEKRAGK LDPHLVLDQLKCNGVLEGITRICRGFPNIVGGSKIFFRAGVLAH LEEERDLKITUTI ITFOROCROTUSETRICOGFPNIVGEFRORVEILTP NAI PRGFMOCKOACERMIRALELDPHLYRIGGSKIFFRAGVLAH LEEERDLKITUTI ITFOROCROTUSETRICOGFPNI IVGGERGEKKINLOG NCAAVLKLRIHOMWRVPYKVKPLLOVTROEBELGAKROLLAKVLOR NCAAVLKLRIHOMWRVPYKVKPLLOVTROEBELGAKROLLAKVLOR NCAAVLKLRIHOMWRVPTKVARPLLOVTROEBELGAKEGLEK IKKKLEEGGLEGEBERANALKRINGVENTISDLEE RIKKKEBKTROELIKSARARKOLGEETRIKKALOOMISDLEE RIKKRESTROELEEKRALGOORGENATALEELSGLEGOLGOAKR FRANLEERNK				FAKDAASLESQLQDTQELLQEETRQKLNLSSRIRQLEEEKNSLQ
KKKLKNDAFALSQRLEEKALAVINLEKTINRILOGELDILTVDLD HOROVASNLEKKO, KKPODLLAEKS IS ARYABERDRABARE KETTALSLARALEEALEAKEEFRONKOLRADMEDLMSS KDDVG KNVHELEKS KRALEQOV, EEMRTQLEELEBILQAFEDAFEDAKELEEV NMQAMRAQFERDLQTRDEONEEKRILIK KOVERLEBAELEDERKG RALAVASKKMEIDLKDLEAGIERAMRARDEVI KOLRKLOAOMK DYGRELEERARSRDEI FAGS KESEKLEBERI LOLGELELAS ERARRHASCERDELADE ITNSASGKSALLDEKRILBAR I JAQLEE ELEEEGSIMMELINDRIFKTITLQVOTLABELAAERSAAQKSDNAR OOLERONKELKARLOELEGAVKSKFKATISALEAKIGQLEEQLE QEAKERAAANKLVRITEKKILKEI FMOVEDERRHADOYKEGMEKA NAMMOLKROLERAEBEATRANASRRIKOELDDATEAKRANDKEGMEKA NAMMOLKROLERAEBEATRANASRRIKOELDDATEAKRANDKEGMEKA NAMMOLKROLEBRABEATRANASRRIKOELDDATEAKRANDKEGMEKA NAMMOLKROLEBRABEATRANASRRIKOELDDATEAKRANDKEGMEKA NAMMOLKROLEBRABEATRANASRRIKOELDDATEAKRANDKODIQ KAMPPKFSKVEDMAELTCLNEASULHALKDRYYSGLIVTTYSGLF CVVINFYNILBIVSENIIEMYNGKKRHEMPRIVATSESSAYRGM LOPREDOSILCTGESGAGKTENTKKVI JAHIVASSKKRODIN 1F08LLERQLLQANFILESFGNARTVONDNSSRFGKFIRINFDV TGYIVAMI ETYLLEKSRAVROANDERHIFYOLLGS, GAGEHL KSDLLLEGFNNYRPLSNGYIPI FOO\QDKOMPROPGEAMHING FSHEEILSMLKVVSSVLOFGNISFKKENTDJORGEAMHING FSHEEILSMLKVVSSVLOFGNISFKKENTDJORGEAMHING FSHEEILSMLKVVSSVLOFGNISFKKENTDJORGEAMHING FSHEEILSMLKVVSSVLOFGNISFKKENTDJORGEAMHING FSHEEILSMLKVVSSVLOFGNISFKKENTDIOAFEFFEIN VATURELFRIDVIRINKALDETKROGGSFIGITENGFPIDFOL DLOPCIDLIERPANPFGVLALLDEECKFFRADKTFUENGLO DLOPCIDLIERPANPFGVLALLDEECKFFRADKTFUENGLO DLOPCIDLIERPANPFGVLALLDEECKFFRADKTFUENGLO DLOPCIDLIERPANPFGVLALLDEECKFFRADKTFUENGLO DLOPCIDLIERPANPFGVLALLDEECKFFRADKTFUENGLO NVATLLHGSSDRFVABLINGVORT IVGLOVTGMTETAFGSAYKT KKGMFTVGQLYKESLITLUNATIRNTNMFVKCII INHEKRAGK LDPHLVLDQLKCNGVLEGITRICRGFPNIVGGSKIFFRAGVLAH LEEERDLKITUTI ITFOROCROTUSETRICOGFPNIVGEFRORVEILTP NAI PRGFMOCKOACERMIRALELDPHLYRIGGSKIFFRAGVLAH LEEERDLKITUTI ITFOROCROTUSETRICOGFPNI IVGGERGEKKINLOG NCAAVLKLRIHOMWRVPYKVKPLLOVTROEBELGAKROLLAKVLOR NCAAVLKLRIHOMWRVPYKVKPLLOVTROEBELGAKROLLAKVLOR NCAAVLKLRIHOMWRVPTKVARPLLOVTROEBELGAKEGLEK IKKKLEEGGLEGEBERANALKRINGVENTISDLEE RIKKKEBKTROELIKSARARKOLGEETRIKKALOOMISDLEE RIKKRESTROELEEKRALGOORGENATALEELSGLEGOLGOAKR FRANLEERNK				EQQEEEEEARKNLEKQVLALQSQLADTKKKVDDDLGTIESLEEA
KETKALSLARALEBALBAKESFERONKOLRAMBEDLMSKODVOS KNUMELEKSKRALSOVO EEMRTOLGELBEDLOATEDAKLRIEV NMQAMKAQFERDLQTRDEQNEEKKRLLI KQVRELBABLEDERKO RALAVASKKMEIDLKOLBAGIEBAMKARDEVI KOLRKLOAQMK DYGRELBEARASRDEI FAGSKESEKKIKSLEABI LOLGELBAS ERARHABOERDELADBI TINSASGKSALLDEKRILBAR IAQLEBE ELBEEGSIMMELINDRIFKTILQVITLBAGSKESKALLDEKRILBAR IAQLEBE ELBEEGSIMMELINDRIFKTILQVITLBAGSKESALKOLBOHRA OOLBRONKELKAKLQELBGAVKSKFKATISALBAKSGAQKSDNAR OOLBRONKELKAKLQELBGAVKSKFKATISALBAKSGAQKSDNAR OOLBRONKELKAKLQELBGAVKSKFKATISALBAKSGAQKSDNAR OOLBRONKELKAKLQELBGAVKSKFKATISALBAKSGAQKSDNAR OOLBRONKELKAKLQELBGAVKSKFKATISALBAKSGAQKSDNAR OOLBRONKELKAKLQELBGAVKSKFKATISALBAKSGAQKSDNAR OOLBRONKELKAKLQELBGAVKSKFKATISALBAKSGAGKSDNAR NABMKOLKROLBERGATTANAGRERLGELDATENBELGE EVSTILMILIRGGSISFSSSRSGRROLHLEGASLELSDDDTESK TSOVBETDOPPOSE  FUSHTINILIRGGSISFSSSRSGRROLHLEGASLELSDDDTESK KLUWIFSSRHOPBAASIKBERGDEVMVELABNGKKAMINKDDIQ KMYPPKFSKVEDMABLITCHINBASVILHARDSKKAMINKDDIQ KMYPPKFSKVEDMABLITCHINBASVILHARDSKYSGLITYTSGLF CVVINPYNILJSENITEMVRGKRRIEMPPHIVAISESAYRCM LQDREDOSILCTIGSSGAGKTENTKKVIQVLAHVASSHKGRKDHN IPGE\LERQLLQANPILLBSFGNARTVONDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAXDERTFHIFYOLLSG\AGBHIL KSDLLLBGFONYRFLIDBANGYIFIPGONGNRFGDPGEAMHING FSHEEILSMLKVVSSVLOPGRIJSFKKRRIVTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRAVPTQAGMREQADFAVEALA KATYREIFERLVARINKALDRTKRQGASFIGILDIAGFETFBIN SFFOLCINYTNEKIQQLFNHTMFILEGEEYQRBGIENFTDPGI DLOPCIDLIBERPANPPGVLALIDBEECHFFRANDTFFEKLVOBO GSHSKFQKPRGLUGKRADFCITHYAGKVDY KADEMIKNMDPLND NVATLLHQSSDRFVABLINKDVDRIVGGSIFFRAGVLAH LEBERDLKITDIIJPQAVCRGYLARKAPAKKQQQLSALKVLQR NCAAYLKLRHWONWFYTKVRYPLQGYTARGEELDAKVELOR GRAFKFOKDELBEKARRLDDPITTAFGGSHIPFAREM RAFLAAKKGELEETILHDLESRVEBEEERNOILOMSKKMAGAHIQ DLEGLDEBERGARKHQLEKVTABAKINKEETILLEDONSKF IKEKKLMEDRIAECSSQLABEEDEKANLAKIRNKQEVMISDLEE EKASINKABROKROLSEELBELKTELDOTLOTTAAQGLERTREE QEVABLKKARLBEETINHEAQIOMRGNHATALBELLSEQLEQAKR FKANLENKQGLETDNKELGEETINGLOOPLAGATELFFRENSIL OKREESTANDABRANGARKROKSHINSTRILEEBEKKRILK FKANDASILSGGALARGDDETLINGBELNONGTHAREELELBELGQLEQAKR FKANLENKGGLETDNKELGEBETRONTOLOORAGSHRK				KKKLLKDAEALSQRLEEKALAYDKLEKTKNRLQQELDDLTVDLD
KNVHELEKSKRALEGOV\EMETICLELEDELGAFEDAKKRLEJ NAGAMRAGPERDLOTRDEONEKKRLLIKGVREREAELEDERKO RALAVASKKMEIDLKDLEAGIEAANKARDEVIKGLRKLGAGMK DYGRELEEARASRDEIFAGSKESKKIKSLEAEILGLGEELASS ERARHAZGERDELADEITNSASGKSKIKSLEAEILGLGEELASS ERARHAZGERDELADEITNSASGKSKIKSLEAEILGLGEELASS ERARHAZGERDELADEITNSASGKSKILASLEAEILGLGEELGE GEAKERAAANKLUKRTEKKIKEITMQVEDERRHADQYKEGMEKA NARMKOLKRGLERAEEBATRANASRRKLGRELDDATEANBGLER EVSTLKNRLRRGGISFSSSRSGRGLHLEGASLELSDDTEKK TSDVWETGPPOSE  FONTHYPTMAGPTGLEDPERVIFVDRAVIYNPATGADMTAK KLWHISERHGFEAASIKEERGDEWWELAENGKKAMVNKDDIG KMMPPKFSKVEDMAELTCLNEASULHNLKDRYYSGLIYTTSGLE CVVINPYNNLDIYSENIIMTNGKKRHEMPPHIVAISESAYRCM LOPREDGSILCTGESGAGKTENTKKVIQVLAHVASSHKGRKDIN IFGE\LERGLLGANPILESFGNARIVONSSFRGKEITRINFDV TGYIVGANIETYLLEKSRAVRGAXDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDFGAMHIMG FSHEEILSMLKVVSSVLOFGRISFKKRRTDGASMPENTVAGKL CHLLGMNVMETTRAILTPRIEVGRDYVQKAGTKEGADFAVEALA KATYERLFRHUVHRINKALDERTREGASTIGLIDGASMPENTVAGKL CHLLGMNVMETTRAILTPRIEVGRDYVQKAGTKEGADFAVEALA KATYERLFRHUVHRINKALDERTREGASTIGLIDIAGFEIFBLN SFEOLCINYTNEKLQLFNHTMFILEGESYGREGIENFTDFDG DLOPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVOED GSHSKPQKPRQLKDKADTCIHYAGKUVKOLDOVTOMTETAFGSAYKT KKOMPRTYGQLYRESIKIKMATLENTPYKCIPHYREKRAGK LDPHLVLDOURCNGVLEGIRICRGGPPNRIVPGCRIPAGNYELIPP NAIPKGFMORGVLEGIRICRGGPPNRIVPGCRIPAGNYELIPP NAIPKGFMORGVLEGUEMERTRAPKCIJ HYTRAGYKKIRAGAKY KKOMPRTYGQLYRESIKIKMATLENTPYKCI PHYREKRAGK LDPHLVLDOURCNGVLEGIRICRGGPPNRIVPGCRIPAGNYELIPP NAIPKGFMORGVLEGUEMERTRADLATRIKGENTISLEE EKGRIKMBRUPTKVSPLLOVTRGEEELQAKDEELLKVK EKGUTKVOEGLEBMERTROQLEEKNILAKTRIKOGENKIFARGEM RARLAKKOGLEEILHDLESKVEBEEERNOILQAEKKMOMAHIO DLEGGLDEEGGASCKLOLEKVILAEAKIKKMEEEILLLEDONSKF IKEKLMEDRIAECSGLAEBEBERANILAKTRIKQEVMISDLEE EKASRIKAERGEKKARKLDGETTDLOQI LBELQAGIDBIKUQL AKKEELGGALARGDDETHINNALKVELQOQI BELKUGLOPEES EKASRIKAERGKARKLOGETTDLOQO LAELGAGOIDBIKUQL AKKEELGGALARGDDETHINNALKVELQOQATBELGEDEE CRASRIKAERGKARKLOGETTDLOQO LAELGAGEELGAKK IKEKLEERTRADLEGGLEGAKK IKEKLEERTRADLEGGERGAKKGIK FKANLEKNGGLEDHERKARKLOGETDNINGELLONVSTILLEEAKKKGIK FKANLEKNGGLEDHERKARLGEBERLEG	1	Í		HQRQVASNLEKKQ\KKFDQLLAEEKSISARYAEERDRAEAEARE
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ERARRHAEGERDELADET TINSASGKSALLIDEKRRLEAR IAQLEE ELEEGSNMELINDERRYTTLYDUTNAELAAERSAAQKSDNAR QQLERQNKELKAKLQELBGAVKSKFKATISALBAKIGQLEEGLE QEAKBRAAANKLVRATEKKLKEIRMQVEDERRHADQYKEMEKA NARMKQLKRQLBABEBEATRANGRKILOPELDDATEANBEJSR EVSTLKNRLRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE  FGNCFFIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLWWIFSERHGPRAASIKEERGDEVMVELAENGKKAMVNIDDIQ KMPPPKPSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPHHYATSESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYJAHVASSHKGRKDHN 1PGG\LERGLLQANPILESFGRARTVONDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLBGFNNYRTLSNSYIPIPGQ\QDKOFFFGDBGAAMHIMG FSHEELISHLKVVSSVLOFGRISFKKERNTDQASMPENTVAQKL CHLLGMNYMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGIUNIGFIFBLN SFEQLCINYTMEKLQQLFNHTMFILEGEEVQREGIEWNFIDPGL DLOPCIDLIERPANPFGULALLDEECHFPKATKKTVEVELVQGG GSHSKFQXPRQLKOKADFCIIHYAGKUTVAKDEWIKNMDPLND NVATLLHQSSDRFVABLUKUDVBIVGLDQVIGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLOOLKGROYLSEIRICROFFNRIVFURGIT INHEKRAGK LDPHLVLOOLKGROYLSEIRICROFFNRIVFURGT LITP NAIPKGFMDGKQACERMIRALELDPNLYRIGGSKIFFRAGVLAH LEEERDLKITDIIFFFFAUCHTGLERVELGGPRORVELLTP NAIPKGFMDGKQACERMIRALELDPNLYRIGGSKIFFRAGVLAH LEEERDLKITDIIFFFFAUCHGLERVELGEGARDEELLKVK EKQTXVEGGLEEBEMERKIGQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERLAKKUQAHIQ DLEEQLDEBEGGARGKCLEKVTAEARIKKMEEFILLLEDONSKF IKKKKLMEDRIAECSSGLAEEBEKANNLAKIRNKGEVMISDLEE RIKKEKERTGELEFKARKLDGETTIJOQ QIAELQAEJDEFES EKASNKAEKQKROLSELEFALKTELEDTUDTTAAQGELRTKEE QEVABLKKALBEETKARKLDGETTIJOQQIAELQEDFESE EKASNKAEKQKROLSELEALKTELEDTUDTTAAQGELRTKEE GEKASNKAEKGKROLSELEALKTELEDTUDTTAAQGELRTKEE GEKARNKAEGKROLSELEALKTELEDTUDTTAAQGELRTKEE GEKARNKAEGKGROLSEELEALKTELEDTUDTTAAQGELRTKEE GEKLKRUEGTONGCHATALEREERGIKAGQU				DYQRELEEARASRDEIFAQSKESEKKLKSLEAEILOLOEELASS
ELEEGSNWELLNDRFRKTTLQVDTLNAELARERSAQKSDNAR OQLERQNKELKAKLQELEGAVKKKKATISALEAKICQLEEQLE QEAKERAAANKUVRTEKKLKEITMQVEDERRIADGYKEQMEKA NARMKQLKRQLERAEEBATRANASGRKLQRELDATEANEGLSR EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE  5931  113  6082  RGNCFWIVPTTMQNTGLEDPERYLFVDRAVIYNPATQADWTAK KLWWIPSERHGPEAASIKEERGDEWMVELAENGKKAMVNKDDIQ KMNPPKPSKVEDMAELTCLNEASVLHNLKDRYYSGLITYTSGLF CVVINPYKHLPIYSENILENTRGKKREMPHIYAISBSAYRCM LOPREDQSILCTGSGGAGKTENTKKVIQYLAHVASHKGRKDHN 1PGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINDV TGYIVGANIETYLLEKSRAVRQAXDEETFHFYQLLSGAGEHL KSDLLLEGFNNYRFISNGYIPIFGQ\QDKGNFFGOPGEMHIMG FSHEELLSHLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMFFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLERWLVHRINKALDRIKRQGASFIGILDIAGFEIFBIN SFEQLCINYTNEKLQQLENHTMFILEGEEVQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECKFFRATDKTTVEKLVQEQ GSHSKFQKPRQLWCKADFCIIHYAGKVDYKADEMLMKNMDPIND NVATLLHGSSDRFVABLMKDVDRIVGLDQVTGMTETAFGSAYKT KKGMPTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK KKGMPTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDOLKCNGVLEGIRICRGGPNRIVPGERQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGGSKIFFRRQULAH LEEEDLKITDIIIPFQAVCRGYLARKAPAKKQQLSALKVUQR NCAAYLKLRHWQWWVTKVKPLLQVTRGBEELQAKDEELLKVK EKQTXVBGGELEEMBRKHQQLLEERNILAGGCAFTELFAEAEM RARLAKKQELEEILHDLESRVEBEEERNOILONEKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKMEERILLEDQNSKF IKKKLMEDRIAGESCLAEEBEKANLAKIRNKGEVHISDLEE RKKKEKTRGBLEKARKLGGETUDQHALAGQIBELLKQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAERQKROLSEELEALKTELEDTLIDTTAAQGELRTKRE QEVABLKKALBEETKRIEQGJCHTGRAHAGRACHAGCELORRT FKANLEKKKQGLFTONKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSBGDRIRVELAKCASKLONELDNVSTLLEERAGKGIK FKANLEKKKGGLFTONKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSBGDRIRVELAKASLKGIKKNLOSSILOEBEEKSILO	1			ERARRHAEQERDELADEITNSASGKSALLDEKRRLEARIAOLEE
OQLERONKELKAKLQELEGAVKSKFKATISALBAKIGQLERQLE GEAKERAANKLVRRTEKKLYFMQVEDERRHADQYKEQMEKA NARMKQLKRQLEAEBEATRANASRRKLQRELDDATEANEGLSR EVSTLINRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVDRTQPPQSE  5931 113 6082 RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLWWIPSERHGFFBASIKEERGDEWWELAENGKKAMVNKDDIQ KMMPPKFSKVEDMAELTCLINGASVLHINLKDRYSGLIYTYSGLF CVVINPYKNLPIYSENIJENYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVJQVLAHVASSHKGRKDHN 1PGE\LERGLLQANPILESFGNARTVQNDNSSFGKFTRINDV TGYIVGANLETYLLEKSRAVRQAKDERTFHIFYOLLSG\AGEHL KSDLLLBGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEMHIMG FSHEELLSHLKVVSSVLOFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYELFRAILVHRINKALDFKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYGREGIEMMFIDFGL DLQPCIDLIERPANPPGVLALLDEECMFFKATDKTFVEKLVQEQ GSHSKFQKPRQKDKDKDFCIHIYAGKUYCHYDENDLAMDLND NVATLHQSSDRFVABLWKDVDRIVGLDOVTGMTETAFGSAYKT KKGMFTTVQQLYKESLTKLMATLRRTHNFFVECIIPNEKRAGK LDPHLVLDOLRCNGVLEGIRICRQGFPNRIVPGFRQRYEILTP NAIPKGFMGKQACERMTRALBELDPNLYRIGGSKIFFRAGVLAH LEEERDLKITDIIIFPQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWMEVPTKVKELQVTRQEEELQAKDEELLKVK EKQTKVGGGLEEMERKHQQLLEERNILAGQLQATELFAEABEM RARLAAKKQELEEILHDLESRVEEEEERNOILONEKKMQAHIQ DLEEQLDEEGGARGRKQLEKVTAEAKIKKMEEFILLLEDQNSKF IKEKKIMEDRIAECSGQLAEEBEKKANLAKIRNKQEWISDLEE RIKKEKEKTRGLEKAKRKLDGETTDLODOIABLQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAKEKQRLEEEILHDLERLEELEDLOTTTAAQQGLRTKRE QEVABLKKALKEETTROLEAKARKLDGETTDLODOIABLGAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELGEDFES EKASRNKAKEKGRIKEETTANLEAOLORGRNATALBELSGDLGDAKR FRANLEKNKQGLEETTRIKEAOLORGRNATALBELSGDLGDAKR FRANLEKNKQGLEETTRIKEAOLORGRNATALBELSGDAR FRANLEKNKQGLETTRIKELGELAKKTLEBLESGDEDARK FRANLEKNKQGLETTRIKELGELAKKTLEBLESGDEDARK FRANLEKNKQGLETTRIKELGENKULDRONTTLLEERBKKGIK FRANLEKNKGGLETTRIKEAOLORGRNATATLEBLESGDEDARK FRANLEKNKGGLETTRIKEAOLORGRNATATLEBLESGDEDARK FRANLEKNKGGLETDNKELAEKASKLONELDNYSTLLEERBKKGIK FRANLEKNKGGLETDNKELAEKASKLONELDNYSTLLEERBKKGIK FRANLEKNKGGLETDNKELAEKASKLONELDNYSTLLEERBKKGIK FRANLEKNKGGLETTRIKEGRETRIKGLEEFSIKGLEE	1			ELEEEQSNMELLNDRFRKTTLOVDTLNAELAAERSAAOKSDNAR
QEAKERAANKLURRTEKKLKEITMQVEDERRHIADQYKEQMEKA NARMKQLKRQLEBAEEBATRANASRRKLQRELDDATEANEGLSR EVSTLINRLRRGGPISFSSSRGRRQLHLEGASLELSDDDTESK TSDVNBTQPPQGE RGNCFWIVPFTMAQRTGLEDPERYLPVDRAVIYNPATQADWTAK KLUWIPSERHGFEAASIKEERGDEVAVELAENGKKAMUNKDDIQ KMMPPKFSKVEDMAELTCLNEASVLINLKDRYYSGLIYTYSGLF CVVINPYKALPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTERTKKVIQVLAHVASSHKGRKOHN IPGE\LERGLLQANPILESFGNARTVONDNSSRFGKFIRINDDV TGYIVGANIETVILEKSRAVRQAKDERTFHIFYQLLSG\ABEHL KSDLLLEGFNNYRFLSNGYIPIPG\QDKORNFGDPGERMHIMG FSHEELISMLKVVSSVLOFGNISFKKERNTDQASMPENTVAQKL CHLLGMNYMEFTRAILTPPRIKVGRDYVQKAQTKEQADPAVEALA KATYERLFRWLVHRINKALDRTKRQASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEGEBYQREGIEMWFIDFGL GSHSKPQKPRQLKDKADFCIIHYAGKVDYKADEWLIMKMDPLND NVATLHIGSSDRFVABLWKDURRIVGLDOVTGMTETARGSAYKT KKSMFTVGQIVKESLTKLMAINTNNPYKELIPMERKAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMGKQACERMTRALELDDRILTRIGGSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAPAKKQQLSALKVLOR NCAAYLKLRHWOWWRVPTKVKPLLQVTRQEBELQAKDEELLKVK EKQTKVBGBLEEMBERKHQQLEERNILLAGQLQAETELFAEAEEM RARLAAKKGELESIHDLEBSFELEBENDNILLAGQLQAETELFAEAEEM RARLAAKKGELESIHDLEBSFELEBENDNILAGQLQATELFAEAEEM RARLAAKKGELESIHDLEBSFELEBENDNILAGQLQATELFAEAEEM RARLAAKKGELESIHDLEBSFELEBENDNILAGQLQAIFELKQL AKKEERLGGALARGDDBTLHKNNALKVVRELQQQIAELQEDFES EKASRNKAEKQKROLSEELHALLESTIDDTTAAQGELRTKRE CRUNZEKKRUGGETDNIKBLACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEAKSKLUGENTOLLDNITLLEEBKKKGIK FKANDASLESGLOTTORGLAECKKVLQQVKAESEHKRKKLDAQV QELHAKVSGGDRLRVELAEACSKLURDNITLLEEBRKKGIK FKANDASLESGLOTTORGLAECKENKLLDNITLLEEBRKKGIK FKANDASLESGLOTTORGLAECKENKULDNITLLEEBRKKGIK FKANDASLESGLOTTORGLAECKENKULDNITLLEEBRKKGIK FKANDASLESGLOTTORGLAECKENKULDNITLLEEBRKKGIK FKANDASLESGLOTTORGLAECKENKULDNITLLEEBRKKGIK FKANDASLESGLOTTORGLAECKENKULDNITLLEEBRKKGIK FKANDASLESGLOTTORGLAECKENKULDNITLLEEBRKKGIK FKANDASLESGLOTTORGLAECKENKULDNITTLLEEBRKKGIK FKANDASLESGLOTTORGLAECKENKULDNITTLLEEBRKKGIK FKANDASLESGLOTTORGLAECKENKULDNITTLLEEBRKKGIK FKANDASLESGLOTTORGLAECKENKULDNITTLLEEBRKKGIK FKANDASLESGLOTTORGLAECKENKULDNITTLLEEBRKKGIK				QQLERQNKELKAKLQELEGAVKSKFKATISALEAKIGOLEEOLE
NARMKQLKRQLEBAEEEATHANASRRKLQRELDDATEAKEGUSR EVSTLKNRLRRGGPISFSSRSGRRQLHLEGASLELSDDDTESK TSDVNBTQPPQSE  5931  113  6082  RGNCFHIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGPEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMMPPKFSKVEDMAELTCLINEASVLIHLKDRYYSGLITYYSGIF CVVINPYKNLPIYSENIIENYRGKKHHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSFGKFTRINDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEELISHLKVVSSVLOPGHISFKKERNTDQASMPENTYAQKL CHLLGMNYMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQBASFIGILDIAGFEIFBLN SFFQLCINYTNEKLQQLFPHFILGDEBYRGGIEWHFIDFGL DLQPCIDLIERPANPPGVLALLDECWFPKATDKTFVEKLVQEQ GSHSKFQKFRQLKDKADFCIIHYAGKVDYKADEMLMKAMDPLIND NVATLHLGSSBFVABLMKDVITVGLDOVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNNFVRCIIPHEKRAGK LDPHLVLLODLRCNGYLEGIRICRQGFPNRIVFGGFRYEILTP NAIPKGFMDSKQACERMIRALDPNLYRIGGSKIFFRAGVLAH LEEERDLKITDIIIFPQAVCRGYLARKAFAKKQQLSALKVLQR NCAAYLKLRHWQWHRVPTKVKBLLQVTRQBEELQAKDEELLKVK EKQTKVBGGLEEMERKHQQLLEEKRILABGLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVBEEEEENOILQNSKF IKEKKLMEDRIAGGSQLAEEEEKAKNLAKIRNCEVMISDLEE RKKKEEKTRGLEEKAKRLLOGETTDLQQIAELQAQIDELKQL AKKEELGGALARGDBTIHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKROLSEELEALKTELEDTLDTTTAQQCERTKKRE QEVABLKKALEETTRNIBQIODMRGHATALBELSSQLEGFRKRE GEVABLKKALEETTRNIBQIODMRGHATALBELSSGLEGAKR FKANLEKNKQGLETDNKBLACGVKVLQQVKAESEHKRKKLDAQV QELHAKVSGGDRLRVELAEKASKLLOENDNTTLLEBAKKGIK FKANDASLESGLOTTQELLGERTRQLENDLDNTTLLEBAKKGIK FKANDASLESGLOTTQELLGERTRGLEDNSTLLEERBKKGIK FKANDASLESGLOTTQELLGERTRGLEDNSTLLEERBKKGIK FKANDASLESGLOTTQELLGERTRGLEDNSTLLEERBKKGIK FKANDASLESGLOTTQELLGERTRGKLEDNSTLLEERBKKGIK FKANDASLESGLOTTQELLGERTRGKLEDNSTLLEERBKKGIK FKANDASLESGLOTTQELLGERTRGKULDNSTLLEBARKKGIK FKANDASLESGLOTTQELLGERTRGKULDNSTLLEBARKKGIK FKANDASLESGLOTTQELLGERTRGKULDNSTLLEBARKKGIK FKANDASLESGLOTTQELGERTRGKULDNSTLLEBARKKGIK FKANDASLESGLOTTQELLGERTRGKULDNSTLLEBARKKGIK FKANDASLESGLOTTQELLGERTRGKULDNSTLLEBARKKGIK	1			QEAKERAAANKLVRRTEKKLKEIFMOVEDERRHADOVKEOMEKA
EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETOPPOSE  FORCFHIVPFTMAGRTGLEDPERYLFVDRAVIYNPATQADWTAK KLWHIPSERHGFBAASIKEERGDEWWELAENGKKAMWINKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKALPIYSENIENYRGKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGO\QDKGMFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKBQADPAVEALA KATYERLFRRLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SPEQLCINYTNEKLQQLFNHTMFILEQEEYQRBGIENMFIDFGL DLQPCIDLIERPANPPGVLALLDEECMFPKATDKTFVEKLVQEQ GSHSKPQKPRQLKDKADFCIIHYAGKVDYKADERLMKNMDPLND NVATLHQSSDRFVABENKUDVRIVGLDOVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRGGFPNRIVFDEFRGNYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGGSKIFFRAGVLAH LEEERDLKITDIIIFPQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQMWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVVEGELEEMERKHQQLLEEKNILABGLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNOILONEKKRMQAHIG DLEEQLDEBEGGAROKLOLEKVTAEAXIKKMEEFILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKANLAKIRKKQEVMISDLEE RLKKEEKTRQELEEKARKLUGETTDLQDQIAELQAQIDELKLQL AKKEEFLQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTLEDTLDTTAAQCELRTKRE QEVABLKKALEEETKNHEAQIODMRGNHATALEELSEDLEOAKR FKANLEKNKQGLETDNKELACEVKVLQOVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEKASKLUGELDNVSTILDEBEKKKILDAQV QELHAKVSEGDRLRVELAEKASKLUGELDNVSTILDEBEKKKILDAQV QELHAKVSEGDRLRVELAEKASKLUGELDNVSTILDEBEKKSLIKA	1			NARMKOLKROLEEAEEEATRANASRRKLORELDDATEANEGLSB
TSDVNETQPPQSE  RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLWWISSERHGFEAASIKEERGDEVMVELAENGKKAMUNKDDIQ KMMPPKPSKVEDMABLTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKHEMPPHIYAISSSAYRCM LQDREDQSILCTGESGGKKTNTKKVIQYLAHVASSHKARKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGY1PIFGQ\QDKGMPRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKRQAPPAVEALA KATYEELFRAUVERINKALDRTKRQGASFIGILDIAGFEIFELN SPEQLCINYTNEKLQQLFNHTMFILEGEEYQREGIEMFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKPQKPRQLKDKADFCIIYYAGKVDYKYDGEFGRAYETLTP NATLHQSSDRFVABLWKNVDRIVGLDQVTGMTETAFGSAYKT KKGMFFTVGQLYKESITKLMATLRITNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFFGRYEILTP NAIPKGFMGGKQACEMMIRALELDPNLYRIGGSKIFFRAGVLAH LEEERDLKITDIIJFPQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWMRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERHHQQLEEKNILAEQLQAFTELFAEAEM RARLAAKKQELEEILHDLESRVEEEEERNOILQNEKKIMQAHIQ DLEEQLDEBEGGRGKUQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIRAECSSQLAEBERKANLAKIRNKQEVMISDLEE RLKKLEEKTRQELEKARKLLDGETTDLQQTAELFLFAEAEM RRLKKLEEKTRGELEKARKLLDGATGLAGATELFAEAEM RRKLKEEKTRGELEKARKLLDGATGLAGATELFAEAEM FRANLEKKLMEDGILGETGLAGCIDTTAAQGELRTKRE GEVABLKKLLEEDTLDTTAAQGELRTKRE EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQGELRTKRE GEVABLKKLLEEBERKHCLGOTTAAQGELRTKRE GEVABLKKALEEETRNHEAQIODMRGRHATALEELSGQLEQDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQGELRTKRE GEVABLKKALEEETRNHEAQIODMRGRHATALEELSGQLEQDAFE FRANLEKNKQGLETDNKELACEVKULQOVKAESEHKRKKLDAQV GELHAKVSEGDRLRVELAEKSKLONELDNVSTILLEEAEKKGILK FRANLEKNKQGLETDNKELACEVKULQOVKAESEHKRKKLDAQV GELHAKVSEGDRLRVELAEKSKLONELDNVSTILLEEAEKKGILK FRANDASLESGLQDTGELLAGETTGNLUNGSRIFROLEEENSLO	1			EVSTIKNRI.RRGGPISESSSRSGPROLHI.EGAGLELCODDTECK
RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLWWIPSERHGFBAAS IKERGDEWAVELAENGKKAMVNKDDIQ KMMPPKPSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKHEMPPHYYAISESAYRCM LQDREQGSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSFFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEELLSMLKVVSSVLOFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMFFTRAILFRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEMNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKRQKPRQLKDKADFCIHYAGKVDYKADEWLMKNMPPIND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFYNCIIPNHERAGK LDPHLVILDQLRCNSVLEGITLCRQGFPNRIVPGEBFQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGGSKIFFRAGVLAH LEEERDLKTTDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGBLEEMERKHQQLLEEKNILABQLQAGTELLFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNOILONEKKKMQAHIQ DLEEQLLEEEGGARQKLQLEKVTAEAKIKMEEEILLLEDONSKF IKEKKLMEDRIAECSGLAEEEEKKANLAKIRNKOEVMISDLEE RLKKEEKTRQELEEBERKKULDECTUDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIOOMRGRAATALEELSEGLEQARR FRANLESNRQGLETDINKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLKVELLAEKASKLQNELDNVSTLLEEABKKGIK FRANDASLESQLQDTOELLQEETRQKLNLSSRIRGLEEEKKRILD				
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KSDLLLEGFNNYRFLSNGYIPIGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEMFIDFGL DLQPCIDLIERPANPPGVLALLDEECMFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQUSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEEGGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSGLAEEBEKAKNLAKIRNCGEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDSTLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQCELRTKRE QEVAELKKALEEETKNIEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKKNKQGLETDNKELACEVKVVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEABKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIRQLEEEKKSLO				TOUR LERGINGANPILES FGNART VQNDNSSRFGKFIRINFDV
FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNYMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEBKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILONEKKKMQAHIQ DLEEQLDEEGGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDBLKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALBEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQOVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEABKKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIRQLEEEKNSLO				IGIIVGANIETILLEKSKAVROAKDERTFHIFYOLLSG\AGEH],
CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQCASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVVGEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFPQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEEEGARQKLQLEKVTAEAKIKMEEEILLLEDONSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIABLQAQIDBLKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEEXSKLQNELDNVSTLLEEAKKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIROLEEEKNSLO				VCDI I I BOEIDING OF CHICAGO
KATYERLFRNLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEBKNILAEQLQAETELFAEAEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKROLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEEVSKLQNELDNVSTLLEEAEKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIROLEEEKNSLO				KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG
SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECMFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVQQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFPQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQBEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEBKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVBEEEERNQILQNEKKKMQAHIQ DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDBTLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEEXSKLQNELDNVSTLLEEABKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIROLEEEKNSLO	I i			KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAOKL
DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCI IHYAGKVDYKADEMLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCI IPNHEKRAGK LDPHLVLDQLRCNGYLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGGSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILOMEKKKNQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDBTLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQELETDNKELACEVKVLQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEEXSKLQNELDNVSTLLEEAEKKGIK FAKDAASLESQLQDTQELLQEETTRQKLNLSSRIROLEEEKNSLO				KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA
GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVARLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIPPQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEEBGARQKLQLEKVTAEAKIKKMEELLLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEBKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIABLQAQIDBLKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKLDAQV QELHAKVSEGDRLRVELAEEXSKLQNELDNVSTLLEEABKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIROLEEEKNSLO				KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN
NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVVDEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFPQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGBLEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNOILQNEKKKMQAHIQ DLEEQLDEEEGGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIABLQAQIDBLKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEABKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIROLEEEKNSLO				KSDLLLEGFNYYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL
KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIPPQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQGELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELACEVKLLQNELDNVSTLLEEAEKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIROLEEEKNSLO				KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLGINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFYEKLVOFO
KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIPPQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQGELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELACEVKLLQNELDNVSTLLEEAEKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIROLEEEKNSLO				KSDLLLEGFNYYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEETLSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKYGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND
LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFPQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEM RARLAAKKQELEEILHDLESRVBEEEERNQILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEBILLLEDONSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDBLKLQL AKKEEELQGALARGDDBTLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEEVKSLONUSTLLEEAEKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIROLEEEKNSLO				KSDLLLEGFNYYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEETLSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKPQKPRQLKDKADFCIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT
NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEEXSKLQNELDNVSTLLEEAEKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIROLEEEKNSLO			·	KSDLLLEGFNYYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPFVRCIIPNIEKRAGK
LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDBTLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEEXSKLQNELDNVSTLLEEAEKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIROLEEEKNSLO			·	KSDLLLEGFNYYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFOEFRORYEILTP
NCAAYLKURHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVBCGELEEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEBEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIABLQAQIDBLKLQL AKKEEKTRQELEKAKRKLDGETTDLQDQIABLQAQIDBLKLQL AKKEEELQGALARGDDBTLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEEXSKLQNELDNVSTLLEEABKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIROLEEEKNSLO			·	KSDLLLEGFNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGOSKIFFRAGVLAH
EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNOILQNEKKKMQAHIQ DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIABLQAQIDBLKLQL AKKEEKTQGLEKAKRKLDGETTDLQDQIABLQAQIDBLKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEABKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIROLEEEKNSLO			·	KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNEKRAGK LDPHLVLDQLRCNGVLEGIRICRGFFNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIFFQAVCRGYLARKAFAKKOOOLSALKVIOR
RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEBEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIABLQAQIDBLKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALBEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEABKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIROLBEEKNSLO			·	KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKMMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGGSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWNVPTKVKPLLQVTRQEEELOAKDEELLKVK
DLEEQLDEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEAEKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIROLEEEKNSLO			·	KSDLLLEGFNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEETLSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGBLEEMERKHQQLLEEKNILAEOLOAETELFAFAFEEM
IKEKKLMEDR IAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQI AELQAQIDBLKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEEVKVLQQVKAESEHKRKKLDAQV FAKDAASLESQLQDTQELLQEETRQKLNLSSRIROLEEEKNSLO				KSDLLLEGFNYYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEETLSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCMGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAPAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGBLEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEEERNQILONEKKKMOAHIO
RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEAEKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIROLEEEKNSLO			·	KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEETLSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEELQAKDEELLKVK EKQTKVEGBLEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEEILLLEDONSKF
AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEABKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIROLEEEKNSLO				KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEETLSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEELQAKDEELLKVK EKQTKVEGBLEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEEILLLEDONSKF
EKASRNKAEKQKROLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEAKKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIROLEEEKNSLO				KSDLLLEGFNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKPQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCMGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGGSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAPAKKQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGBLEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKOEVMISDLEE
QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEABKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIROLEEEKNSLO				KSDLLLEGFNYRPLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNIFFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKPQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGGSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGBLEEMERKHQQLLEBKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLODDIAELOAOIDELKIOL
FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEABKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIROLEEEKNSLO				KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGGSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RIKKEEKTROELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELOAOIAELOEDFES
QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEABKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIROLEEEKNSLO				KSDLLLEGFNNYRPLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGGSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVBEEEERNQILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDBTLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQOGELRTKRE
FAKDAASLESQLQDTQELLQEETRQKLNLSSRIROLEEEKNSLO				KSDLLLEGFNNYRPLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQBEELQAKDEELLKVK EKQTKVEGBLEEMERKHQQLLEEKNILAEQLQAETEIFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDIAELQAQIAELQEDFES EKASRNKAEKQKRDLSELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEDLEOAKR
EQQEEEEEARKNLEKQVLALQSQLADTKKKVDDDLGTIESLEEA				KSDLLLEGFNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKPQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFFQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQBEELQAKDEELLKVK EKQTKVEGBLEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVBEEEERNQILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEEVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTTAAQQELRTKRE QEVAELKKALBEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLOOVKAESEHKRKKLDAOV
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				KSDLLLEGFNYRPLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKPQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGGSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGBLEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNOILQNEKKMQAHIQ DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAIAELQEDFES EKASRNKAERQKRQLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEABKKGIK FAKDAASLESQLQDTGELLQEETRQKLNLSSRIROLEFEKNSLO

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \possible nucleotide insertion)  KKKLLKDAEALSQRLEEKALAYDKLEKTKNRLQQELDDLTVDLD HQRQVASNLEKKQ\KKFDQLLAEEKSISARYAEERDRAEAEARE KETKALSLARALEBALEAKEEFERQNKQLRADMEDLMSSKDDVG KNVHELEKSKRALEQQV\EEMRTQLEELEDELQATEDAKLRLEV NMQAMKAQFERDLQTRDEQNEEKKRLIKQVRELEAELEDERKQ RALAVASKKKMEIDLKDLEAQIEAANKARDEVIKQLRKLQAQMK DYQRELEEARASRDEIFAQSKESEKKLKSLEABILQLQEELASS ERARRHAEQERDELADBITNSASGKSALLDEKRRLBARIAQLBE ELEEEQSNMELLNDRFRKTTLQVDTLNAELAAERSAAQKSDNAR QQLERQNKELKAKLQELEGAVKSKFKATISALEAKIGQLEEQLE QEAKERAAANKLVRRTEKKLKEIFMQVEDERRHADQYKEQMEKA
			NARMKQLKRQLEEAEEEATRANASRRKLQRELDDATEANEGLSR EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE
5932	33	572	RHLEEICFLFLQKGRKLKLSGPRWEEGKPRGTGGLWVKAEANMG FGATLAVGLTIFVLSVVTIIICPTCSCCCLYKTCRRPRPV\APP PHPP/PVVHAPYPQPPSVPPSYPGPSYQGYHTMPPQPGMPAAPY FMQYPPPYPAQPMGPPAYHETLAGGAAAPYPASQPPYNPAYMDA PKAAL
5933		3190	GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD SDMPSRTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK AFSIGKMSTAKRTLSKKEQEELKKKEDEKAAAEIYEEFLAAFEG SDGNKVKTFVRGGVVNAAKEEHETDEKGKIYKPSSRFADQKNP PNQSSNERPPSLLVIBTKKPPLKKGEKEKKKSNLELFKEELKQI QEERDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP LASVKIMMFRTDEERARERNCGFVAFMNRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNFYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLBEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATTRTIQGHLQSENFKQRVM TCFRAWEDWAIYPEPFLIKLQNIFLGLWIIBEKETEDVPDDLD GAPIEEELDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQAVTTSKWELFD QHEESEEEENQNQEEESBDEEDTQSSKSEEHHLYSNPIKEEMTE SKFSKYSEMSEBKRAKLREIELKVMKFQDELESGKRPKKPGQSF QEQVEHYRDKLLQREKEKELEREERDKKDKEKLESRSCHKKEK DECTPTRKERKRRTSTSPSPSRSSGRRVKSPSPKSERSRSRSP KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKFFKKAVTYWKCDLF LCPERSVF
5934	1.	3190	GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD SDMPSRTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK AFSIGKMSTAKRTLSKKEQEELKKKBDEKAAAEIYEEFLAAFEG SDGNKVKTFVRGGVVMAAKEEHETDEKRGKIYKPSSRFADQKNP PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI QEERDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NFQMNLKKCCCQEFGRFGP LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEPVVREGPMFEAMIMNREINNFMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNFYLHGMSBEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPBPFLIKLQNIFLGLVNIIEEKBTEDVPDDLD GAPIEEELDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV

beginning nucleotide location corresponding to first amin acid corresponding to first amin acid residue of amin acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence seq	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No:   nucleotide	_			Amino acto segment containing signal peptide
Corresponding			1	Clutaria Acid E-Phonylel
corresponding to first amino acid residue of residue of amino acid sequence sequence  Popolicine, Collutanine, Radapskragine, Popolicine, Collutanine, Radapskragine, Popolicine, Collutanine, Radapskragine, Popolicine, Collutanine, Radapskragine, Popolicine, Collutanine, Radapskragine, Popolicine, Collutanine, Radapskragine, Popolicine, Collutanine, Radapskragine, Popolicine, Collutanine, Radapskragine, Popolicine, Collutanine, Radapskragine, Popolicine, Collutanine, Radapskragine, Popolicine, Collutanine, Radapskragine, Popolicine, Collutanine, Radapskragine, Popolicine, Collutanine, Radapskragine, Popolicine, Collutanine, Radapskragine, Popolicine, Collutanine, Radapskragine, Popolicine, Collutanine, Radapskragine, Popolicine, Collutanine, Radapskragine, Popolicine, Collutanine, Valuation, Valuation, Popolicine, Collutanine, Valuation, Valuation, Valuation, Popolicine, Science, Popolicine, Collutanine, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Popolicine, Valuation, Po	1			U-Vighiding T. Tooleysian Y. T.
to first amino acid  Codon, /=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletio				n=nistidine, i=isoleucine, K=Lysine,
amino acid residue of amino acid anton acid acquence  PLORITOPION, **POSSIBLE nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide delet	ĺ		1	D Decline, Mamethionine, NaAsparagine,
### ### ##############################				P=Proline, Q=Glutamine, R=Arginine,
amino acid  Sequence    Sequence	1			
Sequence				W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
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SDSGSPVSSRARREKKSKKGRQEALEELKKAGAGEKSKYEVEDE TGYTESVDECOYSLUVOARQDDDHIVDDGIGYVEDGRIFIDDD LEDDALDADEKGCKKAANVOLARQDDHIVDDGIGYVEDGRIFIDDD LEDDALDADEKGCKKAANVOLARVONDDRIGYVEDGRIFIDDD LEDDALDADEKGCKKAANVOKROWNYLALVYNNIKSMFIACA GKKTADKAVOLSKOGLLGDILODLINTETPOITPPPWILIKKERS GGKTADKARVOLSKOGLLGDILODLINTETPOITPPPWILIKKERS GLASPNPFSVHATAVPSGSKLASPYSKREPIVPIKRAEFAG DDVQVESTEEGGSGAMFEDGOFDEPMEVEEVOLEPMAAKAMD KESEPABEVKGABGSKOTVYLGSFLDVEVOLKERDAGA VOEVOUDSSHLPLVKGADEGOVERFYLDAYEDQYNOPVYLF GKWIESABTHVACCAWMKIRETLIJFPENKIDLATGKTGT PISHKOVVERPDEKTATTYKIMFKSKFVERMYAFEIPPVPEKS EYLEVKYSASMPOLPODLAGETFSHYFOTTSISLELFLAMNKKIK GPCHLEVKKSTALNOPVSHCKVEAMALKPELUVIKOVSPPIL WAAFSKKTHQHAKNHONEIIAMALVHISFALDKAAFKPPGSH FCVVSKFMCIFFYAFKEVIEKKNIKVEVAATATETLIGFFLAKY HKIDPDIIVOHNIYGFSLEVILQRINVCKAPHWSKIGRIKKSM FKLGGRSGFGERNATCORMICOVISIASKLILLHAFYKNNY IVPKKITINIAGNIMSFILLHGFKIKKVKVEVAAATETLIGFFLAKY HKIDPDIIVOHNIYGFSLEVILLQRINVCKAPHWSKIGRIKKSM FKLGGRSGFGERNATCORMICOVISIASKLILLHAFYKNNY IVPDKQIFKRPQQKLGDEDEELOGTINKYKKGRKKGAYAGGUL/ DPKVGFVKRFILLLDFSKIJFSIGPENICFTWADALAKYTI IVPDKQIFKRPQQKLGDEDEELOGTINKYKKGRKKGAYAGGUL/ DPKVGFVKRFILLLDFSKIJFSIGPENICFTWADALAKYT IVPDKQIFKRPQQKLGDEDEELOGTINKYKKGRKKGAYAGGUL/ DPKVGFVKRFILLLDFSKIJFSIGPENICFTWADALAKYT VKGREILLGHTKENVOKWALEVIJYODTDSIMINTNSTNILEBVFKL GNVYTKQELKGLDIVRAMCHOLAKOTINNYGQILDSORDTIV YKGREILLGHTKENVOKWALEVIJYODTDSIMINTNSTNILEBVFKL GNVYTKQELKGLDIVRADKODLAKOTINNYGQILDSORDTIV YKGREILLGHTKENVOKWALEVIJYODTDSIMINTNSTNILEBVFKL GNVYTKQELKGLDIVRADKODLAKOTINNYGQILDSORDTIV ENIQRKILETIGBSVANGTYSVIQOGOSINITASQRAYAPBO LQKONATITOTYYLAGOGIRVKAGDFYVIQOGOSINITASQRAYAPBO LQKONATITOTYYLAGOGIRVKAGDFPCKNOTORSTORDERFKCPCP TCOTENIYONVEGSGGTMEPSLIVKGNADALGERFKCPCP TCOTENIYONVEGSGGTMEPSLIVKGNADALGERFKCPCP TCOTENIYONVEGSGGTMEPSLIVKGNADALGERFKCPCP TCOTENIYONVEGSGGTMEPSLIVKGNADALGERFKCPCP TCOTENIYONVEGSGGTMEPSCAGRAFARSANTCYLLAI SKLVKGGLASSTGLAVASGPALTHERVENCHARANGVINANN KLLTHYADHIKGSDRLOFTYTROGSVEVANGOOLLARANGVINANN SKN\LITVIKANGANGANGRANGRONTOPSRAOGRAPPSDDD SDLVIERROPPSSNGLSGOPPCNDLHPCCHPGTRSSLESLDD QCASSGWGRSTROGSGSSU ANGGRKKGG	5025		4400	
TGYTETVEEQYSKLVQARQDDDHIVDDGIGYVEDGRIFDDD LEDDALDADERGDKGKARNUKRUNKUKALTYNNIKSMFIACA GKKTADKAVOLSKUGLLGDILGDLATETPOITPPEWHILKKRES IGASPMPSVARTATAVPSGKIASPYSKREPJITVYPLKRASPAG DDVQVESTEEEQESGAMEFEDGDFDEPMEVEVDLERMAACAMD KESEPAREVKQABSGKATVSILGSFIPDVSKUDIDQEGGSFS VQEVQUSSKILLEVKAGABEGKATVSILGSFIPDVSKUDIDQEGGSFS VQEVQUSSKILLEVKAGABEGVFHEYMLDAVEDQTOMGOVFLF GKWIESSAETHVSCCVMYKRIERTLYFLEREMKIDLINTGKETGT PISMKUVVEEPBEKTATTKYKHKYFKSKPVEKATPEDYVEKS EYLEVKYSAEMPOLPOOLKGETFSRVFGINTSSLELFLMNKTK GPCMLEVKKSTALNOPVSNCKVERMAALKPULVOVSPPPLV WAFSMKIMONAKNIQNEILAMALVHHSFALDKAARKSPIPOSH FCVVSKPKOLTFYARKSVLEKNVKVEVAATERTLIGFFLAKV HKIDPDIIVGHNIYGFELEVLLQRINVCCAPHMSKLIGLKRSHM PKLGGRSGFOERMATCRMICOVETSAKBLIRCKSHHLSBIVOO ILKTERVVITMENIQNIYSESSGLLYLLEHTKADA,KETLGFFLAKV HKIDPDIIVGHNIYGFELEVLLQRINVCCAPHMSKLIGLKRSHM PKLGGRSGFOERMATCAMICOVETSAKBLIRCKSHHLSBIVOO ILKTERVVITMENIQNIYSESSGLLYLLEHTKADA,KETLGFFLAKV HKIDPDIIVGHNIYGFELEVLLQRINVCCAPHMSKLIGLKRSHM PKLGGRSGFOERMATCHMICOVETSAKBLIRCKSHHLSBIVOO ILKTERVVITMENIQNIYSESSGLLYLLEHTKADA,KETLGFFLAKV HKIDPDIIVGHKINSTOPSIOLEDGTHNYKKAGAVAGGLVV UPDKGIFTNOPKILLDFNSLYPSIIQEFNICFTTVORVARSAROKY TEDGGOEGIEPLEDPDSLEMGIIHPERIKKURKANAGAGLVA UPDKGIILOYDINGKALBKLTANSMYGCLGFSYSFYAKPLAALVT YKGREILHGEPDFSLMENILIPFRIKKURKANAGVAGGGAV TEGGGOEGIEPLEPDFSLMENILIPFRIKKURKANAGVAGGGAV TKOGGGOEGIERUNGSYVSYOEPINAALTHOPOYPDKKSLF GNIVTKGELKGLDIVRKAWAGVSPEINKALTHOPOYPDKKSLF HVIVIALAHINGGGRKVKAGDTVSYVI(ODGSNITASGRAYAPBO LQKQNILTIOTYXLAQOHIPVARICEPTICHYDAYATAGRAYAPBO LQKQNILTIOTYXLAQOHIPVARICEPTICHYDAYATAGRAYAPBO LQKQNILTIOTYXLAQOHIPVARICEPTICHYOVARNIATATWEL VDFTGFKWHHYMBEENDALLGGPAQLTTDEKYRDCERFKCPCC TCCTENIYONWEDGGGTDMB PLLITSLOPGFYSVILSKLFRGCAV KS  FGEGFDAEFRRFACLGFGERLQEFSRLEKSNINSDIPVKNOPATI RMMATCCSPFTTTACTGPHQRAPPLLLVQKRRANSGTAFS NSIGRRKGGLIKLBVPABLETTPPLLSINDHPROVSSVIDDULL NETHREVULHKINGSDRPLGFYTROMSVVAPQG\LEEVPOLITI SRLVKGLASSTALLAVSDEILEVKGILEVKLGLEKKILLYSK LVXNAGNETELHLEMMAGLIPDWFEUTEMEVLLELITEMAK LVXNAQNETELHLEMMAGLIPDWFEUTEMEVLLELITEMAK LVXNAQNETELHLEMMAGLIPDWFEUTEMEVLLELITEMAK LVXNAQNETELHLEMMAGLIPDWFEUTEMEVLLELITEMA	5533	] 3	1	SYWLSGWRLSRPPRQFWAGWRGIGRFGTMAPVHGDDCEIGASAL
LEDDALDADEKGKOKARNNKRNYKKLAVTRPNNIKSMPTACA GKKTADRAVOLSKOGLLGDILDDATETOTPOTMILKKMER IGASPMPSVHTATAVPGKIASPVSKREPDLTPVDLKKARSPAC DDVQVESTERGEGSGAMFEGGOFDERMEVEVDLEMAAKAMD KESEPABEVKGEADGGKGTVGYTJGSFLPDVSCWDIDGEGDSSF VOEVQVDSSHLPLVKGADEGKGTVGYTJGSFLPDVSCWDIDGEGDSSFF CKWHISSAETHVSCCVMYKHIGRTLYFLERKKILDHTGKSTGT FISMKDVYEBFDEKTATKYKINKYKSKPYEKNYAFETPDYEKS EYLEVKYSSAEMPOLPOLKGGTSFSVFGTHTSLELFLMNRKIK GPCHLEVKKSTALNOPVSMCKVEAMALKKPDLWTVIKOVSPPLV WAFSMKTWONAKNNQNEI IAMALVHHSFSALDKAAPKEPPOSH FCVVSKPDCI FPYAFKEVIEKKNYKVEVAATERTLIGFILAKY HKLOPDIIVOHNI YOFGLEVLIGRINVCKAPMALKHELJKAPPTONY FKLGGRSGFGERNATCGMICTOVEISAKBLIRCKSYHLBELIVQO LILKTERVVITMENI (SMYESSGLLYLLEHTWKDA KFILQINC ELANLELALQITNIAGNIMSRTLMGGRSSREPELLLHAPYTENNY IVPDKOJFRKPQOKLGDEDEELDGFNYKKKSKKAYAVAGGLVL DEPKVGFTKNF LILLIDFNSLYPSI IQEFNICTTYQRVASEAQKV TEGGROGIFELPDDFSLEMMILPREIRKLVERRKQVKGLMKQOD LNDDLILLYDIRGKALKLTANSWCGLGFSSEARALVAPLAALVT YKGREILMHTKEMVJKANLEVIYGDTDSIKTKKKSKKGAYAKGLVA GNXVISEVNRLYKLLED IDIGVKSLLLIKKAYAKAPLAALVT YKGREILMHTKEMVJKANLEVIYGDTDSIKTNITSTNLEBYFKL GNXVISKGENKLYKLLED IDIGVKSLLLIKKAYAKAPLAALVT YKGREILMHTKEMVJKANLEVIYGDTDSIKTNITSTNLEBYFKL GNXVISKGENKLYKLLED IDIGVFSKLLLIKKAYAKAPLAALVT YKGREILMHTKEMVJKANLEVIYGDTDSIKTNITSTNLEBYFKL GNXVISKGENKLYKLLED IDIGVFSKLLLIKKAYARDLAALVT YKGREILMHTKEMVJKANLEVIYGDTDSIKTNITSTNLEBYFKL GNXVISKGENKLYKLLED IDIGVFSKLLLIKKAYARDLAALVT ENIORALEIGERVLNSSYVPSOFEINKALTKATKOLEPKYKL GNXVISKGENKLYKLIKLED IDIGVFSKLLLIKKAYARDLAALVT LENIORALEIGERVLNSSYVPSOFEINKALTKATKOLEPKYL GNXVISKGENKALLATAGRACH VKGREIKHALLATAGRACH VKGREIKHALLATAGRACH VKGREIKHALLATAGRACH VKGREIKHALLATAGRACH VKHAMATAGARATAGARATAGARATAGARA NSLGRKKGGLIALBAPALERTBPILLISLPQDFRQXSKLAFAS NSLGRKKGGLIALBAPALERTBPILLISLPQDFRQXSKLAFAS NSLGRKKGGLIALBAPALERTBPILLISLPQDFRQXSKLAFAS NSLGRKKGGLIALBAPALERTBPILLISLPQDFRQXSKLAFAS NSLGRKKGGLIALBAPALERTBPILLISLPQDFRQCHFGRSFESDDD SSDLVIENRQPPSSNGLASGAPPSSDDD SSDLVIENRQPPSSNGLAGSGAPPSSDDD SSDLVIENRQPPSSNGLAGGAPPSCHARATHNSTUDULL PETHRAVELHKHKESLKYLSFENSTUDLED PLOTHOPAPI LHIADOVPDPLYSKRPFT FLSEVSRNLKGINLANDHTVEKLKSK LVKNAQOKIEHHLML	1	1	, ,	SDSGSFVSSRARREKKSKKGRQEALERLKKAKAGERYKYEVEDF
GKKTADKAVDLSKOGLIGDILQDLMTETFOTTPPPWILKKRES IGASPMPSVATTATAVPSEKTASPVSRKAPSVPSKAPALSVERKEPOLTPVELKRASFAG DDVQVESTEEGESGAMEFEIGDFDEPMSVEEVDLEPMAAKAMD KESEPAERVKQEADSGKTVSYLSSILPVGMIDGEGDSFF VOEVQVDSSHLPLVKGADEGQVPFFYWLDAYEOQYNQBGVYFLF FISMKDVZEBFDEKLATKYKKMKKKSKEVGMIDGEGDSFF FORWAVESPEDEKLATKYKKMKKSKEVGWIDGEGDSFF FORWAVESPEDEKLATKYKKMKKSKEVGWIDGEGSFF FORWAVESPEDEKLATKYKKMKKSKEVGWIDGEGSFF FORWAVESPEDEKLATKYKKMKKSKEVGWIDGEGSFFINNEKIK GPCHLEVKKSTALNDQVSGKVERMALKEPLDVANIGKSTOPPIN WAFSHKTMONAKHONEILMAALHHISFALDKAAPEPPGSH FORWSKPKDCIFPYARKEVIKKWVEVGWAATERTLLGFFLAKV HKIDPDIIVGHNIYGFELEVLLGRINVCKAPHSKIGRIKKSMM FKLGGSSGGEBNANTGGRIUTVEISAKELIRCKSYHLSELVOO ILKTERVVIPMENIQMWISESSGLLYLLEHTWKDA\KFILQIKC ELAVLPLALQITNIAGNIMSKTLMGGREENBEILLHAPYENNY IVPENGIFRAPQQKLGDBEBEIDGDTNYKKGRKKGAVAGGLVI. DPKVGFYDKTILLLDFNSLYPSIIGFFICFTTVQRVASEAQKV TEDGEGGGIFELPDPSLEBMGILFREIRIKKYKGKKKGAVAGGLVI. DPKVGFYDKTILLLDFNSLYPSIIGFFICFTTVQRVASEAQKV TEDGEGGGIFELPDPSLEBMGILFREIRIKKROVOKLMKQOO LNPDLILGYDIRGKALKLTANSNYGCLGFFYSFTVARVASEAQKV TENGGREGIFELPDPSLEBMGILFREIRIKKROVGKLMKQOO LNPDLILGYDIRGKALKLTANSNYGCLGFFYSFTVARVASEAQKV TENGGREGOFFELPDPSLEBMGILFREIRIKKROVGKLMKQOO LNPDLILGYDIRGKALKLTANSNYGCLGFFYSFTVARVASEAQKV TYKKGRILMHTKERVOKMALGVIVGTDGSHITTSSTNLEBEVPKL GNXVTKQELKGLDIVRROWCLJAKATTOSFTVIGGIISDGKRTIV YKGREILMHTKERVOKMALGVIVGTDGSHITTSSTNLEBVPKL GNXVTKQELKGLDIVRROWCLJAKATTOSFTVIGGIISDGKRTIV YKGREILMHTKERVOKMALGVIVGTDGSHITTANSTNLEBVPKL GNXVTKQELKGLDIVROYATICCPTOSSNLTANGRAVAPSO LOKGONLTIDTOYYLAQGIHPVVARICEPTIGDAVLIATGWEL \DPTOFKWHHYHKBEENDALIGGPAQLITDEKKYRDCEFFKCPCP TCCTENIYONVFGSSTOMPSSLYKGNSTOMSFYDLOLDAVLIATGWEL \DPTOFKWHHYHKBEENDALIGGPAGLTCHNTTHLBLOFPSTTGHLCP ACMKATLOPSFSNSLLTYGLCFYRYIFDPLLSLAFOKVSSVITOVLL PETHRRVELHKHOSDRPLGFYYIRDGMSVRAPGG\LEVGTIFT SRLNKGGLASSTOLLAVBURDFSSKLTANA NSIGRKKKGLLEBPADALTRTPPLLISTLYGKYSSVSVINSLEFFROCH TCSTENIYONAFTSPLLISTLYTPPLLISTLYGKYSSVSVINSLEFFROCH SRLNKGGLASSTOLLAVBURDFSSNSLLSTANA NSIGRKKKGLLEBPADALTRTPPLLISTLYGKYSSVSVINSLEFFROCH SRLNKGLASSTOLLAVBURDFSSTOLLAVBRITTYPLLSGCULDEFTROLTSLISTLYLVELLSK LVKNAQOK IELHFRINALDYSP				TGVYEEVDEEQYSKLVQARQDDDWIVDDDGIGYVEDGREIFDDD
GKKTADKAVDLSKOGLIGDILQDLMTETFOTTPPPWILKKRES IGASPMPSVATTATAVPSEKTASPVSRKAPSVPSKAPALSVERKEPOLTPVELKRASFAG DDVQVESTEEGESGAMEFEIGDFDEPMSVEEVDLEPMAAKAMD KESEPAERVKQEADSGKTVSYLSSILPVGMIDGEGDSFFS VOEVQVDSSHLPLVKGADEGQVPFFYWLDAYEOQYNQBGVYFLF FISMKDVZEBFDEKLATKYKKKKKSKEVGMIDGEGDSFF FORWAVESPEBEKLATKYKKMKKSKEVGMIDGEGDSFF FORWAVESPEBEKLATKYKKMKKSKEVGWIDGEGSFF FORWAVESPEBEKLATKYKKMKKSKEVGWIDGEGSFF FORWAVESPEBEKLATKYKKMKKSKEVGWIDGEGSFFINNEKIK GPCHLEVKKSTALNDQVSGKVERMALKEPLDIAVITGKSTGT FISMKDVGEFPDEPLOLKGETFSHVFGTNTSSLELFMARKIK GPCHLEVKKSTALNDQVSGKVERMALKEPLDVANITGKSTGFPLAKV WAFSSKTMONAKHONEILAMALHISFALDKAARPEPPGSH FORWSKRINGLFFYARKEVIKKNVVEVGAATERTLLGFFLAKV HKIDPDILVGINITYGFLEVLICRIHVCKAPHSKIGRIKRSM FKLGGSSGGFGENANTGGNITWKGANGKSKIKGSKKGMAGGILVL UNDENGIFRQQKLGDBEGELIGDTINYKKGSKKGAVAGGILVL UPDKQIFRQQQKLGDBEGELIGDTINYKKGSKKGAVAGGILVL UPDKQIFRQQQKLGDBEGELIGDTINYKKGSKKGAVAGGILVL UPDKQIFRQQQKLGDBEGELIGDTINYKKGSKKGAVAGGILVL UPKGGFICHFYRQQXLGDBEGELIGDTINYKKGSKKGAVAGGILVL UPKGGFICHFYRQQXLGDBEGELIGDTINYKGGKKGAVAGGILVL UPKGGFICHFYRQQXLGDBEGELIGDTINYKTGSEQLKV TEGGSGGIFFPDPSELEMGLIFRETRIKYKGGKKKGAVAGGILVL UPKGGFICHFYRGQXLGDBEGLIFRETRIKAKQVGLKMKQO LINPULICYDITGKALKUTANSNYGGLGFSYSFYAKDLALUT YKGREILAHFYERWVKMLEVIVOTDGILFREKQVCKIMKQO LINPULICYDITGKALKUTANSNYGGLGFSYSFYAKALALUT YKGREILAHFYERWVKMLEVIVOTDGILFREKQVCKIMKQO LINPULICYDITGKALKUTANSNYGGLGFSYSFYAKALALUT YKKGREILAHFYERWVKMLEVIVOTDGILFREFVIGGILDSKRITU YKKGREILAHFYERWVKMLEVIVOTDGILFREFVIGGILDSKRITU  ENIQKALLEIGGENVLNSVEVSGFILINAKTKOPODYPDKKSLP HUHVALMINNGGGRKVKAGDTUSYJICODGSNILTASGRAVAPSO LOKKOBLITOTOTYLAQGILFVVARICEDIDAVLITATGWEL \DPTOFKWHHYHKBEENDALIGGPAGLITORFTHLDLOFSTTGHLCP ACMKATLOPSFSNSLITYGLCFYRYIFDBLACLEKLTTOHENDK KLIMDIRFIKKYYGGMLICEEFTCANTHILDLOFSTTGHLCP ACMKATLOPSFSNSLITYGLCFYRYIFDPLLILLYQKRBADSSGLAPAS NSLGRKKKGLLEPWALFTRPPLLILSIPGVSSVITUNLL FEHREVRLIKHGSDRPLGFYIRDGMSVRAPAPGLEPGTFS SRLWGGLASSTTLANVENGSSGRLTOPSSGFLAPASFYOUNL SRLWKGGLASSTTLANVENGSSGRLTOPSSGFLAPASFYOUNL SRLWKGGLASSTTLANVENGSSTTLANVENGSSGLAPASFYOUNL SRLWKGGLASSTTLANVENGSSTTLANVENGSSGLAPASFYOUNL SRLWKGGLASSTTLANVE	1			LEDDALDADEKGKDGKARNKDKRNVKKLAVTKPNNIKSMFIACA
IGASPAPESVATATAVPSGKTASPYSKREPLITPULKRAFFAG DDVQVESTEEGOGADERPEGOFDEPENSVEEVDLEPMAAKAMD KESEPAEBVKQEADSGKGTVSTLOSILPDVSCWDIDQEGDSSFS VOEVQVDSSHLPLVKGADEGQVFHFYWLDAVEQOTYPQBVVFLF GKWEISAETHVSCCVMYKNIERTLYFLPERMKIDLATGKSTGT PISMKDVVEEPDEKLATKYKTMKYKSKEVERNTAFSIEDVPEKS EYLEVKYSAEMPQLPQDLKGETFSHYFGTMSLELIFHUMKKIK GPCKLEVKKSTALNOPVSNCKVERMALKEDLVVNI LOWSPPPLV VMAFSHKITMORANCHNORI ILMAALVHISPALDKAAPKPPPOSH FCVVSKPKDCIFPYAPKEVIEKMVKVEVAATERTLLGFFLAKV HKIDPDIIVGHNIYGPELEVLLQRINVCKAPHNSKIGLKKSNM PKIGGRSGFGERNATCGRMICDVEISAEKLIRCKSYHLSELVOO ILKTERVVIPMENIQMYSESSGLUFHTWKDAVARGKSHELVOO ILKTERVVIPMENIQMYSESSGLUFHTWKDAVARGGLKKSNM PKIGGRSGFGERNATCGRMICDVEISAEKLIRCKSYHLSELVOO ILKTERVVIPMENIQMYSESSGLUFTVQKASEAGKV TEGGEOGIPELPDPSLEMGILFTTVQRVASEAGKV TEGGEOGIPELPDPSLEMGILFTTVQRVASEAGKV TEGGEOGIPELPDPSLEMGILFTTVQRVASEAGKV TEGGEOGIPELPDPSLEMGILFTTVQRVASEAGKV TEGGEOGIPELPDPSLEMGILFTTVQRVASEAGKV TEGGEOGIPELPDPSLEMGILFTTVQRVASEAGKV TEGGEOGIPELPDPSLEMGILFTVGTDGTDSINTSTNLEEVFLL GNXVXSEVNKLYKLLEIDIDOVFKSILLLKKKKYAALVVEPTSD GNXYTKGELKGLDIVRROWCLAKTGTGFJGISDGSRDTIV PKORFIVKGLEIDINGSVPVSOPEINKALTKOPPDVPDKKSLP HVIVALMINISGGRKVKAGDTUTSVYLCOGGIISDGSRDTIV ENIQKRLEGGENTUNGSVPVSOPEINKALTKOPPDVPDKKSLP HVIVALMINISGGRKVKAGDTUTSVYLCOGERFKOPOP TCGTENIYDAVFPGSSTDMEPSLYKCSNIOCKASPLTFTVOLSIN KLIMDIRRFIKKYYDGMLICEPTCRNRTHRLPLOFSRTGPLCP ACMKATLGPESYSSLSTVGCFFYRIPDEAKHITDIEKDK KLKMPTFFKKYYDGMLICEPTCRNRTHRLPLOFSRTGPLCP ACMKATLGPESYSSLSTVGCFFYRIPDEAKHITTDIEKDK KLKMPTFFKKYYDGMLICEPTCRNRTHRLPLOFSRTGPLCP ACMKATLGPESYSSLSTVGCFFYRIPDEAGSVEVNLSKLFAGCAV KS  13936 1124 139 RGEEOFDAEFRRFACLGFGERLQEFSRLLRAVHRSRAWTCYLAY RMMATCCPSPTTTACTGPMQRAPPLRLLVQKRRADSSGLAFAS NSLQRKKKGLLEPVAPALFRTPPLLISLPGVSSVIDVDLL PETHRRVELIKHGSSDPLGFYIRDGMSVRAPOG\LEKVFGTFI SRLVKGGLASSTTLLAVGFPSAGLOPACDSVIDULL PETHRRVELIKHGSDRPPLGFFYRPLLSLENGVSSVIDVDLL PETHRRVELIKHGSSDPLGFYIRDGMSVRAPOG\LEKVFGTFI SRLVKGGLASSTTLLAVGRSTFALLAUFTRSLSLELTFVULSTFYULLIL CHAQOOPLYSKRTSIFLLOWSFFALRKKSYSDIDVKNDFAPI LHLADOVPLYSKRTSIFLLOWSFFALRKSKYSDIDVKNDFAPI LHLADOVPLYSKRTSIFLLOWSFFALRKSKYSSIDVKNDFAPI LHLADOVPLYSKRTSIFLLOWSF	1			GKKTADKAVDLSKDGLLGDILQDLNTETPQITPPPVMILKKKRS
DDUQVESTEEQESGAMEFEIGDFDEPMEVEEVILEPMAACAMU KESEPAEEVKQEADSKAFTSYLSGLIPUGDGSSFS VOEVOUDSSHIPLVKGADEGOYEFFWILDAYEDQYNQPOVYFLY GKWAISSAETUVSCCWUKNIERTLYFLPREMKILDAYDQYNQPOVYFLY GKWAISSAETUVSCCWUKNIERTLYFLPREMKILDAYDQYNQPOVYFLY GKWAISSAETUVSCCWUKNIERTLYFLPREMKILDAYDQYNQPOVYFLY GKWAISSAETUVSCCWUKNIERTLYFLPREMKILDAYDQXYGESTSHUMGATTSELEIFMARKIK GPCHLEVKKSTALNQPVSMCVERMAALKPULWYIHOVSPPFLV WAFSHKTMONAKNHONEILAMAALVHHISFALDKAAPKPPGSH FCVVSKPKOLTFYPAFKEVTEKKNVVEVENARTHILOFFFLAKV HKIDPDIIVGHNIYGFELEVLLQRINVCKAPHWSKIGRLKSSHM PKIGGSGFGERNATGGRINICOVEISAKETKTLLOFFFLAKV HKIDPDIIVGHNIYGFELEVLLQRINVCKAPHWSKIGRLKSSHM PKIGGSGFGERNATGGRINICOVEISAKETKTLLOFFILAKY IVPDKQIFRKPQQKLGDBDEEIDGTNNYKGRKKGAYAGGLVI. DENGFYDKFILLLDFNSLYSSIJGFFNICFTTVQXNSEAQKY IVPDKQIFRKPQQKLGDBDEEIDGTNNYKGRKKGAYAGGLVI. DENGFYDKFILLLDFNSLYSSIJGFFNICFTTVQXNSEAQKY TEDGEGGGIFELPDPSELEMGILFRENGILFREKSYHLGHAYENGY ONVYSEUNKLYKLLEIDIDQVFKSGLILLKKKKYAALVVBPTSD GNYUTNGELAGLDIVRRDWCOLLAKOTONFVIGQILSDQSKDTIV YKGREILMHYKENVQKMLEVIVGDDGINTASTORAYAPPO LQKOPALTIDTOYYLAQQIHPVVARICEPIDAVLIATGWEL VDFTOFKVHHYHHDEENDALLGGPAQLIDEEKYRDCEFFKCPCP TCGTENIYONVFGSSTIMPSSIJKGSNIDAVLIATGWEL VDFTOFKVHHYHHDEENDALLGGPAQLIDEEKYRDCEFFKCPCP TCGTENIYONVFGSSTIMPSSIJKGSNIDAVLIATGWEL VDFTOFKVHHYHHDEENDALLGGPAQLIDEEKYRDCEFFKCPCP TCGTENIYONVFGSSTIMPSSIJKGSNIDAVLIATGWEL VDFTOFKVHHYHHDEENDALLGGPAQLIDEEKYRDCEFFKCPCP TCGTENIYONVFGSSTIMPSSIJKGSNIDAVLIATGWEL VDFTOFKVHHYHHDEENDALLGCPFRILLAVHRSRANTCYLAI RMMATCCPSPITTACTGPWQRAPPLRILLQVRRADSSILAPAS NSLQRKKKGLLEPVADLFTRYPPLLISLGPOPFQVSSVIDVDLL PSTHRKVELKKHGSDRPLGFYYIROMSVRAPQGLEEVPGIFI SRLVKGGLASSAGSTINGGSGFSI SSDLVIERRQPPSSBLSQCPPCWOLHPGCRHFTRSSLESLDD SSDLVIERRQPPSSBLSCQPPCWOLHPGCRHFTRSSLESLDD SSDLVIERRQPPSSBLSCQPPCWOLHPGCRHFTRSSLESLDD SSDLVIERRQPPSSBLSCQTPSVILLEVNIERTYVELLKSK LVKNQOKSTRINGSSFSU	1			IGASPNPFSVHTATAVPSGKIASPVSRKEPPLTPVPLKPARFAG
KESSPAEUVGGADSGKGTVSYLGSFLEDVSCMDIDGEDSSES VOEUVOUSSHIPLIVKGADEROVHPHOVYFLE GKWIESABTHVSCCWAVKNIERTLYFLPREMKIDLITGKETGT PISMKDVYEEFDEKIATKYKIMKYKSKEVEKYAPEIPDVEKS EYYEVKYSAEMPOLPODLKGETFSHVSTNTSSLELFIMMRKIK GPCMLEVKKSTALNOPVSMCKVEMAALKPDLWAYIKOVSPPDLV WMAFSMKIMONAKHONGHIIAMAALVHISVALDKADKEPPOSH FCVVSKPKDCIFPYAPKEVIEKKNYKVEVAATRETLLGFFLAKV HKIDPDIJGMINIGGFLEVLLQRINVGHWSKIGKLKSMM PKLGGRSGFGERNATCGRMICDVEISAKELIRCKSYHLBELVQO ILKTERVVIPMENIQMYSESSQLLYLLEHTIKKALKSIMLSELVQO ILKTERVVIPMENIQMYSESSQLLYLLEHTIKALKSYHLBELVQO ILKTERVVIPMENIQMYSESSQLLYLLEHTIKALKSYHLBELVQO ILKTERVVIPMENIQMYSESSQLLYLLEHTIKALKSYHLBELVQO ILKTERVVIPMENIQMYSESSQLLYLLEHTIKALKSYHLBELVQO ILKTERVVIPMENIQMYSESSQLLYLLEHTIKALKSYHLBELVQO ILKTERVVIPMENIQMYSESSQLLYLLEHTIKALKSYHLBELVQO ILKTERVVIPMENIQMYSESSQLLYLLEHTIKALKSYHLBELVQO ILKTERVVIPMENIQMYSESSQLLYLLEHTIKALKSKYAALVVIPTENY IVPDKGIFRKPQGKLGDEDEELDGDTMKYKKGRKKGAYAGGLVL DPKVGFYKOFKIILLDIDGAVFKSLLLLKKKKYAALVVIPTENY IVPDKGIFRKPQGKLGDEDEELDGTTMKYKKGRKKGAYAGGLVL YKGREILMHTKEMVOKMULEVIYGDTDSIMINTNSTNLEEVFKL GNIVKKSEVNAL YKLLEIDIDGAVFKSLLLLKKKYAALVVEPTED GNYVTKQELKGLEIVTENDEOLALAGAPALTEGPISGFSKFYARCHEALDT YKGREILHGERVINGSSYPVSGFINKALTKDPQDYPDKKSLP HVIVALMINSGGGRVKAAGDTVSYVICOGSILTASGGAVAPO LOKODILTIDTOYYLAQOIHPVVARICEPIDGIDAVLIATGMEL \DPTOFKHHYHADEENDALLGGPAQLTDEENYRDCEPFKCPCP TCGTENIYDNVFDGSGTDMEPSLYRCSNIDCKASFIPLCF ACMATLGPEYSNKSLYTDLCFYRYIFGCALBKLTTDHEKOK LKKGFFTFKVLQDYRKLKNTAEGFLSRSGYSEVNLSKLFAGCAV KS  SGERKKGLLEPVAPALRTRPPLALLSLPOPFCVSSVILVOLL PETHRRVELHHHGSDRPLGFITRGMSVRVAPOG LERVPGIFI SRLVRGGLESTGLLAVSBEILEVNGTEVAGKTINQVTOMMAN SIN\LIVTVKPANGRNVVRGASGRITGPPSAGGPAEPDSDDD SSDLVIERROPPSSMGLSGFPTCAGGFPGTRSSLPSLDD QEQASSGWGSRIRGDGSGFSL LKHANGORSLESTGLLAVGENDVENDEVELLEN SSLLNEGGLESTGLLAVGYSPELLEKENNSDIPDVKNDFAPI LHLADOYDPLYSKRFSIFFILSEVSENKIKGINLNEKWINDS LUNNADGRIKGLEHDFMINGLENDVPELITEMEVLSLELIPEVILPS AVSOLVALKELRYHSSLVVDHPALAFLEENLKILRLKFTEMK LVKNAQORSLEHLFMINGLENDVPELITEMEVLSLELIPEVILPS AVSOLVALKELRYHSSLVVDHPALAFLEENLKILRLKFTEMK ILHANGORSLEHLFMINGLENDVFELITEMEVLSLELIPEVILPS AVSOLVALKELRYHSSLVADHPALAFLEENLKIL	1			DDVQVESTEEEQESGAMEFEDGDFDEPMEVEEVDI.EPMAAKAWD
VOEVQVDSSHLPLVKGADEGQVHFYLDAYEDQNQGGVVFLF GKWHISASHTWSCCWANNIERTLYFLPERMKIDLINTGKETGT PISMKDVMEEPDEKIARKYKIMKPKSKPVERNYAPEIPDVPEKS EYLEVKYSAEMPQLPQDLKGETFSHVFGTNTSSLELFLMMRKIK GPCWLEVKKSTALNQPVSMCKVEAMAKRPLVWYIKDVSPPLV WMAFSHKIMQNAKHHQNEIIANAKPPLWNIKDVSPPLV WMAFSHKIMQNAKHHQNEIIANAKPPLWNIKDVSPPLV WMAFSHKIMQNAKHHQNEIIANAKPPLWNIKDKLKRSM PKLGGRSGGERNATCGRHICDVEISAKELIRCKSYHLSELVQ ILKTERVVIPMENIQMMYSESSQLLYLLEHTMKDA\KFILGIKKSMM PKLGGRSGGERNATCGRHICDVEISAKELIRCKSYHLSELVQ ILKTERVVIPMENIQMMYSESSQLLYLLEHTMKDA\KFILGIKC ELAVUPLALQITNTAGNHINSRTLMGGSERNBFLLLHAPYENNY IVPDKQIFRPRQQKLEGDEBEIDGTHKKGRKKGAKGAYAGGLVL DPKVGFYDKFILLLDRNSLYPSIJQEFNICFTTVQRVASEAQKV TEDGEGGDIPELPOPSLEMGILPREIKLKGRKKYAALVWSPTSD LNPDLILQYDIRQKALKLTANSMIGCLGFYSRFYTAKQLALVT YKGREILMHTKEMVQKMALEVIYGDTDSIMINTNSTMLEEVFKL GNIVKSENNKLYKLLEIDIDGVFKSLLKKKYAALVWEPTSD GNIVTKQELKGLDIVRRDDCLJAKANTADPODYPDKKSLP HVHVALWINSQOGRKVKAGDTVSYVICODGSNLTASQRAYAPEQ LQKODNLTIDTGYTLAQQIHVVARICEPTCNTALTDPODYPDKSLP HVHVALWINSQOGRKVKAGDTVSYVICODGSNLTASQRAYAPEQ LQKODNLTIDTGYTLAQQIHVVARICEPTCNTHLPLOFSRTSPLCP TCGTENIYDNVFDGSSTDMEPSLKYRSDHILDFLOFSRTSPLCP ACMKATLQPEYSDKSLYTQLGFYRYIFDAGCALEKLTTDLEKOK KLIMDIRFRIKKYYDGWLICEPTCNTHLPLOFSRTSPLCP ACMKATLQPEYSDKSLYTQLGFYRYIFDAGCALEKLTTDLEKOK KKQFFFPKVLQDYRKLKNTAEQFISRGYSEVLINGVTDMYAN SIN\LIVTIVKPANGRNNVVRGASGRLTGPPSAGGPAEPDSDD SSDLVIERRYGPSSNGLYTQLGFYRGMSVRVAPQG\LERPFGTFI SRLVRGGLAESTGLLAVSDEILEVNGIEVAGKTLNQVTDMYAN SIN\LIVTIVKPANGRNNVVRGASGRLTGPPSAGGPAEPDSDD SSDLVIERRYGPSSNGLAGGPFCCHPGTRSSLPSLD OCAASSGRGSRIKGDSGGFSL VXNAQOKISLHLFMINGLPDNYFELITENINLEHVLSELIFEVKLPS AVSGLVNLKELRVYHSSLVVDHPALAFLEENIKLICHKTENGK LVNAQOKISLHLFMINGLPDNYFELITENINLELLSLEIPEVKLPS AVSGLVNLKELRVYHSSLVDHPALAFLEENIKLLKLKTYENGK IPRWYEHLANLKELYJSGCVUPSQLSTMQLEGGPQDLKMILRTLYLL KSSLSRIPOVTDLDFSLQKLISLDENISCLELLEPKILSLE LLESCDLERIPHSIFSISLANDLEFDLENNIKLTUREISFOMLO NISCKKWHANNIAYIPAGGALBNNIKTVEETISFOMLO NISCKKWHANNIAYIPAGGALBNNIKTVEETISFOMLO NISCKLWHANNIAYIPAGGALBNNIKTVEETISFOMLO NISCKLWHANNIAYIPAGGALBNNIKTUETISFOMLOH				KESEPAEEVKOEADSGKGTVSYLGSFLPDVSCWDIDOFGDSSFS
GKWWIESAETHVSCVWKNIERTKYFLPREMKILDLNTGKETGT PISMKDVYEEFDEKLATKYKIMKPKSRVBYAEFIDYDVEKS EYLEVKYSAEMPQLPQDLKGETFSHVFGTNTSSLELFLMMRKIK GPCWLEVKKSTALMQPVSMCKVEMAMLKPDLWVIKDVSPPDLV WMAFSKKIKMQMKNHOMEN IAMAALVHISPALDKADKEPPGSH FCVVSKPKDCIFPYAPKEVIEKKNVKVEVAATERTLLGFFLAKV HKIDPDIJUGNINIYGFELEVLLQRINVARHNSKIGLKRSMM PKLGGRSGFGERNATCGRMICDVEISAKELIRCKSYHLBSLVQQ ILKTERVVIPMENIQMNYSESSQLLYLLEHTKMOLKEILGLKRSMM PKLGGRSGFGERNATCGRMICDVEISAKELIRCKSYHLBSLVQQ ILKTERVVIPMENIQMNYSESSQLLYLLEHTKMOLKEILGLKRSMM PKLGGRSGFGERNATCGRMICDVEISAKELIRCKSYHLBSLVQQ ILKTERVVIPMENIQMNYSESSQLLYLLEHTKMOLKKSIKMAGGLVL DPKVGFYDKFILLLDTNISTYSIJGERNICPTTVQRVASEAQKV TEDGEQEQIPELPDPSLEMGILPREIRKLVERKQVXQGLMKQQD LNPDLILQYDIRGKALKLTANSMYGCLGFSYSEFYAKQLAALVI YKGRELIHHTEMVQKMLEVIYGGTISHININISTUREVYFLL GNNVYKSEVNKLYKLLEIDIDGYFKSLLLLKKKXYAALVVEPTSD GNVYKSEVNKLYKLLEIDIDGYFKSLLLLKKKXYAALVVEPTSD GNVYKSEVNKLYKLLEIDIDGYFKSLLLLKKKXYAALVVEPTSD GNVYKSEVNKLYKLLEIDIDGYFKSLLLLKKKXYAALVVEPTSD GNVYKSEVNKLYKLLEIDIDGYFKSLLLLKKKXYAALVVEPTSD GNVYKSEVNKLYKLLEIDIDGYFKSLLLLKKKXYAALVVEPTSD GNVYKSEVNKLYKLLEIDIDGYFKSLLLLKKKYAALVVEPTSD GNVYKSEVNKLYKLLEIDIDGYFKSLLLLKKKYAALVVEPTSD GNVYKSEVNKLYKLLEIDIDGYFKSLLLKKKYAALVVEPTSD GNVYKSEVNKLYKLLEIDIDGYFKSLLLLKKKYAALVVEPTSD GNVYKSEVNKLYKLLEIDIDGYFKSLLLLKKKYAALVVEPTSD GNVYKSEVNKLYKLLEIDIDGYFKSLLLKKKYAALVVEPTSD GNVYKSEVNKLYKLLEIDIDGYFKSLLLLKKKYAALVVEPTSD GNVYKSEVNKLYKLLEIDIDGYFKSLLLLKKKYAALVVEPTSD LOKOONLITOTYYLLQOGIPPVVAILEDGIDIDAVILATGYBEL \DETTGYTENTATUTTOTYYLLQOGIPPVVAILEDGIDAVILATGYBEL \DETGGERKYKLTUTTOTYYLLQOGIPPVVAILEDGIDAVILATGYBEL \DETGGERKYKLTUTTOTYYLLQOGIPPVVAILEDGIDAVILATGYBEL \DETGGERKYKLTUTTOTYYLLQOGIPPVVAILENGTBADVILANG KLIMDIRRFIKKYYDGWLICEEPTCRNTRHLBLQFFSTOLOG ACMAATLQPEYSDKSLYTTQLCFYRYIFDLDALAKLTTOTHENDK KKUMPTTOTYTTOTYYLLQOGIPPVVAILATGYBOLOGIPPOTTATOTYTOTYTOTYTOTYTOTYTOTYTOTYTOTYTOTY	1			VOEVOVDSSHLPLVKGADEEOVFHFYWLDAVEDOVNORGWIFT P
FISHKDVÆEFDEKLATKKKINKKSKPUSKAYAFEIDDVEKS EYYLEVKYSAEMPOLIPODLKGETTSSVEGTATSSLEIFLMNRKIK GPÜLEVKKSTALNOPUSMCKVEAMALKPDLINVIKDVSPPDLV WAFSHKTMORAKHONEIIAMALVEVBAATKRILEFLANKKIK GPÜLEVKKSTALNOPUSMCKVEAMALKPDLINVIKDVSPPDLV WAFSHKTMORAKHONEIIAMALVEVBAATKRILEFTLAKV HKIDPDITUGINIYGFELVELLORINVCKAPHHSKIGRLKRSSM FKLGGRSGGERNATCGRHICTDVEISAELIRCKSYHLSELVOO ILKTERUVIPMENIONMYSESQLLYLLEHTWKDA\KFILQIKC ELNVLPLALQITHIAGNIHSRTLMGGRSERNEFLLHAPYENNY IVPDKQIFKRPOQKLEDBEDEIDDGTHKYKKGKKGRYAGGIVL DPKVGFYOKFILLIDFNSLYPSIJQEFNICFTTVORVASEAQKV TEDGEGGJTELPDPSILEMMILPPRIKYRKGKVGKKGAYAGGIVL DPKVGFYOKFILLIDFNSLYPSIJQEFNICFTTVORVASEAQKV TEDGEGGJTELPDPSILEMMILPPRIKYRKGKVGKKGAYAGGIVL OPKVGFYOKFILLIDFNSLYPSIJQEFNICFTTVORVASEAQKV TEDGEGGJTELPDPSILAMINGTGGFSYSRFYAKPLAALVT YKGREILMHTKEMVOKMILEVIYGDTDSIMINTNITBILEBUFKL GINVXSEVNKLYKLLEIDIDGVFKSLLLIKKKXYAALVVBPTDD GNVYTKQELKGLDIVRRDWCDLAKOTONFVIGQILSDOSRDTIV ENIQRKLIEGIBENIANSVYSOGEINKITDPODYPREKSLP HVHVALWINSGGGRKVKAGDTVSYVICOGSSILTASQRAYAPEO LQKODNITIDTOYYLAQQIHPVVARICEPPIGNEKIPD-PREKSLP HVHVALWINSGGGRKVKAGDTVSYVICOGSSILTASQRAYAPEO LQKODNITIDTOYYLAQQIHPVVARICEPPIGNEKIPD-PREKSLP HVHVALWINSGGGRKVKAGDTVSYVIOCASSILTASQRAYAPEO LQKODNITIDTOYYLAQQIHPVVARICEPPIGNEKIPD-PGFSTEPLCP ACMKATLQDEVSSKSLYTQLCFYRYIPDAGCALBEKTTOLIEKOK LKKOFFFTKVLQDYRKLKNTAEQFISRGSYSEVNILSKLFRAGCAV KS  139 RGEGGFDAEFRFRACLGFGERLQEFSRLLRAVHRSRAWTCYLAI RMIMATCOPSYTTACTGFBVQRAPPIRHLPLOFSRTSPLCA KS MSLQRRKKGLLLBPVAPLRTRPPLLISLPOPFGOVSSVIDVDLL PETHRVENLYHKHGSDENJCGYPCVOLTAPQG\LERVPGIFI SRLVRGGLAESTGLLAVSDEILEVNGIEVAGKTLNQVTDMAVAN SIN\LIVTVVRAMQRNNVVRGASGRLTGPPSAGGPAEPDSDDD SSDLVIERROPSSNGLAGGSPCCHPGTRSSLPSLDD QCASSGWGSRIKGDSGGFSL VXNAQOKISLHFFMUAGCPDNVELTETHEVLISLELIPEVKLPS AVSGLVNLKELRVYHSSLVVDHPALAFLEENIKLLRIKFTENGK LVNAQOKISLHLFMUAGLPDNYFEUTIEMEVLSLELIPEVKLPS AVSGLVNLKELRVYHSSLVVDHPALAFLEERIKLLRIKFTENGK IPPWFHLANLKELIYLSGCVVPEQLSTMQLEGFQDLKNILRILVLK SSLSRIPQVVTDLLPSLQKLSDLDNSTENLELJOLFIL NSSCLKEMHNILAYIPAGGLAGLISNINIKTVEETISFOHLO NISSCKLEMHNILAYIPAGGLAGLISNINIKTVEETISFOHLO NISSCKLEMHNILAYIPAGGLAGLISNINIKTVEETISFOHLO NISSCKLEMHNILAY	1			GKVWIESAETHVSCCVMVKNTERTI.VET.DDEMKIDI.NTCVETCT
EYYEVKYSAEMPOLEODIKGETESHYEGINTSSLEILFLMNRKIK K GPCHLEVKKSTALNOPVSMCKVEMAKPDLVNVIKDVSPPILV VMAFSMKTMQNAKNHQNEIIAMAALVHHSFALDKAAEKPPEQSH FCVVSKPKDCIFPYAPKEVIEKKNIKVEVAAAERTLLGFILAKV HKIDPIJIGHIN YGPELEVILQRINVCKAPHWSKIGRLKSSM FKLGGSGGGENATCGRMICDVEISAKBLIRCKSYHLSELVOO ILKTERVJTPMENIQNWYSESSQLLYLLEHTWKDA\KFILQIMC ELNVLPLALQITNIAGNIMSTLINGGRSERNEFILLIHAPYENNY IVPDKQIFRKPQQKLGDEDELIDGDTNYKYKKRKKGRYAGGUNL DPKVGFYDKFILLIDFNSLYPSIIQBFNICPTTVQRASEAQKV TEDSEQGSIPELPDPSLEMGILPREIRKLVRRRKQVXQLMKQOD LNPDLILQYDIRKALKLTANSMYCCLGFYSRFYARPLAALVT YKGREILMHTKEMVQKMNLEVIGDTDSIMINTSTRLEEVFKL GNKVKSEVNKLYKLLEIDIDOVFKSLLLKKKKYAALVVEPTSD GNYVTKGELKGILTVRDWCDLAKORVFVIQOILSOSRDTIV ENIQKSLIEGENVLNGSVPYSQPEINKALTKDPQDYPDKKSLP HVHVALMINSQGGRKVKAGDTVSYVICQDSNITASGRAYAPEQ LOKQDNLTIDTQYTLAQQIHPVVARICEPIDGIDAVILATGWEL \DPTOPKVHHYHKDEENDALLGGPAQLTDEEKYDCCEFKCPCP TCSTENIYONVPOSGSTDMPSSLYNGCNSDVAGSRAYAPEQ LOKQDNLTIDTQYTLAQQIHPVVARICEPIDGIDAVILATGWEL \DPTOPKVHHYHKDEENDALLGGPAQLTDEEKYDCCEFKCPCP TCSTENIYONVPOSGSTDMPSSLYNGCNSDVAGSAGFYASPEQ EKKELTHTENDKYDGSTDMPSSLYNGCNSDVAGSAGFYAFPG KLIMDIRRFIKKYYDGWLICEEPTCRNRTRHLPLQFSRTGPLCP ACMATLQPEYSDKSLYTQLCFYRYIFDAECALBKLTTDHEKOK LKKQFFTFKVLQDYRKLKNTAECFISFRSYSEVULSLFAGCAV KS  SGEOPDAEFRFFACLGFGERLQEFSRLLRAVHESRAWTCYLLAY RMLMATCCPSPTTTACTGPWQRAPPLRLLVQKREADSSGLAFAS NSLQRKKKGLLLRVAPALRTRPPLLISLPQDFFQVSSVIDVDLL PSTHRKVRLHHNISGDRPLGFYIRDGVAVAPQG\LEFUPGGFF SRLVRGGLAESTGLLAVSDBILEVNGIBVAGKTLNQVTDMWAN SIN\LIVTVKPANQRNINVVRGASGRLTOPPSAGFGPAEDSDDD SSDLVIENRQPPSSNGLSQSPPCWLHFGCRHCTRSSLPSLDD QCQASSGGGSRIRGDGSGFSL PTSLLKSTVOLMCELLDDKYNGVVRAPGAGERPCFPSDDDD SSDLVIENRQPPSSNGLSQSPPCWLHFGCRHCTRSSLFSLDS LUKNAQDKIELHLFMLNGLDDKNYRLTEVLLSLKKKKK LLKLADQYDPLYSKRFSIFISEVSEKKLKQINLANDRYVEKLKKK LVXNAQDKIELHLFMLNGLDDKNYRCHGLGFGODLKNLTLYL LKSSLSRIPOVVTDLLPSLQKLSLDNESKLVVILNILKKMVNLKS LLVXNAQDKIELHLFMLNGLEDDLKSLUKHVESIISFOHLQ KSSLSRIPOVTDLLPSLQKLSLDHNIENILLELLKVTENGK IPRWFHHKINKLELLYJAGCULFEGLSLDHNIENILDFLQLLFL KSSLSRIPOVTDLLPSLQKLSLDHNIENILDFLQLLFL	1			
GPCMLEVKKSTALINOPVSMCKVERMALKPDLUNVILKDVSPPDIJV VMAPSMKTMONAKNHONE I IAMAALVHHSFALDKAPKPPFOSH FCVVSKPKDCI FPYAFKEVI EKKNYVEVAATERILLGFFLAKV HKIDPDI IVGHNI YGFELEVILORI INVCKAPHUSKIGRLKRSMM PKILGGSGGGENANTCORMICOVELISARBLIRKCSYSHLSELVOO ILKTERVVI PMEN IQNNYSESSQLLYLLEHTWKDA\KFILQIMC ELNVLPLALQI TNIAGNIMSRTIMGGRSERNEFILLHAPYENNY IVPDKQI FRKPQOKLGEDBEE IDDOTNKYKKGRKKGAYAGGLUL DPKVGPYDKFI ILLDFNSLYPSI IQFFNICTTYORVASEAQKV TEGEGGGOT PELPPDSLEMGILLBERI RLLVERRKQVKQLMKQQD LNPDLILQYDI RQKALKLTANSMYGCLGFSYSRYPAKPLAALVT YKGREI LMHTKEMVQKNNLEVI YGDTDSIMINTHSTALEEVPKL GNUKSECVNKLYKLLEI DIDODYKSLLLLKKKKYAALVVEPTSD GNVATKOELKGLDI VRRDWCDLAKDTGNFVIGQI ILSDQSRDTIV ENIQKRLIEI GENVLNGSVPVSQFEI INKALTKRPQDYPDKKSLP HVIVALWINSQGGKVKAGDTVSYVI CODGSNLTASGRYAPEO LORODNITIDTOYYLAQOI HPVVARI CEPPI GIJ IDAVLI ATGMEL \QPTOTEVHTHKHE GENDALLGGAPQLTDEEKYRDCEPFKCPCP TCGTENI YDNVFDGSGTDMEPSLYRCSNIDCKASPJITFTVQLSN KLIMDIRRFI KKYYDGHLI CEEPTCRNTETRILLQFSRTGPLCP ACKMATLQEEYSDSLYTOLCFYRI YFDAECALEKLTTDHEKDK KKS FTFKVLQDYRKLKNTAEQFLSRSGYSEVNLSKLFAGCAV KS  1124  139 RGEEOFDAEFRRFACLGFGERLQEFSRLLRAVHRSRAWTCYLAI RMMATCCPSPTTTACTGPWORAPPLIRLLVCKRRADSSGLAFAS NSLGRKKGLLIEPSVLDLTYTY IFDAECALEKLTTDHEKDK KKSFTPKVLQDYRKLKNTAEQFLSRSGYSEVNLSKLFAGCAV KS  5936  1124  139 RGEEOFDAEFRRFACLGFGERLQEFSRLLRAVHRSRAWTCYLAI RMMATCCPSPTTTACTGPWORAPPLIRLLVCKRRADSSGLAFAS NSLGRKKGLLIEPSVRDLAVRAPGS LEERVSJUDDLL PETHRRVRLHKHGSDRPLGFYTICMSWVRAPGG \LERVPGIFI SRLVRGGLABSTGLLAVSDE ILEVKSILDQDFRQVSSVIDVDLL PETHRRVRLHKHGSDRPLGFYTICMSWVRAPGG \LERVPGIFI SRLVRGGLABSTGLLAVSDE ILEVKSILDQDFRQVSSVIDVDLL PETHRRVRLHKHGLIPSVISURGLEVKSILDQDFRCYSSLIDDDI SSDLVIENRQPPSSNGLSQOP PCWDLHFGCRHPGTRSSLPSLDD GQQASSGWGSRTRGDGSGTSL  5937  31 1600 PTSLLKSTVOLMCELLQDKRYQCVYSLAETFKVLASFYVILVIL LHLADQYDPLYSKRFSI FILSEVSENKLKQINLRNETYKEKKSK LLVKNAQOKIELHLFMLNGLEGVDLEVGLEGDEDOLKDRLTLYL LKSSLSRIPOVYTDLLPSLQKLSLDHNESKLIVLLRIKLELKTEMGK IPRWFHHIKMIKELIJLSGCVLPEGLSLDHNI IERNGLKTURETISFOHLQ LKSSLSRIPOVYTDLLPSLQKLSLDHNIENINLETURLLKKMVNLKS LELISCDLERI PHSI FSLINLHELDLLERINLKTURETISFOHLQ KSSLSKIPOVYTDLLPSLQKLSLDHNIENINLE				
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DPKYGYPUKFILLIDFNSLYPSITQEFNICFTTYQRVASEAQKV TEDGEQEQIPELPDPSLEMGILPREIRKLVERRKQVKQLMKQQD LNPDLILQYDIRQKALKITANSMYGCLGFSYSRYYAKPLAALVT YKGREILMHTKEMVQKMNLEVIYGDTDSIMINTNSTNLERVFKL GNKVKSEVNKLYKLLEIDIGVFKSLLLLKKKXYAALVVBETSD GNYVTKQELKGLDIVRRDWCDLAKDTGNFYIGQILSDQSRDTIV ENIQKRLIEIGENVLNGSVPVSQFEINKALTKDPQDYPDKKSLP HVHVALMINSQGGRVKAGDTVSYVICQDGSNLTIASQRAYAPEQ LQKQDNLTIDTQYYLAQQIHPVVARICEPIGGIDAVILATUWEL \DPTQFKVHHYHKDEENDALLGGPAQLTDEEKYRDCERFKCPCP TCGTENIYDNVFDGSGTDMEPSLYRCSNIDCKASPLTTVQLSN KLIMDIRRFIKKYYDGWLICEEPTCRNRTRHLPLQFSRTGPLCP ACMKATLQPEYSDKSLYTQLCFYRYIFDAECALEKLTTDHEKDK KKWGFFTPKVLQDYRKLKNTAEQFLSRSGYSEVNLSKLFAGCAV KS  1124 139 RGEEQFDAEFRRFACLGFGERLQEFSRLLRAVHRSRANTCYLAT RMIMATCCPSPTTTACTGPMQRAPPLRLLVQKRRADSSGLAFAS NSLQRRKKGLLLRPVAPLRTRPPLLISLPQDFRQVSSVIDVDLL PETHREVRLHKHGSDRPLGFYIRDGMSVRVAPQG\LERVPGIFI SRLVRGGLAESTGLLAVSDRILEWGIEVAGKTINQVTDMMVAN SHN\LIVTVKPANGRNVVVRGASGRTGPPSAGFGPAEPDSDDD SSDLVIENRQPPSSNGLSQOPPCWDLHPGCRHPGTRSSLPSLDD QEQASSGWGSRIRGDGSGFSL  5937 31 1600 PTSLLKSTVQIMGRLLQDKRYQCVYSLÄEIFKVLASFYVILVIL YGLTSSYSLWMLRSSLKQVSFEALRKSNYSDIPDVKNDFAPI LHLADQYDPLYSKRFSIFLSEVSENKLKQINLNNEWTVEKLKSK LVKNAQDKIELHLFMLNGLPDNVFELTEMEVLSLELIPFEVKLPS AVSQLVNLKELRVYHSSLVVDHPALAFLEENIKLIRLKFTEMGK IPRWFHLKNLKELYLSGCVLPFQLSTMQLEGFQDLKNLRTLYL KSSLSRIPQVVTDLLPSLQKLSLDNEGSKLVVLNNLKKMVNLKS LELISCDLERIPHSIFSLNNLEEDLLENNLKTVEEIISFQHLQ NISCKLWHNNTAYIPAQTGALSNLEQLSLDHNNIENLPLQLFL				IVPDKQIFRKPQQKLGDEDEEIDGDTNKYKKGRKKGAYAGGLVI.
TEGGEGETIELPDPSLEMGILPREIRKLVERRKQVKQLMKQQD LNPDLILQYDIRQKALKLTANSMYGCLGFSYSRFYARDLALVT YKGREILMHTKEMVQKMMLEVIYGDTDSIMINTNSTKLERVFKL GNXVKSEVNKLYKLLEIDIDGVFKSLLLLKKKKYAALVVEPTSD GNYVTKQELKGLDIVRRDWCDLAKDTGNFVIGQILSDQSRDTIV ENIQKRLIEIGENVLMGSVPVSQFEINKALTKDPQDYPDKKSLP HVHVALWINSQGRKVKAGDTVSYVICQDGSNITASGRAYAPEQ LQKQDNITIDTQYYLAQQIHPVVARICEPIDGIDAVILATGWEL \[ \begin{array}{c} \DPTQFKVHHYHKDEENDALLGGPAQLTDEEKYRDCERFKCPCP \text{TCSTENIYDNVFDGSGTDMEPSLYRCSNIDCKASPLTFTVQLSN} KLIMDIRRFIKKYYDGWLICEEPTCRNRTRHLPLQFSRTGPLCP ACMARATLQPEYSDKSLYTQLCFYRYIFDAECALEKLTTDHEKDK KLKQFFTPKVLQDYRKLKNTAEQFISRSGYSEVNLSKLFAGCAV KS \[ \text{S} \text{139} \text{RGEEGFDAEFRRFACLGFGERLQFFSRLLRAVHRSRAWTCYLAT} \text{RMIMATCCPSPTTTACTGFWQRAPPLRLLVQKRRADSSGLAFAS} \text{NSLGRKKGLLLRPVAPLRTRPPLLISLPQDFRQVSSVIDVDLL} \text{PETHRRVRLHKHGSDRPLGFYIRDGMSVRVAPQG\LERVPGIFI} \text{SRLVRGGLAESTGLLAVSDEILEWGIEVAGKTLNQVTDMVAN} \text{SIN\LIVTVXPANQRNYVVGASGRLTGPPSAGGPAPAEDDDD} \text{SSLVIENRQPPSSNGLSQGPPCWDLHPGCRHPGTRSSLPSLDD} \text{QEQASSGWGSRIRGDGSGFSL} \] \text{SSLVIENRQPPSSNGLSQGPPCWDLHPGCRHPGTRSSLPSLDD} \text{QEQASSGWGSRIRGDGSGFSL} \text{LYKNAQDKIELHHYMLRGLPDNVFELTEMEVLSLEIPEWKLPS} \text{LYKNAQDKIELHHYMLRGLPDNVFELTEMEVLSLEIPEWKLPS} \text{LYKNAQDKIELHHYMLRGLPDNVFELTEMEVLSLEIPEWKLPS} \text{LYKNAQDKIELHHYMLRGLPDNVFELTEMEVLSLEIPEWKLPS} \text{LYKNAQDKIELHHYMLRGLPDNVFELTEMEVLSLEIPEWKLPS} \text{LYKNAQDKIELHHYMLRGLPDNVFELTEMEVLSLEIPEWKLPS} \text{LYKNAQDKIELHHYMLRGLPDNVFELTEMEVLSLEIPEWKLPS} \text{LYKNAQDKIELHHYMLRGLPDNVFELTEMEVLSLEIPEWKLPS} LYKNAQDKIELHHYMLKELYLSGCVLPEQLSTMQLEGFQDLKNLRTLVIL \text{KSSLSRIPQVVTDLLPSLQKISLDNEGSKLVVLNNLKKMVNLKS \text{LPHVFHLKNLKELYLSGCVLPEQLSTMQLEGFQDLKNLRTLVIL \text{KSSLSRIPQVVTDLLPSLQKLSLDNEGSKLVVLNNLKKMVNLKS \text{LPLISCDLERIPSIFSPLLDRENNLKTVEEIISFQHLQ \text{NISCLKLWHNNIAYIPAQIGALSNLEQLSLDMNNIENLEPLQLILIF \text{LISCDLERIPSIFPALGEQLSLDMNNIENLEPLQLILIF \text{LYKNAGDKIELPQLISLDMSGSKLVVLNNILKMVMILKS \text{LYKNAGDKIELPQLISLDMSGSKLVVLNNILKMVMILKS \text{LYKNAGDKIELPQLISLDMSGSKLVVLNNILKMVMILKS \text{LYKNAGDKIELPQLISLDMSGSKLVVLNNILKM	1	i i		DPKVGFYDKFILLLDFNSLYPSIIOEFNICFTTVORVASEAOKV
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YKGREILMHTKEMVQKMNLEVIYGDTDSIMINTNSTNLEEVFKL GNKVKSEVNKLYKLLEIDIDGVFKSLLLIKKKKYALAUVBPTSD GNYVTKQELKGLDIVRDWCDLAKDTGMFVIGGILSDQSRDTIV ENIQKRLIEIGENVLNGSVPVSQFEINKALTKDPQDYPDKKSLP HVHVALWINSQGGRKVKAGDTVSVVICQDGSNLTASQRAYAPEQ LQKQDNLTIDTQYYLAQQIHPVVARICEPIDGIDAVLIATGWEL \DPTQFKVHHYHKDEENDALLGGPAQLTDEEKYRDCERFKCPCP TCGTENIYDNVPDGSGTDMEPSLYRCSNIDCKASPLTFTVQLSN KLIMDIRRFIKKYYDGWLICEPPTCRNRTRHLPLQFSRTGPLCP ACMKATLQFEVSDKSLYTQLCFYRYIPDAECALEKLTTDHEKDK LKKQFFTPKVLQDYRKLKNTAEQFLSRSGYSEVNLSKLFAGCAV KS  SGEEQFDAEFRRFACLGFGERLQEFSRLLRAVHRSRAWTCYLAT RMLMATCCPSPTTTACTGFWQRAPPLRILVQKRRADSSGLAFAS NSLQRRKKGLLLRPVAPLRTRPPLLISLPQDFRQVSSVIDVDLL PETHRRVRLHKHGSDRPLGFYIRDGMSVRVAPQG\LERVFGIFI SRLVRGGLAESTGLLAVSDEILEUNGIEVAGKTLNQVTDMWAN SIN\LIVTVKPANQRNNVVRGASGRLTGPPSAGPGPAEPDSDDD SSDLVIENRQPPSSNGLSQGPPCWDLHPGCRHPGTRSSLPSLDD QEQASSGWSRIRGDGSGFSL JEGASGWGSRIKGDGSGFSL LHLADQYDPLYSKRFSIFLSEVSENKLKQINLNEWTVEKLKSK LVKNAQDKIELHLFMLNGLPDNVFELTEMEVLSLELIPEVKLPS AVSQLVNLKELRVYHSSLVVDHFALAFLEENLKILRIKFTEMCK IPRWVFHLKNLKELYLSGCVLPEQLSTMQLEGFQDLKNLRTLYL KSSLSRIPQVVTDLLPSIQKLSLDNEGSKLVVLNNILKKMVNLKS LELISCDLERIPHSIFSLNNLHELDLRENNLKTUEEIISFQHLQ NISCKKUMHNNIAYIPAQIGALSNLEQLSLDHNIENDLQLFL		1		I-NPDI-II-OYD I ROKAI-KI-TANSMYGGI-GEGYGD EVAKDI AAT 1777
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LKKQFFTPKVLQDYRKLKNTAEQFLSRSGYSEVNLSKLFAGCAV KS  RGEEQFDAEFRRFACLGFGERLQEFSRLLRAVHRSRAWTCYLAI RMLMATCCPSPTTTACTGPWQRAPPLRLLVQKREADSSGLAFAS NSLQRRKKGLLLRPVAPLRTRPPLLISLPQDFRQVSSVIDVDLL PETHRRVRLHKHGSDRPLGFYIRDGMSVRVAPQG\LERVPGIFI SRLVRGGLAESTGLLAVSDEILEVMGIEVAGKTLNQVTDMMVAN SHN\LIVTVKPANQRNNVVRGASGRLTGPPSAGFGPAEPDSDDD SSDLVIENRQPPSSNGLSQGPPCWDLHPGCRHPGTRSSLPSLDD QEQASSGWGSRIRGDGSGFSL  S937  31  1600 PTSLLKSTVQLMCRLLQDKRYQCVYSLAEIFKVLASFYVILVIL YGLTSSYSLWWMLRSSLKQYSFEALREKSNYSDIPDVKNDFAPI LHLADQYDPLYSKRFSIFLSEVSENKLKQINLNNEWTVEKLKSK LVKNAQDKIELHLFMLNGLPDNVFELTEMEVLSLELIPEVKLPS AVSQLVNLKELRVYHSSLVVDHPALAFLEENLKILRLKFTEMGK IPRWVFHLKNLKELYLSGCVLPEQLSTMQLEGFQDLKNLRTLYL KSSLSRIPQVVTDLLPSLQKLSLDNEGSKLVVLNNLKKMVNLKS LELISCDLERIPHSIFSLNNLHELDLRENNLKTVEEIISFQHLQ NLSCLKLWHNNIAYIPAQIGALSNLEQLSLDHNNIENDPLQLFL				ACMKATLQPEYSDKSLYTQLCFYRYIFDAECALEKLTTDHEKDK
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139 RGEEQFDAEFRRFACLGFGERLQEFSRLLRAVHRSRAWTCYLAI RMLMATCCPSPTTTACTGPWQRAPPLRLLVQKRBADSGLAFAS NSLQRRKKGLLLRPVAPLRTRPPLLISLPQDFRQVSSVIDVDLL PETHRRVRLHKHGSDRPLGFYIRDGMSVRVAPQG\LERVPGIFI SRLVRGGLAESTGLLAVSDEILEVMGIEVAGKTLNQVTDMMVAN SHN\LIVTVKPANQRNNVVRGASGRLTGPPSAGPGPAEPDSDDD SSDLVIENRQPPSSNGLSQGPPCWDLHPGCRHPGTRSSLPSLDD QEQASSGWGSRIRGDGSGFSL QEQASSGWGSRIRGDGSGFSL LHLADQYDPLYSKRFSIFLSEVSENKLKQINLNNEWTVEKLKSK LVKNAQDRIELHLFMLNGLPDNVFELTEMEVLSLELIPEVKLPS AVSQLVNLKELRVYHSSLVVDHPALAFLEENLKILRLKFTEMGK IPRWVFHLKNLKELYLSGCVLPEQLSTMQLEGFODLKNIRTLYL KSSLSRIPQVVTDLLPSLQKLSLDNDEGSKLVVLNNLKKMVNLKS LELISCDLERIPHSIFSLNNLHELDLRENNLKTVEEIISFQHLQ NLSCLKLWHNNIAYIPAQIGALSNLEQLSLDHNNIENLPLQLFL				
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NSLCRRKKGLLLRPVAPIRTRPPLLISLPQDFRQVSSVIDVDLL PETHRRVRLHKHGSDRPLGFYIRDGMSVRVAPQG\LERVPGIFI SRLVRGGLAESTGLLAVSDBILEVWGIEVAGKTLNQVTDMYVAN SHN\LIVTVKPANQRNNVVRGASGRLTGPPSAGPGPAEPDSDDD SSDLVIERRQPPSSNGLSQGPPCWDLHPGCRHPGTRSSLPSLDD QEQASSGWGSRIRGDGSGFSL  5937 31 1600 PTSLLKSTVQLMCRLLQDKRYQCVYSLAEIFKVLASFYVILVIL YGLTSSYSLWWMLRSSLKQYSFEALREKSNYSDIPDVKNDFAFI LHLADQYDPLYSKRFSIFLSEVSENKLKQINLNNEWTVEKLKSK LVKNAQDRIELHLFMLNGLPDNVFELTEMEVLSLELIPEVKLPS AVSQLVNLKELRVYHSSLVVDHPALAFLEENLKILRLKFTEMGK IPRWVFHLKNLKELYLSGCVLPEQLSTMQLEGFODLKNLRTLYL KSSLSRIPQVVTDLLPSLQKLSLDNEGSKLVVLNNLKKMVNLKS LELISCDLERIPHSIFSLNNLHELDLRENNLKTVEEIISFQHLQ NLSCLKLWHNNIAYIPAQIGALSNLEQLSLDHNNIENLPLQLFL				RMIMATCCPSPTTTACTGDWODADDI DI I VOVDDADGOCA SES
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QEQASSGWGSRIRGDGSGFSL  5937 31 1600 PTSLLKSTVQLMCRLLQDKRYQCVYSLAEIFKVLASFYVILVIL YGLTSSYSLWWMLRSSLKQYSFEALREKSNYSDIPDVKNDFAFI LHLADQYDPLYSKRFSIFLSEVSENKLKQINLNNEWTVEKLKSK LVKNAQDKIELHLFMLNGLPDNVFELTEMEVLSLELIPEVKLPS AVSQLVNLKELRVYHSSLVVDHPALAFLEENLKILRLKFTEMGK IPRWVFHLKNLKELYLSGCVLPEQLSTMQLEGFQDLKNLRTLYL KSSLSRIPQVVTDLLPSLQXLSLDNEGSKLVVLNNLKKMVNLKS LELISCDLERIPHSIFSLNNLHELDLRENNLKTVEEIISFQHLQ NLSCLKLWHNNIAYIPAQIGALSNLEQLSLDHNNIENDFLQLFL				SHIN (LI VIVKPANQKNNVVKGASGRLTGPPSAGPGPAEPDSDDD
9337 31 1600 PTSLLKSTVQLMCRLLQDKRYQCVYSLAEIFKVLASFYVILVIL YGLTSSYSLWWMLRSSLKQYSFEALREKSNYSDIPDVKNDFAFI LHLADQYDPLYSKRFSIFLSEVSENKLKQINLNNEWTVEKLKSK LVKNAQDKIELHLFMLNGLPDNVFELTEMEVLSLELIPEVKLPS AVSQLVNLKELRYHSSLVVDHPALAFLEENIKILRLKFTEMGK IPRWVFHLKNLKELYLSGCVLPEQLSTMQLEGFQDLKNLRTLYL KSSLSRIPQVVTDLLPSLQKLSLDNEGSKLVVLNNLKKMVNLKS LELISCDLERIPHSIFSLNNLHELDLRENNLKTVEEIISFQHLQ NLSCLKLWHNNIAYIPAQIGALSNLEQLSLDHNNIENIPLQLFL			į	
YGLTSSYSLWMMLRSSLKQYSFEALREKSNYSDIPDVKNDFAFI LHLADQYDPLYSKRFSIFLSEVSENKLKQININNEWTVEKLKSK LVKNAQDKIELHLFMLNGLPDNVFELTEMEVLSLELIPEVKLPS AVSQLVNLKELRVYHSSLVVDHPALAFLEENLKILRLKFTEMGK IPRWVFHLKNLKELYLSGCVLPEQLSTMQLEGFQDLKNLRTLYL KSSLSRIPQVVTDLLPSLQKLSLDNEGSKLVVLNNLKKMUNLKS LELISCDLERIPHSIFSLNNLHELDLRENNLKTVEEIISFQHLQ NLSCLKLWHNNIAYIPAQIGALSNLEQLSLDHNNIENDFLQLFL	F-5005			
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AVSQLVNLKELRVYHSSLVVDHPALAFLEENLKILRLKFTEMGK IPRWVFHLKNLKELYLSGCVLPEQLSTMQLEGFQDLKNLRTLYL KSSLSRIPQVVTDLLPSLQKLSLDNEGSKLVVLNNLKKMVNLKS LELISCDLERIPHSIFSLNNLHELDLRENNLKTVEEIISFQHLQ NISCLKLWHNNIAYIPAQIGALSNLEQLSLDHNNIENLPLQLFL	i l		I	
IPRWVFHLKNLKELYLSGCVLPEQLSTMQLEGFQDLKNLRTLYL KSSLSRIPQVVTDLLPSLQKLSLDNEGSKLVVLNNLKKMVNLKS LELISCDLERIPHSIFSLNNLHELDLRENNLKTVEEIISFQHLQ NLSCLKLWHNNIAYIPAQIGALSNLEQLSLDHNNIENLPLQLFL			1	
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CTKLHYLDLSYNHLTFIPEEIQYL\SNLQYFAVTNNNIEMLPDG	]		1	
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	L		· l	CIRLHILDLS YNHLTFIPEEIQYL\SNLQYFAVTNNNIEMLPDG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LFQCKKLQCLLLGKNSLMNLSPHVGELSNLTHREPIG\NYLETL
			PPELEGCQSLKRNCLIVEENLLNTLPLPVTERLQTCLDKC
5938	395	1865	YKGEGFFCNQEARGERRKKKKAMSSPNIWSTGSSVYSTPVFSOK
			MTVWILLLSLYPGFTSQKSDDDYEDYASNKTWVLTPKVPEGDV
			TVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINME
			YTIDIFFAQTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRN
			SKKADAHWITTPNRMLRIWNDGRVLYSLRLTIDAECQLQLHNFP
1	}	ļ	MDEHSCPLEFSSYGYPREEIVYQWKRSSVEVGDTRSWRLYQFSF
1			VGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLI
ŀ			VVLSWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVS
-	i		YVTAMDLFVSVCFIFVFSALVEYG\TLHYFVSNRKPSKDKDKKK
			KNPAPTIDIRPRSATIQMNNATHLQERDEEYGYECLDGKDCASF
			FCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPTAFCLFNLVYW
ľ			VSYLYL
5939	66	1404	IRPGYLKEVQENSPGHRAGLEPFFDFIVSINGSRLNKDNDTLKD
			LLKANVEKPVKMLIYSSKTLELRETSVTPSNLWGGQGLLGVSIR
ļ			FCSFDGANENVWHVLEVESNSPAALAGLRPHSDYIIGADTVMNE
l			SEDLFSLIETHEAKPLKLYVYNTDTDNCREVIITPNSAWGGEGS
ł			LGCGIGYGYLHRIPTRPFEEGKKISLPGQMAGTPITPLKDGFTE
I			VQLSSVNPPSLSPPGTTGIEQSLTGLSISSTP\PAVSSVLSTGV
İ			PTVP/LLPPQVNQSLTSVPPMESSYLHLPGLMPFTRQGLPNLPQ
ł			PSTFNLPR\PTHSWPGVGLYQEFVKPGVLPPLSSMPPRNLPG\I
}			APLPLPSEFLPSFPLVPESSSAASSGELLSSLPPTSNAPSDPAT
1			TTAKADAASSLTVDVTPPTAKAPTTVEDRVGDSTPVSEKPVSAA
			VDANASESP
5940	145	717	RRSASRSASPRQSAGTAVTTGTRAGGTCLAAAHHRMRWRADGRS
3310	143	/ * /	
			LEKLPVHMGLVITEVEQEPSFSDIASLVVWCMAVGISYISVYDH
l	İ		QGIFKRNNSRLMDEILKQQQELLGLDCSKYSPEFANSNDKDDQV
			LNCHLAVKVLSPEDGKADIVRAAQDFCQLVAQKQKRPTDLDVDT LA\VYLVOMVVLILI
5941	13	6147	MCLGRMGASSPRSPEPVGPPAPGLPFCCGGSLLAVVVLLALPVA
3311	1	0147	WGQCNAPEW\LPFARPTNLTDEFEFPIGTYLNYECRPGYSGRPF
1			
	İ		SIICLKNSVWTGAKDRCRRKSCRNPPDPVNGMVHVIKGIQFGSQ
			IKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPP
1			TITMODEL COMPENSION OF THE PROPERTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE P
1			TITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIY
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGQBVFYSCEPGYDLRGAASMRCTPQGDW
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGQBVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGQBVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGQBVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCOPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGQBVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTORDKDNFSPGGBVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFFIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGGEVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPI
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGGEVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGQBVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE CREFYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGKPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCOPGFVMKGPRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGQBVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSAECILGNAAHWSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGBPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIIL VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGBPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCBPGYDLRGAA
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGQBVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFFIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGKPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCBFGYDLRGAA SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGA
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGGEVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFFIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNFGSGGRKV FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCBPGYDLRGAA SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSP
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGGBVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMYH VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNFGSGGRKV FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCBPGYDLRGAA SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSP PVIPNGRHTGKFLEVFFFGKAVNYTCDPHPDRGTSFDLIGESTI
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGGEVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKKKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCBPGYDLRGAA SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSP PVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTOTNASD
		·	CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCQPGFVMKGPRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGQBVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGBPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCBPGYDLRGAA SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLPPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSP PVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTOTNASD FPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKT
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSEQGEVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGBPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFYMKGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCBPGYDLRGAA SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLPPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSP PVIPNGRHTGKFLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD FPIGTSLKYECRPEYYGRPFSTTCLDNLVWSSPKDVCKRKSCKT PPDDVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGQBVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSAECILSGNAAHWSTKPPI CQRIPCGLPPTIANGDFISTNREHFHYGSVVTYRCNPGSGGRKV FELVGKPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFYMKGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCBPGYDLRGAA SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSP PVIPNGRHTGKPLEVFFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD FPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDDVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFFIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPI CQRIPCGLPPTIANDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCBFGYDLRGAA SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSP PVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD FPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGGEVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFFIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNFGSGGRKV FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTQRKDNFSPGQEVFYSCBFGYDLRGAA SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSP PVIPNGRHTGKPLEVFFFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNSVWSSPAPRCGILGHCQAPDHFLFAKLKTOTNASD FPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC
		·	CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCOPGFVMKGPRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGQBVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE CREYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSSAECILGGNAAHWSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCBPGYDLRGAA SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLPPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSP PVIPNGRHTGKPLEVFFFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD FPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILGGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVYTYR CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLMEVVEFRCQPGFVMKGPRRVKCQA LNKWEPELPSCSRVCQPPPEILHGEHTPSHQDNFSPGQEVFYSC
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCQPGFVMKGPRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGQBVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSSAECILGSNAAHWSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGBPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCBPGYDLRGAA SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLPPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSP PVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTOTNASD FPIGTSLKYECRPBYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQA LNKWEPELPSCSRVCQPPPEILHGEHTPSHQDNFSPGQEVFYSC EPGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGQLPHGRV
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCOPGFVMKGPRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGQBVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE CREYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSSAECILGGNAAHWSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCBPGYDLRGAA SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLPPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSP PVIPNGRHTGKPLEVFFFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD FPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILGGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVYTYR CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLMEVVEFRCQPGFVMKGPRRVKCQA LNKWEPELPSCSRVCQPPPEILHGEHTPSHQDNFSPGQEVFYSC
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCQPGFVMKGPRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGQBVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGBPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCBPGYDLRGAA SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLPPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSP PVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTOTNASD FPIGTSLKYECRPBYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQA LNKWEPELPSCSRVCQPPPEILHGEHTPSHQDNFSPGQEVFYSC EPGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGQLPHGRV

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to first amino acid residue of amino acid residue of amino acid amino acid sequence  #Tryptophan, %=Typrosine, X=Unknown, *=Stop Codon, %-possible nucleotide deletion,		1		LaLeucine, Mamethionine, NaAsparagine,
amino acid residue of amino acid sequence  Sequence  Codon, /-possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide disection, \possible nucleotide nucleotide disection, \possible nucleotide nucleotide disection, \possible nucleotide nucleotide disection, \possible nucleotide nucleotide nu	ļ			1
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### Apposable mucleotide insertion  ### FFALGEST RECTSPENGWWISSPARGELSPRAGHEKTPEQP #### PFASPTTP INDFEPPWGTSLINVECRPCYPGEMPS ISCLENLUMS #### SVERDER/RECTSPENGWWISTPTCPSTVTYCGNESSEL IGSPSTTCLVSGNNVTMDKKAPICELISCEPPPTISMODYSVM #### RTSPINGTVTYTGCHTGPDGGGLEFLUMGERSITCTISKODYSVM #### RTSPINGTVTYTGCHTGPDGGGLEFLUMGERSITCTISKODYSVM #### SSPPRCISTNCTAPEVENALTAVENSSTSTEILTRECOPG FVMVSSHTVQCOTINGEMGGLEFLUMGERSITCTISKODYSVM #### SSPPRCISTNCTAPEVENALTAVENSSTSTEILTRECOPG CDPFLOGLHENGVLLPLANGLASSINCTPPGGMSPEARCTVKS CDCPLOGLHENGVLLPLANGLASSINCTPPGGMSPEARCTVKS USTTCOMPLEMENT LOSSTITERSTEPHONGWASSPARGEL ##### PVGAACHPEPKIONGSTJCGHTISTTCDPGTLLVGK GFIFTOGGINSGLUMICKENNOSPHENOISSELEMEKVYHY ODVOTLKCEGOYTLESSTMSGCQADDROPPLAKGTSRTHDALI USGTLSGTIFFILLITISKSTLINERKONAREEPRECAVILHISG GGSSWPRTTGOTSTSCHTOSTTTCHTTCHTALLAGT USGTLSGTTFILLITISKSTLINERKONAREEPRECAVILHISG GGSSWPRTTGOTSTSCHTOSTTTCHTUSTTCHTALLAGT ####################################	1	amino acid	seguence	Codon, /=possible nucleotide deletion.
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GGSSWPRTLOTNEENSKULP  YLYVRMRANFILAYGISHKAYQIDPFIL\RKHREQ\LVIE\VGRKL DK\AQMIRFERRTGYPSSTDLGRTASHYYIKYATIETYNELFDA HKTEGDIFAIVSKAEEFDQIKVREEPIEELDTLLSNFCELSTFO GVENSYGKINLLQTYINRGMOSFSILDSAYVAQNAARIVRA LFEIALRKRUPTMYTRLLINLSKAIDKRLMGHASBLAQFSILPPI MLTRLEEKKLTVOKLEOMREDEGSTLIDSAAYVAQNAARIVRA LFEIALRKRUPTMYTRLLINLSKAIDKRLMGHASBLAQFSILPPI MLTRLEEKKLTVOKLEOMREDGSTLIDGAKVAQCVIGIP SVMMEAFIQPITRTVLRVTLSIYADFTWMDQVGGTVGEFWHIW EDPTNDHIYHSEYFLALKKQVISKEAQLLVFTIPIFPPLDSGVY IRAVSORMIGARANCI INFQHLILPPRHIPPHTELLDLQPLPITA LGCKAYEALIYNFSHFNPVQTQIFHTLYHTDCNVLLABPTGGKT VAAELAIRFVONNYPPSKAVIAPLALVAYRIAPLGAVPGRWDFWKY QOVTILI IDETHLLGEEROPLEVIVSKTNISSHTEKRVIVV QOVTILI IDETHLLGEEROPLEVIVSKTNISSHTEKRVIVV QOVTILI IDETHLLGEEROPLEVIVSKTNISSHTEKRVIVV LSTALANARDLADWLMIKQMGINFRPSVRPVPLEVHIOGFPGQ HYCPRMASMNKPAFQAIRSHSPAKVULIFVSRSTQTLTALLELI AFLATEEDPKQWLMMDRERMENI IATVEDSNLKLTLAGGIGMH AGLHEDRKTVEBLFVNCKVQVLIATSTLAWGVNFPAHLVIIKS TEYYDGKTRRTVOPPITDVLQMMARGARPDQGGKAVLVHDI KKDPYKKFLYSPFPVSSSLLGVLSDHLNAELAGGTITARQDALD YITMTYFFRRINNPSYTULDQMARGARGPDQGGKAVLVHDI KKDPYKKFLYSPFPVSSSLLGVLSDHLNAELAGGTITSKQDALD YITMTYFFRRINNPSYTULDQMARGARGFNKTLEBSLIEESL LSYCIBIGEDRRSIEPLTYGRIASYYYLKHOTVKMFKOELKPEC STEELLSILSDABEYTDLPVRHNEDHMSELAKCLPIESNPHSF DSPHTKAHLLQAHLSRAMLECPDYTDITVTULDQALRVCQAHL HLPKKKKFI MRGPRAAGRTSIECLPELIHAGGKDUFVFSSWVES ELHAAKTGQANFISBLEPINGISVKGSWDDLVECHNELSVST LTADKRDDNKRIKLHADQGVVLQVSLGAWFISKWES ELHAAKTGQANFISBLEPINGISVKGSWDDLVECHNELSVST LTADKRDDNKRIKLHADQVVLQVSLGAWFIKKHENSELT LTADKRDDNKRIKLHADQVVLQVSLGAWFIKKHENSELT LTADKRDDNKRIKLHADGVVLQVSLGAWFIKKHENSUCTT VAERFFTSSTSLTLKHAAWYPSEILDPHVVLLTSDNVIRIYSLR EPQTPTTNVIIISSBAKMAAAEGPVGDGELWOTWLPHVVFLRLR GEDSSFLVVRLRGGSGGGEPPLLSQVQRLLCTNPPLFFIYOU. LSPPGHVALIGINGMUVLLDFRKWKKISPGGKSTVUCSTFT VAERFFTSSTSLTLKHAAWYPSEILDPHVVLLTSDNVIRIYSLR EPQTPTNVIIISBABESELVINKGRAYTASIGETRAVAPEFGPLA AVPRILFGGONKDEVVAYPLLIPPRWGKGTGGKSTVTACTSTFT VAERFFTSSTSLTLKHAAWYPSEILDPHVVLLTSDNVIRIYSLR EPQTPTNVIIISBABESELVINKGRAYTASIGETRAVATDFGPLA AVPRILFGGONKDEVVAYPLUTLIPPRWGGGGSGKSTVACTSTFON HKANGGSEDDHTSGLYBERDHTSGFKAMTASIGTRVALLCOQ A			1	
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HKTEOLIFAIUSKAEPPOJIKUREETIBELDTLLSNYCELSTPE GVENSYGKINILLQTYINRGEMDSFSIISDAYVAQNAARIVRA LPEIALRKRWFTMTYRLLMLSKAIDKINGWASPLRQSSILPH MLTRLEEKKLTVDKLKDMKRDEIGHILHHUNIGLKVGCCVHQIF SVMMEAFIGPITRTVLAVTLSIYAAPTWINDQVUGTVGEPWIW EDPTNDHIYHSEYFLALKKQVISKEAQLLVFIFJFEPLBSQYY IRANDRWIGABAVCIITOPHLILDERHPTELLDLQIPITA LGCKAVEALYNFSHFNPVQTQIFHTLTHTDCNVLLGAPTGSGKT VAAELAIFRVPNKYPTSKAVYIAPLKALVXERNDDWKVRIEEKL GKKVIELTGDVTPPMKSIARADLIVTFENDGVSRSGMORNIYV QQVTILLIDEHHLIGEERGPV_EVIVSRTNFISSHTEKPVRIVG LSTALANADLADHAINIKQMGJFFNFSWDVYDSKTHOGFPGG HYCPRMASMNKPAPQAIRSHSPAKPVLIFVSSRQOTRLTALELI AFLATEEDPKGWLMMDERBMENIIATVEDSNIKATLIARGIGMHH AGLHERDRKTVEBLFVACKVQVLLATSLLAWGNFPAHLVIIKS TEYYDGKTRTVUDFPITDULQMWGRAGRPGPDDQGKAVILVHDI KKDPYKKFLYSFFVESSLIGVISSHNEAGGGTITSKQNALU YITMTYFFRILMPSYYNLGDVSHDSVNKFLSHLIERSLIELE LSYCIBIGEDNRSIEPLTYGRIASYYYLKOTVKMFKOPLKKE STEELLSILSDABEYTDLEVRINGEHNNSSLAKCIPIESNPHSF DSPHTRAHLLLQAHLSRAMLPCPDYDTDTTKTVLDQALRVCQAHL DVAANGGMUTVTUHITILIQMVIGGKNDSSUDLVEGHRIECVST LTADKKDONKNIKLHADQEVVLQVSLGRVHFFFHKORLAKSE ELHAAKTKQAMPFLAGHLILIQMVIGGKNDDLVEGHRELOVST LTADKKDONKNIKLHADQEVVLQVSLGRVHFFFHKOKRESCAVT PRFFKSKDEGWFLILGSVDKRELIALKRVGYIRNHVASLSFYT PEIFGRYITTYFMSDCYLGLDQVOYDLANGRAFGESCAVT PRFFKSKDEGWFLILGSVDKRELIALKRVGYIRNHVASLSFYT PEIFGRYITTYTFMSDCYLGLDQVOYDLANGRYTESSCTTONGH GL  SPOTTIVTLITSFSTSILKHAAMYBERJLALKRVGYIRNHVASLSFYT VARFFTSSTSILTKHAAMYBELJALKRVGYIRNHVASLSFYT VARFFTSSTSILTKHAAMYBELJALKRNGRYTSETGOHGPLA AVPKTLFGQNGKDEVVAYPLYILYENGGTFLTTVSCTTFV VARFFTSSTSILTKHAAMYPSELJALKRNGRYTSINNIRIYSLR EPOTTIVYILSESBERSJULNKGRAYTSALGFTAVATDFOFPLA AVPKTLFGQNGKDEVVAYPLYILYENGGTFLTTVISLLHSPGN/I WKAWGSIAHAS\AARDNYGYDACAVLCLPCVRNILVIATESGML ASGDDPFDSDFSCVELHRDKKCPSRYHCTHLEXGYHSVGLIMI HKLKKFLGSBEDDHISGSBEDLINGRATSSKORSTILDITSINVIRTYSLR EPOTTIVYILISEAGEBEDDHISGSBULDELSTROKCFULLCTLECTREDELALKL ASGDDPFDSDFSCVELHRDKCPSRYHCTHLEXGYHSVGLIMI HKLKEFLGSBEDDHISGSDELGSTROKCFULLCTLCTLECROPAP IRGPWIVPDILGPTMICTTSTYECLINPLLSTVHPASPPLLATE EDVEVARSPLRVLAETDGSFEKHIRSILGRSVAMPAFLKASEKO TAPPPEECULQLSKATOVFREGVILLKDOLLECE		1	1	-
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SEO	Predicted	Predicted end	Amino pold coment
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	1	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
· l	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
			KLLHSFHSELPVLSDSERDMKKELQLIPDQLRHLGNAIKQVTMK
			KDYQQQKMEKVLSLPKPTIILSAYQRKCIQSILKEEGEHIREMV
Long.			KQINDIRNHVNF
5944	167	3428	FSIATFTDEPEVLTEPPSATTTTTIGISATWTTLAGSHGKRNNT
			ITTTSSKRKNRKNKITPENVQIIFDDPLPISYSQPEKVNGESKS
	ŀ	ì	SSTSESGDSDNMRISSCSDESSNSNSSRKSDNHSPAVVTTTVSS
			KKQPSVLVTFPKEERKSVSGKASIKLSETISEGTSNSLSTCTKS
		Ì	GPSPLSSPNGKLTVASPKRGQKREEGWKEVVRRSKKVSVPSTVI
1			SPUTCECCOMINA TERRESONAL VASPARGUARES WARRANT TO THE SPUTCE CONTINUE TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESONAL TERRESON
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			TRQATQLINALIKDPDKEIDELIPKNRLKSSSANSKIGSSAPTT
	1	,	TAANTSLMGIKMTTVALSSTSQTATALTVPAISSASTHKTIKNP
}		l	VN\NVRPGFPVSFP\LAYPPPQFAHALLAAQTFQQIRPPRLPMT
			HFGGTFPPAQSTWGPFPVRPLSPARATNSPKPHMVPRHSNQNSS
1	1		GSQVNSAGSLTSSPTTTTSSSASTVPGTSTNGSPSSPSVRRQLF
1			VTVVKTSNATTTTVTTTASNNNTAPTNATYPMPTAKEHYPVSSP
1			SSPSPPAQPGGVSRNSPLDCGSASPNKVASSSEQEAGSPPVVET
1			TNTRPPNSSSSSSSSSAHSNQQQPPGSVSQEPRPPLQQSQVPPP
İ			EVRMTVPPLATSSAPVAVPSTAPVTYPMPQTPMGCPQPTPKMET
			PAIRPPPHGTTAPHKNSASVQNSSVAVLSVNHIKRPHSVPSSVO
			LPSTLSTQSACQNSVHPANKPIAPNFSAPLPFGPFSTLFENSPT
			SAHAFWGGSVVSSQSTPESMLSGKSSYLPNSDPLHQSDTSKAPG
	1		FRPPLQRPAPSPSGIVNMDSPYGSVTPSSTHLGNFASNISGGOM
			YGPGAPLGGAPAAANFNRQHFSPLSLLTPCSSASNDSSAOSVSS
1			GVRAPSPAPSSVPLGSEKPSNVSQDRKVPVPIGTERSARIRQTG
			TSAPSVIGSNLSTSVGHSGIWSFEGIGGNQDKVDWCNPGMGNPM
İ			IHRPMSDPGVFSQHQAMERDSTGIVTPSGTFHQHVPAGYMDFPK
			VGGMPPSVYGNAMIPPVAPIPDGAGGPIFNGPHAADPSWNSLIK
			MVSSSTENNGPQTVWTGPWAPHMNSVHMNQLG
5945	1461	197	GVTHLFLFGKRKLRNGIAEDLKGQADFFFLLVSEAVVATGSPRA
			WLTCLILPLPGIIFSVLPKAMSRPLLITFTPATDPSDLWKDGQQ
1			QPQPEKPESTLDGAAARAFYEALIGDESSAPDSQRSQTEPARER
1			VEVVEDIMENDARARAF TEALIGDESSAPDSQRSQTEPARER
i l			KRKKRRIMKAPAAEAVAEGASGRHGQGRSLEAEDKMTHRILRAA
			QEGDLPELRRLLEPHEAGGAGGNINARDAFWWTPLMCAARAGQG
			AAVSYLLGRGAAWVGVCELSGRDAAQLAEEAGFPEVARMVRESH
1 -			GETRSPENRSPTPSLQYCENCDTHFQDSNHRTSTAHLLSLSQGP
1	·		QPPNLPLGVPISSPGFKLLLRGGWEPGMGLGPRGEGRANPIPTV
			LKRDQEGLGYRSAPQPRVTHFPAWDTRAVAGRE\TPPRVATLSW
5946	641	2000	REERRREE\KDRAWERDLRTYMNLEF
046	541	1666	ILGSYSSIQPEEYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLP
1 1			SEGSPQRVNSIDFV\EL\EHLQPDVLVHAVLRVVDF/TILTEAV
			YSYRGQKQKKVMLTVEQAQDQHYALVLWGPGAAW\YPQLQRKKG
1			YIWEFKYLFVQCNYTLENLELHTTPWSSCECLFDDDIRAITFKA
i i			KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASO
			KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDENRIYKOCF
			SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA
ļ			DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL
L l			DENSYPLQQDFSLLDFYPDIVKHGANARL
5947	3	1317	RGIPDRRRRGPIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKEK
<u> </u>			CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT
j			KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA
	1	į	PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD
			QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG
			PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG
			DDATVAFDAGVDVI MUDA GOUGGOOGGOOGGOOGGOOGGOOGGOOGGOOGGOOGGOO
	1		DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG
j j		]	RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI
1	Į		LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN
5948		225	NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS
3348	39	3370	YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ
1	1		GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAOAORM
	1		VEIEIEGRLHRISIFDPLEIILEDDLTAOEMSECNSNKENSERP
L			PVCLRTKRHKNNRVKKKNEALPSAHGTPASASALPEPKVRIVEY
			The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	Amino acto segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	Grutamic Acid, Fernenylatanine, GeGlycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid		P=Proline, Q=Glutamine, R=Arginine,
1		residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
			SPPSAPRRPPVYYKFIEKSAEELDNEVEYDMDEEDYAWLEIVNE
			KRKGDCVPAVSQSMFEFLMDRFEKESHCENQKQGEQQSLIDEDA
1	İ		VCCICMDGECQNSNVILFCDMCNLAVHQECYGVPYIPEGQWLC/
			RAHCLQSRARPADCVLCPNKGGAFKKTDDDRWGHV\VCALW\IP
			E\VGFANTVFIEPIDGVRNIPPARWKLT\CNLCKEKGR/VGACI
1	1		OCHENICAL ELITECTORIST CONTRACT CONTRACT
1	1		QCHKANCYTAFHVTCAQKAGLYMKMEPVKELTGGGTTFSVRKTA
1	1		YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVRSTSKVR
1	l		KKAKKAKKALAEPCAVLPTVCAPYIPPQRLNRIANQVAIQRKKQ
İ	1		FVERAHSYWLLKRLSRNGAPLLRRLQSSLQSQRSSQQRENDEEM
	į		KAAKEKLKYWQRLRHDLERARLLIELLRKREKLKREOVKVEOVA
į			MELRLTPLTVLLRSVLDQLQDKDPARIFAOPVSLKEVPDYLDHI
ì			KHPMDFATMRKRLEAQGYKNLHEFEEDFDLIIDNCMKYNARDTV
ł	ļ		FYRAAVRLRDQGGVVLRQARREVDSIGLEEASGMHLPERPAAAP
	1		RRPFSWEDVDRLLDPANRAHLGLEEQLRELLDMLDLTCAMKSSG
		1	SRSKRAKLLKKEIALLRNKLSQQHSQPLPTGPGLEGFEEDGAAL
1			GPEAGEEVLPRLETLLQPRKRSRSTCGDSEVEEESPGKRLDAGL
			TNGFGGARSEQEPGGGLGRKATPRRRCASESSISSNSPLCDSS
			FNAPKCGRGKPALVRRHTLEDRSELISCIENGNYAKAARIAAEV
1			GOSSMUTSTDAASSU PRI VIRNANGGOVERNA TARAKTAAKV
1			GQSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV
			PGHHNGVTIPAPPLDVLKIGEHMQTKSDEKLFLVLFFDNKRSWQ
			WLPKSKMVPLGIDETIDKLKMMEGRNSSIRKAVRIAFDRAMNHL
5949	39	3370	SRVHGEPTSDLSDID
2243	39	3370	YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ
			GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM
. ]			VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP
			PVCLRTKRHKNNRVKKKNEALPSAHGTPASASALPEPKVRTVEV
1			SPPSAPRRPPVYYKFIEKSAEELDNEVEYDMDEEDYAWLEIVNE
			KRKGDCVPAVSQSMFEFLMDRFEKESHCENQKQGEQQSLIDEDA
			VCCICMDGECQNSNVILFCDMCNLAVHQECYGVPYIPEGQWLC/
			RAHCLQSRARPADCVLCPNKGGAFKKTDDDRWGHV\VCALW\IP
i			E\VGFANTVFIEPIDGVRNIPPARWKLT\CNLCKEKGR/VGACI
1 1			QCHKANCYTAFHVTCAQKAGLYMKMEPVKELTGGGTTFSVRKTA
1 1	' I		YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVRSTSKVR
			KKAKKAKKALAEPCAVLPTVCAPYIPPQRLNRIANQVAIQRKKQ
1			FVERAHSYWLLKRLSRNGAPLLRRLQSSLQSQRSSQQRENDEEM
1 1			KAAKEKLKYWQRLRHDLERARLLIELLRKREKLKREQVKVEQVA
1			MEI DI TRI TRI DOU DOU ODENDARI DA ODUST MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE LA COMOTA MONTO DE L
1			MELRLTPLTVLLRSVLDQLQDKDPARIFAQPVSLKEVPDYLDHI
1			KHPMDFATMRKRLEAQGYKNLHEFEEDFDLIIDNCMKYNARDTV
			FYRAAVRLRDQGGVVLRQARREVDSIGLEEASGMHLPERPAAAP
			RRPFSWEDVDRLLDPANRAHLGLEEQLRELLDMLDLTCAMKSSG
[ ]			SRSKRAKLLKKEIALLRNKLSQQHSQPLPTGPGLBGFEEDGAAL
			GPEAGEEVLPRLETLLQPRKRSRSTCGDSEVEEESPGKRLDAGL
		-	TNGFGGARSEQEPGGGLGRKATPRRRCASESSISSSNSPLCDSS
		ĺ	FNAPKCGRGKPALVRRHTLEDRSELISCIENGNYAKAARIAAEV
			GQSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV
{		ľ	PGHHNGVTIPAPPLDVLKIGEHMQTKSDEKLFLVLFFDNKRSWO
j l			WLPKSKMVPLGIDETIDKLKMMEGRNSSIRKAVRIAFDRAMNHL
			SRVHGEPTSDLSDID
5950	1166	373	ESRSLTMSTSQPGACPCQGAASRPAILYALLSSSLKAVPRPRSR
			CLCRQHRPVQLCAPHRTCREALDVLAKTVAFLRNLPSFWQLPPQ
1		ļ	DORRLLOGCWGPLFLLGLAQDAVTFEVAEAPVPSILKKILLEEP
		j	SSSGSSGQLPDRPQPSLAAVQWLQCCLESFWSLELSPKE\YACL
1	İ		KGPILFNPDVPGLQAASHIGHLQQEAHWVLCEVLEPWCPAAQGR
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5951	143		LTRVLLTASTLKSIPTSLLGDLFFRPIIGDVDIAGLLGDMLLLR
2321	143	5449	WNVKPSLLVVQLFKFSDKEEHEQNDSISGKTGETGVEEMIATRK
	1		VEQDSKETVKLSHEDDHILEDAGSSDISSDAACTNPNKTENSLV
1			GLPSCVDEVTECNLELKDTMGIADKTENTLERNKIEPLGYCEDA
1			ESNRQLESTEFNKSNLEVVDTSTFGPESNILENAICDVPDONSK
]	1	}	QLNAIESTKIESHETANLQDDRNSQSSSVSYLESKSVKSKHTKP
	İ	(	VIHSKONMTTDAPKKIVAAKYEVIHSKTKVNVKSVKRNTDVPES
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			QQNFHRPVKVRKKQIDKEPKIQSCNSGVKSVKNQAHSVLKKTLQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion) DQTLVQIFKPLTHSLSDKSHAHPGCLKEPHHPAQTGHVSHSSQK
			QCHKPQQQAPAMKTNSHVKEELEHPGVEHFKEEDKLKLKKPEKN
			LQPRQRRSSKSFSLDEPPLFIPDNIATIRREGSDHSSSFESKYM
			WTPSKQCGFCKKPHGNRFMVGCGRCDDWFHGDCVGLSLSQAQQM
ĺ		ĺ	GEEDKEYVCVKCCAEEDKKTEILDPDTLENOATVEFHSGDKTME
	İ		CEKLGLSKHTTNDRTKYIDDTVKHKVKILKRESGEGRNSSDCRD
			NEIKKWQLAPLRKMGQPVLPRRSSEEKSEKIPKESTTVTCTGEK
			ASKPGTHEKQEMKKKKV\EKGVLNVHPAASASKPSADQIRQSVR
]	]		HSLKDILMKRLTDSNLKVPEEKAAKVATKIEKELFSFFRDTDAK
			YKNKYRSLMFNLKDPKNNILFKKVLKGEVTPDHLIRMSPEELAS
			KELAAWRRENRHTIEMIEKEQREVERRPITKITHKGEIEIESD
			APMKEQEAAMEIQEPAANKSLEKPEGSEK\RKEEVDSMSKDTTS
			QHRQHLFDLNCKICIGRMAPPVDDLSPKKVKVVVGVARKHSDNE
			AESIADALSSTSNILASEFFBEEKQESPKSTFSPAPRPEMPGTV EVESTFLARLNFIWKGFINMPSVAKFVTKAYPVSGSPEYLTEDL
			PDSIQVGGRISPQTVWDYVEKIKASGTKEICVVRFTPVTEEDQI
			SYTLLFAYFSSRKRYGVAANNMKQVKDMYLIPLGATDKIPHPLV
			PFDGPGLELHRPNLLLGLIIRQKLKRQHSACASTSHIAETPESA
			PPIALPPDKKSKIEVSTEEAPEEENDFFNSFTTVLHKQRNKPQQ
		ļ	NLQEDLPTAVEPLMEVTKQEPPKPLRFLPGVLIGWENQPTTLEL
			ANKPLPVDDILQSLLGTTGQVYDQ\AQSVMEQNTVKBIPFLNEQ
			TNSKIEKTDNVEVTDGENKEIKVKVDNISESTDKSAEIETSVVG
1			SSSISAGSLTSLSLRGKPPDVSTEAFLTNLSIQSKQEETVESKE
			KTLKRQLQEDQENNLQDNQTSNSSPCRSNVGKGNIDGNVSCSEN
			LVANTARSPQFINLKRDPRQAAGRSQPVTTSESKDGDSCRNGEK HMLPGLSHNKEHLTEQINVEEKLCSAEKNSCVQQSDNLKVAQNS
		İ	PSVENIQTSQAEQAKPLQEDILMQNIETVHPFRRGSAVATSHFK
			VGNTCPSEFPSKSITFTSRSTSPRTSTNFSPMRPQQPNLQHLKS
			SPPGFPFPGPPNFPPQSMFGFPPHLPPPLLPPPGFG\FA\QNPM
			VPWPPVV\HLP\GQPQRMMGPLSQASRYIGPQNFYQVKDIRRPE
			RRHSDPWGRQDQQQLDRPFNRGKGDRQRFYSDSHHLKRERHEKE
			WEQESERHRRRDRSQDKDRDRKSREEGHKDKERARLSHGDRGTD
			GKASRDSRNVDKKPDKPKSEDYEKDKEREKSKHREGEKDRDRYH
F050	2206		KDRDHTDRTKSKR
5952	3226	639	PPARRSARDLPRALSMEAARPSGSWNGALCRLL\LVTL\AFLIF
1			ASDACKNVTLHVPSKLDAEKLVGRVNLKECFTAANLIHSSDPDF QILEDGSVYTTNTILLSSEKRSFTILLSNTENQEKKKIFVFLEH
			QTKVLKKRHTKEKVLRRAKRRWAPIPCSMLENSLGPFPLFLOOV
			QSDTAQNYTIYYSIRGPGVDQEPRNLFYVERDTGNLYCTRPVDR
			EQYESFEIIAFATTPDGYTPELPLPLIIKIEDENDNYPIFTEET
			YTFTIFENCRVGTTVGQVCATDKDEPDTMHTRLKYSIIGQVPPS
1			PTLFSMHPTTGVITTTSSQLDRELIDKYQLKIKVQDMDGQYFGL
			QTTSTCIINIDDVNDHLPTFTRTSYVTSVEENTVDVEILRVTVE
			DKDLVNTANWRANYTILKGNENGNFKIVTDAKTNEGVLCVVKPL
			NYEEKQQMILQIGVVNEAPFSREASPRSAMSTATVTVNVEDQDE
			GPECNPPIQTVRMKENAEVGTTSNGYKAYDPETRSSSGIRYKKL
			TDPTGWVTIDENTGSIKVFRSLDREAETIKNGIYNITVLASDQG
			GRTCTGTLGIILQDVNDNSPFIPKKTVIICKPTMSSAEIVAVDP DEPIHGPPFDFSLESSTSEVQRMWRLKAINDTAARLSYONDPPF
1			GSYVVPITVRDRLGMSSVTSLDVTLCDCITENDCTHRVDPRIGG
			GGVÇLGKWAILAILLGIALFFCILFTLVCGASGTSKQPKVIPDD
			LAQQNLIVSNTEAPGDDKVYSANGFTTQTVGASAQGVCGTVGSG
			IKNGGQETIEMVKGGHQTSESCRGAGHHHTLDSCRGGHTEVDNC
			RYTYSEWHSFTQPRLGEESIRGHTLIKN
5953	330	811	PLLCNPDPGWYWWVKQESEISKESQEMDARPKLDLGFKEGQTIK
			LCIGNITNKKGGASKPRTARGGGLSLLPPPPPGGKVTIPPPSS/V
1			KLPSTNHVTPPSIPKSNHGGSDADILLDLDSPAPVTTPAPTPVS
			VSNDLWGDFSTASSSVPNQAPQPSNWVQF
5954	32	2130	PPPPPPKLANMADLEAVLADVSYLMAMEKSKATPAARASKRIVL
			PEPSIRSVMQKYLAERNEITFDKIFNQKIGFLLFKDFCLNEINE
1	<u></u>		AVPQVKFYEEIKEYEKLDNEEDRLCRSRQIYDAYIMKELLSCSH
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to first amino acid residue of amino acid residue of amino acid sequence  #Tryptophan, Y-Tyrosine, X-Unknown, *=Stop Codon, /=possible nucleotide deletion, \possible nucleotide insertion)  #PFSKQAVEHVOSHLSKKQVTSTLF(DTYTEE)CESLRGDIFQKFM ESDKFTRFCQMKAVELNIKHTNMFSYHRI IGRGGFGEVYGCFK ADTGKWYAMKCLIKKRINMFSYHRI IGRGGFGEVYGCFK ADTGKWYAMKCLIKKRINMFSYHRI IGRGGFGEVYGCFK ADTGKWYAMKCLIKKRINMFSYHRI IGRGFGEVYGCFK ADTGKWYAMKCLIKKRINMFSYHRI IGRGFGEVYGCFK ADTGKWYAMKCLIKKRINMFSYHRI IGRGFGEVYGCFK ADTGKWYAMKCLIKKRINMFSYHRI IGRGFGEVYGCFK ADTGKWYAMKCLIKKRINMFSYHRI IGRGFGEVYGCFK ADTGKWYAMKCLIKKRINMFSYHRI IGRGFGEVYGCFK ADTGKWYAMKCLIKKRINMFSYHRI IGRGFGEVYGCFK ADTGKWYAMKCLIKKRINMFSYHRI IGRGFGEVYGCFK ADTGKWAMAPEN VALLEBINGTHTUTWINELPTSPELKSILEGLI CRUVSKRIGGGGGSGEVKEHSFF KGVDMGHYYLQKYPPPLIPP RGEWNAADAFDIGSFDEDTKGIKLLDCDQELYKFFPLISER QQEVTETTYYEAVRADTDKIEAKRAKNKGLGHEEDYALGKDIM HGYMLKINFFIGSFDEDTKGIKLLDCDQLIKKFPLINKFPELMSER QQEVTETTYYEAVRADTDKIEAKRAKNKGLGHEEDYALGKDIM HGYMLKINFFIGSFDEDTKGIKLLDCDQLIKKFPLINKSNGL  #REEFERLAVCPLRYFSAYESSFOTELEGGLCRSGGBFDCFR PANRQDVLLSWINLDVLLTKDFIKTHGRGVTVLNSKARLAKHSLASS VLAVACQSCLLIWTLDFTSLSTAFSSGCAQVISHFGITTYTILA MASSLIGSIFPHISIRSEDLIAEFAQVTNNSSCLAVETASGAMLALCR WASSLIGSIFPHISIRSEDLIAEFAQWWTCAGWALLACR WASSLIASFPSAYDARIYWDSTETCVELPHFRGGGVTNLIW SPDOSKLIATTPSAVFRWEAGAWTCERNFTLSGRCGTGKSPD GSRLFTVLGFPLITYLSFFPRGGBKGKALAKWFDSAS VLAVACQSCLLIWTLDFTSLSTAFSSGCAQVISHFGITTYTTILA MASSLEDLWENLSKAPANSPHVNISATLSPQVINWWLCL RGQYRNOWMRGIGBELTPWSGTPVGWWWLCL RGQYRNOWNRGIGBELTPWSGTPVGWWWLCL RGQYRNOWNRGIGBELTPWSGTPVGWWWLCL RGQYRNOWNRGIGBELTPWSGTPVGWWWLCL RGQYRNOWNRGIGBELTPWSGTPVGWWWLCL RGQYRNOWNRGIGBELTPWSGTPVGFSVAQXPFGSA TYWSSIINTLQTQVEVKKRRHLKRNNCPVGSRAVDTFSHL LGNKYRGDVDIPRAKVWRVQALMNYKPEAVPTKVPGSKKPT FEDSSCSLYRFTINNGSGCKHALTYSPAYADALFKSDIN SASLEDLWENLSKAPANSPHVNISATLSPQVINEVNGETIGL LGLIKLIDPGNREFFRILLYFMAVAANPSFFKLQKESDNRNVK RIFSKATUNNGNLSKKTDLWFFLYBALTHOL VS\VK\LLMPLATIAGDPGVYEVKHFACHTLVRKTTLDFETTLYK US\VK\LLMPLATIAGDPGVYEVKHFACHTLYNKSNTLDGILFFF SKKSDCSLBWRGSNRKKPNINLYGRMYDVLUMISLGILBFFF SKKSDCSLBWRGSNRKKFNINLYGRMYDVLUMISLGILBFFF
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residue of amino acid sequence   Codon, /-possible nucleotide deletion, %=stop   Codon, /-possible nucleotide deletion, %=stop   FFSKQNEHYQSHISKKQYTSTLFQFYTBETCESLRGDIFQKFM   ESDKFTRFCQMKNVELNIHLIMDEFSVHIS IGRGGGGEVYGCRK   ADTGKMYAMKCLNKKRIKMKQGETLALMBRIMLSLVSTGDCFFT   VCMTYAFHTPDKLCFILLDHMOGDLHYHLSILDHGGMFSEKRMRYYA   TEILGLEMMINRFVYTRDLKFANILLDEHGBRIS JBLGLACD   FSKKEPHASVATHGWYAB-VLQKGTAYDSSADWFSLGCHLYKLL   RGHS-PRQHKCXDKHBIDBMILTUTWELDFTFSPELKSLLEGLI.   QRDVSKRLGCHGGGSQEVKEHSFPKGVDWGHYYLQKYPPDLIPE   RGEWNAADAFDIGSFDEEDTKGIKLLDCDQELYKNFPLVISERW   QQEVTETVYEAVNADTDKLEARRANKQLGHEEDYHQKKYLDKSLIK   HGYMLKLGMFPLTWGRKFYFLTPMREKENGGESSRQNLLITMED   ILSVERTQIKDKKCLIFRIKGGKGFVLQCESDPEPTVGMKKLINE   HGYMLKLGMFPLTWGRKFYFLTPMREKENGGESSRQNLLITMED   ILSVERTQIKDKKCLIFRIKGGKGFVLQCESDPEPTVGMKKLINE   FYKEAGRILBAFFFLTWGRKFYFLFVNERHENGGGESSRQNLLITMED   ILSVERTQIKDKKCLIFRIKGGKGFVLQCESDPEPTVGMKKLINE   WARSIGNAADAFDISSFDLTWGRKFSGTVELDFWSLGKRNSNGL   KREEFFILAVCPLKFFSAVESSPGTELREGGLCSGGGBFADCRR   PANRODVLEGATIN.PVLGTHERGTGTVLFUKRTAFHHREQ   VWRCINIWRDWGLFGVLIKDPLTTGRACGTGTGTGTBFD   NKFAVALLDDSVRYYMASSTIVFSLKHRLQRNVASLAMKPLSAS   VLAVACQSCLILWHLDFTSLSTRFSSCCAQVLSHPGRTVTSLAM   WASSIGRLEASSPUDANIKDWDSTSTCYTHREGGGTTGTGTSFD   GRALLFTVLGSPLTYSLSFPERGCGCKGAGDRAUCK   ROSYRHOMWRGLGERLTPWSGTVEDVBFRGGGTTVLLM   SPDSSKILATTPSAVFRVWEAQMMTCERMFTLSGRCQTGCMSPD   GRALLFTVLGSPBLTYSLSFPERGCEGKGAADAINSCALBFRGGGSTANDLST   GGGWGGRAMATVSTRAUNDSTSTCYTHSCHGCTGCMSPD   GRALLFTVLGSPBLTYSLSFPERGCEGKGAADAINSCALBFRGGGSTANDLSTALBFRGGGTMLL   LQUMDLFLLDSILLDSILAVQCAADAINSCALBFRGGGSTANDLSTANDLS HARPOGGDKTDTLW   SASLEDLMENNISLKPANSPHVNISTATSLSPANADALFKSSDIR   SASLEDLMENNISLKPANSPHVNISTATSLSPANADALFKSSDIR   SASLEDLMENNISLKPANSPHVNISTATSLSPANADALFKSSDIR   SASLEDLMENNISLKPANSPHVNISTATSLSPANADALFKSSDIR   SASLEDLMENNISLKPANSPHVNISTATSLSPANADALFKSSDIR   SASLEDLMENNISLKPANSPHVNISTATSLDVNINKFTETTALBE   LQUMDLFLLDSILLAGGGTFTT   LGUMDLFLLDSILLAGGGTFT   SASLEDLMENNISLKPANSPHVNISTATSLSPANADALFKSDIR   FERSTATUNDENLEKKETTALLWGRTFTERFGGTSLEFFF   PTVSNTRLAGLEFYLHFTALNKTYFFFSKARFFLEKERFERME
residue of amino acid sequence   Codon, /-possible nucleotide deletion, %=stop   Codon, /-possible nucleotide deletion, %=stop   FFSKQNEHYQSHISKKQYTSTLFQFYTBETCESLRGDIFQKFM   ESDKFTRFCQMKNVELNIHLIMDEFSVHIS IGRGGGGEVYGCRK   ADTGKMYAMKCLNKKRIKMKQGETLALMBRIMLSLVSTGDCFFT   VCMTYAFHTPDKLCFILLDHMOGDLHYHLSILDHGGMFSEKRMRYYA   TEILGLEMMINRFVYTRDLKFANILLDEHGBRIS JBLGLACD   FSKKKPHASVATHGWYAB-VLQKGTAYDSSADWFSLGCHLYKLL   RGHS-PRQHKCXDKHBIDBMILTUTWELDFTFSPELKSLLSGLL   GRDVSKRLGCHGGGSGEVKEHSFPKGVDWGHYYLGXYPPPLIPF   RGEWNAADAFDIGSFDEEDTKGIKLLDCDQELYKNFPLVISERN   QGEVTETVYEAVNADTDKLEARRANKGLGHEEDYHQKKYLDKSLL   HGYHLKLGMFPLTWGRKFYFLTWGRKFYFLFNRLEWGGGSSRQNLLITMED   ILSVERTQIKDKKCLIFFIKGGKGFVLQCESDPEPTVGKKELDE   HGYHLKLGMFPLTWGRKFYFLFNRLEWGGGSSRQNLLITMED   ILSVERTQIKDKKCLIFFIKGGKGFVLQCESDPEPTVGKKELDE   FYKEAGRLERAFKFINKFSGTVELPKSLGKGGGSGROUDER   PANGOVLEGATNLPVLGIKDFTLTGREGGICKSGGGFADCRR   PANGOVLEGATNLPVLGIKDFTLTGREGGICKSGGGFADCRR   WASSLIKGSIFFHLSIRSFDLIKBFALTARFCGTVELPKSLGKTRANKFLAR   WASSLIKGSIFFHLSIRSFDLIKBFALTARFCGTVELPKFALGKTRANKFLAR   VLAVACQSCILIWILDFTSLSTRFSSCCAQVLSHFGRTVTSLAM   WASSIGNLASSTURGBHINSPLKFRWDVSTSTCVTGTGTSPD   GRRLLFTVLGSPLTYSLSFPERGGGCKSGVLSHFGRGVTLLLW   SPDSSKILATTPSAVFRVWEAQMMTCERWFTLSGRCQTGCMSPD   GRRLLFTVLGSPLTYSLSFPERGCGCKGAGDKTVLLW   SPDSSKILATTPSAVFRVWEAQMMTCERWFTLSGRCQTGCMSPD   GRRLLFTVLGSPLTYSLSFPERGCGCKGAGDKTVLLW   SPDSSKILATTPSAVFRVWEAQMMTCERWFTLSGRCQTGCMSPD   GRRLLFTVLGSPLTYSLSFPERGCGCKGADKTVLL   RQGYRGGMRAMFTVOKKARALNISALLSFPARGFADEFTGGGSVTDLLW   SPDSSKILATTPSAVFRVWEAQMMTCERWFTLSGRCQTGCMSPD   GRRLLFTVLGSPLTYSLSFPERGCEGKGADKTVK   RLJCDLGFLGLDSLLAGGAANLDTSALTSFPERGGFSVAQKFFGA   TYVWSIINTLQTQVEVKKRRHLKRHNDCFVGSEADVIPSH   LQMAVMANDALDSLVKFKTALNISALNISALDSAPRATADALFKSSDIR   SASLEDLMENNISLKPANSHVNISGATLANGKTYFFSKDELAKK   LQMAVMAVAVALCANGKTELALBAT   QLLLKLLLDGGGGRAFMATSAPRATADALFKSSDIR   SASLEDLMENNISLKPANSHVNINTGRTCHANKTHANDEFTIGRCTLAKK   RTKAKLMBLGGGFTANLLTHALBODLYKLKNINTRFEDGTSLEFF   PTVSNTRLAGLEFYLHFTALNKTYFFFSKARFFLEKERFRINTENTH   LJEWSPSLDLATRRTHLASDDLYKLKKNINTHFTEDGTSLEFF   PTVSNTRLAGLEFYLHFTA
amino acid sequence    Codon, /-possible nuclectide deletion,    -possible nuclectide insertion    PFSKQAVEHVQSHLSKKQVTSTLFQFYIEEICESLRGDIFQKFM     ESDKFTRFCQMKNVELNIHLIMMNEFSVHRIIGRGGGEVYGCRK     ADTGKMYMAKCLNKRIK HKKQGETLALINERIMISLUSTGDCFF     VCMTYAFHTPDKLCFILDLMNGGDLHYHLSQHGYFSEKMRFYA     TEILIGLEMMINRFVVYRDLKFANILLDEHGRARIS DLGLACD     FSKKKHASVGTHGHYMAPPVLQKGTAYDSSADWFSLGGMLFKLL     RGHSPFRQHKTKDKHBIDMTLTVNVELPDTFSPELKSLLEGLL     CRUDYSKLGCHGGGSGGVKEHSFFKGVDWQHVYLQKYPPPLIPP     RGEVNAADAPDIGSFDEEDTKGIKLLDCDGLIKNFSPPLKSLLEGGL     CRUDYSKLGCHGGGSGGVKEHSFFKGVDWQHVYLQKYPPPLIPP     RGEVNAADAPDIGSFDEEDTKGIKLLDCDGLIKNFSPPLKSLLEGGL     CRUDYSKLGCHGGGSGGVKEHSFFKGVDWQHVYLQKYPPPLIPP     RGEVNAADAPDIGSFDEEDTKGIKLLDCDGLIKNFSPLKSLLEGGL     CRUDYSKLGCHGGGSGGVKEHSFFKGVDWQHVYLQKYPPLIPP     RGEVNAADAPDIGSFDEEDTKGIKLLDCDGLIKNFSVGLIME     CRUDYSKLGCHGGGSGGVKEHSFFKGVGSGANLLCK     CRUDYSKLGCHGGGSGGVKEHSFFKGKGGKGVLCGESDFFVQMKKEHS     TFKEAQRLLBRAPKFLNKPSGTTVELDKRGGGSGANLLCK     CRUDYSKGWINLPVLQLTKOPLKYPSLCHENSNGL     TFKEAQRLLBRAPKFLNKPSGTTVELDKRSCLCHRNSNGL     VKRCLTIHRDVGLFGVLDLTARGAVTHNSSCCLRVFAMHPHT     NKFAVALLDDSVRYVNASSTLVPSLKHRLQRRVASLAKKFLSAS     VLAVACQSCLILWTLDDTSLTFRSSCCAQVLSHPGHTPVTSLA     APSSGGRLLSASPVDAAIRVNDVSTETCVPLPWFRGGGVTNLW     SPDGSKLLATTPSAVPRVWEAQMWTCERNFLSGRCQTGCMSW     APSGGRLLSASPVDAAIRVNDVSTETCVPLPWFRGGGVTNLW     SPDGSKLLATTPSAVPRVWEAQMWTCERNFLSGRCQTGCMSW     SPDGSKLLATTPSAVPRVWEAQMWTCERNFLSGRCQTGCMSW     CRUGYGGRARMATVQKKAALINSALLSFARLFFKFFFFSVAQKFFGA     TYVMSSIINTLGTGVBVKKRRHRLKRHNDCFVGSGAVDVIFSH     CRUGYGGRARMATVGVEKAALINSALLSFAHREFFFSVAQKFFGA     TYVMSSIINTLGTGVBVKKRRHRLKRHNDCFVGSGAVDVIFSH     CRUGYGGRARMATVGVEKAALINSALLSFAHREFFFSVAQKFFGA     TYVMSSIINTLSKYCYCQALLDVBVKYGKFETALDEAT     CLLLLLLKLTDDGSCLSAKEKKYLLLGGFYNFKVFGGKKKKYT     FEDSSCSLVRPTTFNODSGLGKRNLYSPARADADAFKSDIR     SASLEDLWENLSKYPANAPHTSATLSDHVNISTMTENTTXD     CLLPDLATGGVTSSEFFRLLLYPMAAANPSEFKLQKEEGDNRMVK     RIFSKALVNINNLSKKKTLULLULFLINMUNFKTETALDEAT     CLLPDLATGGVTSTSFRFTLULFTFNODSGCBCFFFTLULKKYCOTTRONT     SEKSBCSLLBRFGSSNACTR
Sequence
PFSKOAVERVOSHLISKKGVTSTLEOPYIEICESLAGDIFOKEM ESDKTTRPCQWKOVELIHLITMERFSVHIGGGGGEGVEGVEGE ADTGKWYAMKCLNKKRIKMKQGETLALMERIMLSLUSTGDCPPI VCMTYAFHTPDKLCFILDLMMGGGLHYHLSQHGVTSEKMRYYA TEIILGLEMHMIRFUYVARDLKANILLEHGHGARAIS\DLGLACD FSKKKPHASVATHGYWAPFULQKGTAYDSSADWFSLGKLEKLL RGMSPROKKYKOHRIDEMTLTUNVELDEDTSSELKSLLEGLL GRUSKRIGCHGGGSGEVKEHSPFKGVMGHYTJGKYPPLIPP RGEVNAADAFDIGSFDEDTKGIKLLDCDGLYKNPPLUYSERW QGEVTETTYVEAVNADTDKIEARKRANKQLGHEEDTALGKDCIM HGYMLKIGNPPLTQWGRRYFTLFPNRLEWGGGSFSAGNLITMEG ILSVERTGIKOKKGLIFFRKGKGKGFVLGCESDPFFVGHKKENG TFKEAQRLLRRAPKFINKPRSGTVELPKPSLCHRANGGL  SP55  1726  444  KREEPFILAVCLEYPSPAYESSPOTELEREGGGSSAGNLAITMEG ILSVERTGIKOKKGLIFFRKGKGKGVFLGCESDPFFVGHKKENG TFKEAQRLLRRAPKFINKPRSGTVELPKPSLCHRANGGL VKRCINIWRUVGLIFGULNELANSEEVFFWUKTASGWALALCR WARSSLINGSIPPHDSLASEDLIAFPAQVTKASGWALALCR WARSSLINGSIPPHDSLASEDLIAFPAQVTWASSCLARVFMHHT NKFAVALLDDSVRVYNASSTIVPSLKHRQRIVASLAKFJEAS VLAVACQSCILIWTLDDTSLETRPSSCAQVISHPGHTPVTSLA WAPSGGRILISASPVDAAIRVMDVSTBTCVPLPWRFGGVTMLW SPOGSKILLATTPSAVTRWEAQMMTCERMFTLSGRCQTGCMSD GSRLLFTVLGBPLIYSLSPPERCGECKGVALEVGSQWFRUMOUTCL RQYYHQMVRRGLGERLTPWSGTPYGNVWLCL SQYHQMVRRGLGERLTPWSGTPYGNVWLCL SQYHQMVRRGLGERLTPWSGTPYGNVWLCL TQNYYFGDVD FPRAKVYRVQCALMDVKVPCFAVFXVPGKKPFT FEDSSCSLVRFTTIPNOBOGJGKENKLYSPARVADALFKSSDIR JGSRLEDLAGRYSSBEPLIAHLSDHWGIARLLVMGKTETLALEAT QLLLKLUTDGDVBEFFRELLYPHAVAANPSEFKLQKESDHRMVKY RIFSKALVUNKNLSKGKTDLJUFLIMMGDVFKIFGTLUNKV BLLPDALGGYYSSBEPLIAHLSDHWGIARLLVMGKTETLALEAT QLLLKLLDDGGNKRSSSERKKLLLGGPYGNFKLYRTDDFTENTERDE LGUNVAMDTLDRVVKPKFKRARRLEKRENDCFKGESDHRMVK RIFSKALVUNKNLSKGKTDLJUFLIMMGVKFETLALEAT QLLKLLLDGGGGVYSSBEPLILLYFLAGDDFDYTERNTEKTTEDE LLENLATTLDGDGKLSKFKKLLLGGFYGNFKLIPTIFTEDTSLEFF SKKSDCSLEWFGSNKKKRYNINLUTGRYDDYKFKIFGTLUNKT LGGRANATVTKVLKDVYALKKFYGGLYKKNITSHTDE LLENLATTLDGGGGSKYLLTFAGDDFDVTEDYRRLESLTDFFR PTVSNITLAGLGFYLHTALNOKTYFFREXKKLLLDFFRG PTVSNITLAGLGFYLHTALNOKTYFFREXKKLLLKKRSCTURFTE LEEWSPSLDLULARRTHAGNDLYKLGNKKNITHTDE LEEWSPSLDLUTRRTHLAGDDLYKLGNKKNITHTDE LEEWSPSLDLURARRANGSPGTFTE LEEWSPSLDLUTRRTHLAGDLYKKKRNITHTDE LEEWSPSLDLURARRANGTHENNOLOTERNYTHTEDTSLE
PFSROAVERVOSHLISKROPTSTLEOPYTETICESLRODIFOKEM ESDKTTRPCQWKOVELINILIMERSFUHICRGGGGEOVEGORE ADTGRWYAMKCLNKKRIKMKQGETLALMERIMLSLUSTGDCPFI VCMTYAFHTPDKLCFILDLMRGGGLHYHLSQRGFGEVEGGE TETILGLEMHNIRFVYTHOLKPANILLEHGHGARAIS\DLGLACD FSKKKPHASVATHGYWAPEVLQKGTAYDSSADWFSLGCHLFKLL RGHSPFROKKYKDHRIDEMTLTVNVELBEDTSFELKSLLEGGL RGHSPFROKKYKDHRIDEMTLTVNVELBUTTSFELKSLLEGGL RGHSPFROKKYKDHRIDEMTLTVNVELBUTTSFELKSLLEGGL RGHSPFROKKYKDHRIDEMTLTVNVELBUTTSFELKSLLEGGL RGHSPFROKKYKDHRIDEMTLTVNVELBUTTSFELKSLLEGGL RGHSPFROKKYKDHRIDEMTLTVNVELBUTTSFELKSLLEGGL RGHSPFROKKYKDHRIDEMTLTVNVELBUTTSFELKSLLEGGL RGEVNAADAFDIGSFDEEDTKGIKLLDCDGLYKNFPLVISERW CQEVTETYVEAVNADTDKIERKRRANKQLGHEEDTALGKDCIM HGYMLKIGNFPLTUMGRRYFTLFRNKLEWGGGSFANLLTWEO ILSVERTGIKOKKCLIFFRIKGGKGFVLQCESDPEFVQMKKEND TYKEAQRLLRRAPKFLNKPRSGTVELPKPSLCHRANSGL TYEAQRALRRAPKFLNKPRSGTVELPKPSLCHRANSGL VKRCINIWRLVGLIFGVLNELANSEEVFEWVKTASGWALALCR WARSLINGSIPPHISLRSEDLLARFAQVTWASSCLARVFLAMBHT NKRAVALLDDSVRVYNASSTIVPSLKHRIQRRVASLAKFLSAS VLAVACQSCILIWTLDPTSLTSRSSCAQVISHPGHTPVTSLA WAPSGGRILLSASPVDAAIRVMDVSTBTCVPLPBFRGGVTMLBW SPOGSKILLATTPSAVTRWEAQAMTCERMFTLSGCQTGCMSB URAVACQSCILIWTLDPTSLTSRSSCAQVISHPGHTPVTSLA WAPSGGRILLSASPVDAAIRVMDVSTBTCVPLPBFRGGVTMLBW SPOGSKILLATTPSAVTRWEAQAMTCERMFTLSGCQTGCMSB GSRLLFTVLGGBLIYSLSFPERCEGCKGVALBVQSQQRLWQICL RQYYHQWYRRGLGERTPMSGTPYGNVWLCL RQYYHQWYRRGLGERTPMSGTPYGNVWLCL RQYYHQWYRRGLGERTPMSGTPYGNVWLCL RQYYHQWYRRGLGERTPMSGTPYGNVWLCL RQYYHQWYRRGLGERTPMSGTPYGNVWLCL RQYYHQWYRRGLGERTPMSGTPYGNVWLCL RQYYHQWYRRGLGERTPMSGTPYGNVWLCH RCHAMBART TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMAN TO RAMA
ESDKFTRPCOWKNELNITHLTNNEFSVRR I IGRGGGGEVYGCRK ADTGKMYAMKCLNKKRI KKRKQETLALMER IMLSLVSTGDCPFI VCMTYAPHTPDKLCF ILDLMGGDLHYLLSGHGVFSEKMRFYA TEILGLEMMINFVYTDLKEANILLDEHGHARIS \DLGLACD FSKKKPHARVSTGHGMAP EVLQKGTASDMFSIGGCHLYKLL RGHSPROCHKTKDKHEIDRITTUVNFLPDTTSPELKSLLEGLLI ORDVSKRLCHGGGSGEVEXHSPFKOVDWGHVYLQKYPPPLIPP RGEVNAADAFDIGSFDEEDTKGI KLLDCDQELYKNFPLVISERW QOEVTETVYEAVNADTDKIEAKRAKNKQLGHEEDYALGKDCIM HGYMLKLGSPFLTOWGRYFYTLFPRIKGEGESSRQHLITMEQ ILSVETTGI KOKKCILFRI KGGGVPVLQCESDPEPVGWKKELNE FSKEAGRLERAPKFLANKPRSGTVELPSFLGKRISNGL  5955 1726 444 KREREFRLAVCPLRYFSAYESSPGTELRECGLCRSGGEFADCRR PANRQDVLSGWINLPVLQLIKUPLKTFGRLDHGTRTAFIHHREG VMKRCINTHRUDGLEFGVUNENSSCLEAVFAWHEHT NKFAVALLDDSVRYVNASSTVPSLKHGRVAVSLAWKEPLAS VLAVACQSCILLWTLDPTSLSTRPSSGCAQVLSHPGHTPVTSLA WAPSGGRLLASPVDAAIRVWDVSTETCVPLPWFRGGGVTNLLW SPOBSKILATTPSAVFRVWEAGMATCERWFTLSGRCQTGCKSPD GSRLLFTVLGBELIYSLSFPERGEGKG\ALBVOGQRRWGICL RQQYRHQMYRGLGERITPWSGTPVONVLCL  SPOSS 139 GVGWGRARMATVOEKKARALNSALHSPAHEPFFSVAGKPFGA TYWMSS IINTLOTOWEKKRHHLKANDLPVGSGARAVGYFGA FEDSSCSLKRPTTIPNGDSQLGKENKLYSPARTADALFKSSDIR LQNKYFGDVDIPRAKVVRVQQALMDYKVFEAVPTKVFGKDKKPT FEDSSCSLKRPTTIPNGDSQLGKENKLYSPARTADALFKSSDIR SASLEDLBENSLKERANSPHNINSATLSPQVINEWXQEETIGRL LQLVDLPLLDSLLKQGRAVPKIPQFRRGSTVNISSNYLDRGILK AYSISGBEMISAAI TOESET HYPOGYTKENYDETTIGRL LQLLKLLDFQNREEFRELLYFMAVAANPSEFKLQKESDNRNVK RIFSKAI VINNKLESGKTDLLVLFL,WHOHROVFKTPGTLLHERI VS\VK\LMAIQNGRDPNRDAGYIYCQCTLQNDYKNTEKTTKDE LLENDATGRYYTSSRPPLLINHLISDVINGIARLLUNGKTEILAEAT QLLLKLLDFQNREEFRELLYFMAVAANPSEFKLQKESDNRNVVK RIFSKAI VINNKLESGKTDLLVLFL,WHOHROVFKTPGTLLHERI VS\VK\LMAIQNGRDPNRDAGYIYCQCTLQCHDRDYNNTEKTTKDE LLENDATGRYTKVLKOVYALKKPYGVUKKNITSPFDOTSLEFF SKKSDCSLFPRGSHNKKRPNNLVIGRMYDHVLDMIELGIENFV SLKDI KNSKCPEGTKPMLIFAGDDPVTEDTRALKSLIIDFFRG PTVSNITILGGLEYVLHFALANGKITFRSYKLLKKKSCTTRIE LSEWGPSLDLVLRRTHLASDDLYKLTWRYSGPKOSYFGVADFHIPD TGTTYGTHMAKODLGKLGTTRIM,KGLKKRPABRITEDHEKS KRIKKKMBLSQPLLFRFCLLKRTIKTAGDFPRAVYCPAPARTSGPDIVESGRFRIE LSEWGPSLDLVLRRTHLASDDLYKLTYYGOPKASTFORDHEKS KRIKKKLMBLSQPLLFRFALOKLTYTYGOPKASTFORDHEKS KRIKKLMBLSQPLLFRANGSDPIVE
ADTOKNYANKCINKKRI KMRQGETLALIMER IMLSLUSTBOCPFI VCMTYAPHTPKKLCFILDLMNGGDLHYHLSQHGYFSEKEMRYYA TEIILGLEMMINRFVVYRDLKFANI LLDEHGHARIS   DLGLACD FSKKKPHASVGTHGYMAPEVLQKGTAYDSSADMFSLGCMLFKLLL RGHSPFRGIKKTÖKHE IDRNITJVAVDELPDTFSPELKSLLÖGLL ORDVSKRLGCHGGGGGEVXBHSFFKGVDWGHVYLQKYPPPLIPP RGEVNAADAFDIGSFDEEDTKGIKLLDCDGLYKNFPLVISERW QOEVTETVYEAVNADTDKIE BAKRAKNQLGHEEDYALGKDCIM HGYMLKLGNFFLTOWQRRYFYLFPRNLEWRGGGSGRNGLLTMEQ LLSVEETGIKDKKCLIPER IKGGGVPLQCESDPEFVOMKKEINE TFKEAQRLLERAPKFLMKPRSGTVELPKPSLCHRNSNGL KREREFRLAVCPLRYFSAYESSPGTELREGGLGRSGGBFADCRR PANRQDVLSGMINLPVLQLIKDPLKTPGRLDHGTRTAFIHHREQ VWKRCINIHRDVGLIFGVLINSILANSEEEVFEWVETASGWALALCR WASSLHGSIPPHLSLRSEDLIABFAQCVLSHPGHTPATFIHHREQ VWKRCINIHRDVGLIFGVLINSILANSEEEVFEWVETASGWALALCR WASSLHGSIPPHLSLRSEDLIABFAQCVLSHPGHTPWTSLA WAPSGGRLLSASPVDAAIRVWDVSTETCVPLPWFRGGGVTNLLW SPDOSKILATTPSAVFRWEAQMWTCERWPTLSGRQOTGCMSPD GSRLLFTVLGSPLIVSLSFPERGGESGK\ALEVGSQGVMIQTCL RQQYRHQMVRRGLGERLTPWSGTPVGNVWLCL  SPOOSKILATTSAVFRWEAQMWTCERWPTLSGRQOTGCMSPD GSRLLFTVLGSPLIVSLSFPERGGSGK\ALEVGSQQNLWGTCL RQQYRHQMVRRGLGERLTPWSGTPVGNVWLCL  SQUVRHQMVRRGLGERLTPWSGTPVGNVWLCL  5956  1705  139 GVGVRGARAMATVQEKAALINLSALHSPAHRPFGFSVAQKPFGA TYWSSIINTLQTQUFUKKRRHELKRHDCFVGSEAVDVIFSHL IQNNYFGDVDIFRAKVVRVQQALMDYKVFEAVPTKVFGKDKAPT FEDSSCSLYRPTTIFNDSGLGKERKHPARAVDRYKYFEAVPTKVFGKDKAPT FEDSSCSLYRPTTIFNDSGLGKERKHPARAVDRYKFSDSTLAEA QLLIKLLDGDNEBFRERLLYFMAVAANPSEFKLQKESDRMAVK RIFSKALVONKNLSKGYTDLLVFL\MDHQKDVFKIPGTLAEAT QLLIKLLDFQNREBFRERLLYFMAVAANPSEFKLQKESDRMAVK RIFSKALVONKNLSKGYTDLLVFL\MDHQKDVFKIPGTLAEAT QLLIKLLDFQNREBFRELLYFMAVAANPSEFKLQKESDRMAVK RIFSKALVONKNLSKGYTDLLVFL\MDHQKDVFKIPGTLAEAT QLLIKLLDFQNREBFRERLLYFMAVAANPSEFKLQKESDRMAVK RIFSKALVONKNLSKGYTDLLVFL\MDHQKDVFKIPGTDLYK ELLPDAIGRYYSSREPLLINHLSDVINGIABLJUNGKTELALEAT QLLIKLLDFQNREBFRERLLYFMAVAANPSEFKLQKESDRMAVK RIFSKALVONKNLSKGYTDLLVFL\MDHQKDVFKIPGTLAEAT QLLIKLLDFROREBFRERLYFMAVANNSKNTEKTTKDE LLINLLKYLDEDSKLSAKEKK\LLLGGYFKCHEDFIFEHGD SKKSDCSLPMFGSHKKRPRINKLYRIKKNATHFFEOTSGLFFF SKKSDCSLPMFGSHKKRPRINKLYRKNKTNAMPLIKKNATHFFEOTSGLFFF SKKSDCSLPMFGSHKKRPRINKLYRKKKNISHD TFG
VCMTYARHTPDKICFILDLAMGGDLHYHLSQHGVFSBKEMRFYA TBIILGLEHMHNRFVYYRDLKPANILLDEHGARIS\DIGLACD FSKKKPHASVGTHGYMAPEVLQKGTAYDSSADMFSLGCMLFKLL RGHSPFRQHKTXDKHEIDRHTITVWVELPDTTSPELKSLLEGLL. QRDVSKLGCHGGGSQEVKHSFFFKOVDMQHVYLQKYPPLIPF BGEWNAADAFDIGSFDEEDTKGIKLLDCDQELYKNFPLVISERW QQEVTETVYAAVNADTDKIEARKRAKNKQLGHEEDVALGKDCIM HGYMLKIGNFPLTUMQRRYFYLFPBRLEMRGEGESRQNLIMMED ILSVERTQIKDKKCILFRIKGGKQFVLQCESDFEFVQMKKELNE TFKEAQRILRRAPKIKHKPRSGTVELPSFJCHRNSNGL  5955 1726 444 KREEFFALWCPLRYFSAYESSFGTELÆEGLGKSGBFADCRR PANRQDVLGWTINLVGLKTPLLTVBLHGHTGTTAFTHHEQ VWRCINIHRUVGLFGVLRYFSAYESSFGTELÆEGLCKSGGEFADCRR PANRQDVLGWTNLDLGKVDLLTVBLHTSLHGHTGTTAFTHHEQ VWRCINIHRUVGLFGVLRHEIANSEEVFEWVKTASGWALALCR WASSLHGSLFPHISLRSEDLIAFFAQVTNMSSCCAVPAMHPHT NKFAVALLDDSVRYVNASSTIVPSLKHELQRNVASLAKKPLSAS VLAVACQSCILUMTLDFTSLSTRPSSGCAQVLSHPGHTYTVSIA APSGGRILASSPVDAATRVWDVSTETCVPLPWFRGGGVTVLLW SPDGSKILATTPSAVFRVWEAQMWTCERWFTLSGRCQTGCMSPD GSRLLFTVLGSPLIYSLSFPERGEGKG\ALBVYSQGRLWQICL APSGGRAMATVQEKKAALNISALHSPAHEPFFSVAQKFGG GSRLLFTVLGSPLIYSLFPSGTPVONVMLCL  5956 1705 139 GUGWGGARAMATVQEKKAALNISALHSPAHEPFFSVAQKFGA VLONYFGDVDIPRAVVVRVQQALMDVKVPEAVPTKVFGKDKKPT FEDSSCSLYRPTTIPNQDSQLGKENKLYSPARYADALFKXSDIR SASLEDLMENSLKRANSPHVNISATLSPQVINEVNQEETIGRL LQLVDLPLLDSLLKQGEAVPKTQFFRGSTTWNSSNYLDRGILK AYSDSQBEMLSAATDCSFLLPWANGTSSFFFEQDFTDLVK ELLFDATGRYYSSRFPLINHLSDVINGIARLLVNGKTELALEAT QLLKLKLDEDSKLSAREKKK\LLAGPYKKTEPFELDGFRILVSH KAYSDSQBEMLSAATDCSFLLPWANGTSSFFFEQDFRILVKH VS\VK\LMAIQMGRDPMRDAGYIYCGRIDGRDYNTEKTTKDE LLINLLKTLDEDSKLSAREKKK\LLAGPYKKTHEPFELDGSLEFF SKKSDCSLPMFGSHNKKRPNNLVIGRMYDTHVLDMIELGIENFV SLKDINNSKCPBGTKPMLIFRAGDDPVTEDTRALKSLLIDFFR SKKSDCSLPMFGSHNKKRPNNLVIGRMYDTHVLDMIELGIENFV SLKDINNSKCPBGTKPMLIFRAGDDPVTEDTRALKSLLIDFFR FOTVSNITALGGLEYVLHFTALNGKITFELSSLLILDFFR SKKSDCSLPMFGSHNKKRPNNLVIGRMYDTHVLDMIELGIENFV SLKDINNSKCPBGTKPMLIFRAGDDPVTEDTRALKSLLIDFFR FOTVSNITALGGLEYVLHFTALNGKITFERSYKLLKKNISHD TFGTTYGRITHMAXODLSKLOTKMYNGLKKRPRFKKNISHD TFGTTYGRITHMAXODLSKLOTKMYNGLKKRPRFKKNISHD TFGTTYGRITHMAXODLSKLOTKMYNGLKKRPRFKKNISHD TFGTTYGRITHMAXODLSKLOTKMYNGLKKRPRFKKNISHD TFGTTYGRITHM
TEILLGLEIMHNRFVVYRDLKFANILLDEHGHARIS\DLGLACD FSKKKPHASVGTHGYMAPEVLQKGTAYDSSADMFSLGCMLFKLL RGHSPFRQHKT.KDKHEIDRMLTUTWVSLEDTFSPELKSLLEGGLI QRDVSKRLGCHGGGSQEVKEHSFFKGVDWQHYVLQKYSPPLIPF RGEVNAADAPDIGSFDEDTKSILLDCDQELYKHSPFLVISERW QQEVTETVYRAVNADTDKIEARKRANKQLGHEEDYALGKDCIM HGYMLKLGNFFLTQWQRRYFYLFFNRLEWRGEGSERQNLITMEQ ILSVEETQIKDKCLLFRIKGGGCFVLQCESDPEFVQWKKELNE TFKEAQRLERRAPKFINRPRGGTVELPKPSJCHGRNSNGL KREEFFLAVVCPLRYSAYESSFDTELREGGLCRSGOFADCRR PANRQDVLSGWINLPVLQLTKDPLKTPGRLDHGTRTAFIHHEQ VWKRCININHUVGLHGVLNEIANSEEEVFEWVKTASGWALALCR WASSLHGSLFPHLSIRSEDLIAFRAQVTNNSSCLCRVPAMHPHT NKFAVALLDDSVRVYNASSTIVFSLKHRLQRWASLALCR WASSLHGSFPHLSIRSEDLIAFRAQVTNNSSCLCRVPAMHPHT NKFAVALLDDSVRVYNASSTIVFSLKHRLQRWASLAKKPLSAS VLAVACQSCILLWTLDFTSLSTREGACQVS.HGHOTCH RGQYRHGMVRRGLGERLIPWSGTFVGNVWLCL GGRULFTVLGFPLIVSLSPEPLSCEGKG\ALEVGSQCHMGICL RQQYRHGMVRRGLGERLIPWSGTFVGNVWLCL GGRULFTVLGFPLIVSLSFPERCEGKG\ALEVGSQCHMGICL RQQYRHGMVRRGLGERLIPWSGTFVGNVWLCL GGVRGRAMATVQEXAALHSPAHRPFGFSVAQKFFGA TYVWSSIINTLQTQVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVQALMDYKVFFGADVFKVFGKDKKPT FEDSSCSLYRFTTIRPOSQLGKENKLYSPANYLDGGLKK AYSDSGEDWLSAAIDCSBYLPDQMVVEISRSFPEQDPTDLVK ELLFDATGRYYSSREPLLNHLSDVHNIARLLVNGKTEIALEAT QLLLKLLDFQNREFFRILLYFMANSFSFKLQKSSDNRWVK RIFSKAIVDNKNLSKGKTDLLVLFI\NDHQKDFFKIDTLVK ELLFDATGRYYSSREPLLNHLSDVHNIARSEFKLQKESDNRWVK RIFSKAIVDNKNLSKGKTDLLVLFI\NDHQKDFFKTFTGDT JCLLKLLDFQNREFFRILLYFMANSFSFKLQKSSNNRWVK RIFSKAIVDNKNLSKGKTDLLVLFI\NDHQKDFKTFTGTL VS\VK\LMAIQNGDPNDDAGYIYKKNITTFFFTDDTSLEFF SKKSDCSLFMFGSHKKRPNNLVIGGRYDYHVLDMTEIGIENFV SLKSDCSLFMFGSHKKRPNNLVIGGRYDYHVLDMTEIGIENFV SKKSDCSLFMFGSHKKRPNNLVIGGRYDYHVLDMTEIGIENFV SKKSDCSLFMFGSHKKRPNNLVIGGRYDYHVLDMTEIGIENFV SKKSDCSLFMFGSHKKRPNNLVIGRRYDYHVLDMTEIGIENFV SKKSDCSLFMFGSHKKRPNNLVIGRRYDYHVLDMTEIGIENFV SKKSDCSLFMFGSHKKRPNNLVIGRRYDKHVLDMTEIGIENFV SKKSDCSLFMFGSHKKRPNNLVIGRRYDKHVLDMTEIGIENFV SKKSDCSLFMFGSHKKRPNNLVIGRRYDKHVLDMTEIGIENFV SKKSDCSLFMFGSHKKRPNNLVIGRRYDKHVLDMTEIGIENFV SKKSDCSLFMFGSHKKRPNNLVIGRRYDKHVLDMTEIGIENFV SKKSDCSLFMFGSHKKRPNNLVIGRRYDKHVLDMTEIGIENFV SKKSDCSLFMFGSHKKRPNLVIGRSCAYYTCPWBAEGSAC
TEILLGLEIMHNRFVVYRDLKFANILLDEHGHARIS\DLGLACD FSKKKPHASVGTHGYMAPEVLQKGTAYDSSADMFSLGCMLFKLL RGHSPFRQHKT.KDKHEIDRMLTUTWVSLEDTFSPELKSLLEGGLI QRDVSKRLGCHGGGSQEVKEHSFFKGVDWQHYVLQKYSPPLIPF RGEVNAADAPDIGSFDEDTKSILLDCDQELYKHSPFLVISERW QQEVTETVYRAVNADTDKIEARKRANKQLGHEEDYALGKDCIM HGYMLKLGNFFLTQWQRRYFYLFFNRLEWRGEGSERQNLITMEQ ILSVEETQIKDKCLLFRIKGGGCFVLQCESDPEFVQWKKELNE TFKEAQRLERRAPKFINRPRGGTVELPKPSJCHGRNSNGL KREEFFLAVVCPLRYSAYESSFDTELREGGLCRSGOFADCRR PANRQDVLSGWINLPVLQLTKDPLKTPGRLDHGTRTAFIHHEQ VWKRCININHUVGLHGVLNEIANSEEEVFEWVKTASGWALALCR WASSLHGSLFPHLSIRSEDLIAFRAQVTNNSSCLCRVPAMHPHT NKFAVALLDDSVRVYNASSTIVFSLKHRLQRWASLALCR WASSLHGSFPHLSIRSEDLIAFRAQVTNNSSCLCRVPAMHPHT NKFAVALLDDSVRVYNASSTIVFSLKHRLQRWASLAKKPLSAS VLAVACQSCILLWTLDFTSLSTREGACQVS.HGHOTCH RGQYRHGMVRRGLGERLIPWSGTFVGNVWLCL GGRULFTVLGFPLIVSLSPEPLSCEGKG\ALEVGSQCHMGICL RQQYRHGMVRRGLGERLIPWSGTFVGNVWLCL GGRULFTVLGFPLIVSLSFPERCEGKG\ALEVGSQCHMGICL RQQYRHGMVRRGLGERLIPWSGTFVGNVWLCL GGVRGRAMATVQEXAALHSPAHRPFGFSVAQKFFGA TYVWSSIINTLQTQVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVQALMDYKVFFGADVFKVFGKDKKPT FEDSSCSLYRFTTIRPOSQLGKENKLYSPANYLDGGLKK AYSDSGEDWLSAAIDCSBYLPDQMVVEISRSFPEQDPTDLVK ELLFDATGRYYSSREPLLNHLSDVHNIARLLVNGKTEIALEAT QLLLKLLDFQNREFFRILLYFMANSFSFKLQKSSDNRWVK RIFSKAIVDNKNLSKGKTDLLVLFI\NDHQKDFFKIDTLVK ELLFDATGRYYSSREPLLNHLSDVHNIARSEFKLQKESDNRWVK RIFSKAIVDNKNLSKGKTDLLVLFI\NDHQKDFFKTFTGDT JCLLKLLDFQNREFFRILLYFMANSFSFKLQKSSNNRWVK RIFSKAIVDNKNLSKGKTDLLVLFI\NDHQKDFKTFTGTL VS\VK\LMAIQNGDPNDDAGYIYKKNITTFFFTDDTSLEFF SKKSDCSLFMFGSHKKRPNNLVIGGRYDYHVLDMTEIGIENFV SLKSDCSLFMFGSHKKRPNNLVIGGRYDYHVLDMTEIGIENFV SKKSDCSLFMFGSHKKRPNNLVIGGRYDYHVLDMTEIGIENFV SKKSDCSLFMFGSHKKRPNNLVIGGRYDYHVLDMTEIGIENFV SKKSDCSLFMFGSHKKRPNNLVIGRRYDYHVLDMTEIGIENFV SKKSDCSLFMFGSHKKRPNNLVIGRRYDYHVLDMTEIGIENFV SKKSDCSLFMFGSHKKRPNNLVIGRRYDKHVLDMTEIGIENFV SKKSDCSLFMFGSHKKRPNNLVIGRRYDKHVLDMTEIGIENFV SKKSDCSLFMFGSHKKRPNNLVIGRRYDKHVLDMTEIGIENFV SKKSDCSLFMFGSHKKRPNNLVIGRRYDKHVLDMTEIGIENFV SKKSDCSLFMFGSHKKRPNNLVIGRRYDKHVLDMTEIGIENFV SKKSDCSLFMFGSHKKRPNNLVIGRRYDKHVLDMTEIGIENFV SKKSDCSLFMFGSHKKRPNLVIGRSCAYYTCPWBAEGSAC
FSKKKPHASVGTHGYMAP BULQKGTAYDSSADWFSLGGMLFKLL RGHSPFRQHKTKDKHBIDRMITLTVNUELPDTFSPELKSLLEGLL QRDVSKRLGCHGGSGEWYEHSF KGVDMQHYYLQKYPPPLIPF RGEWNAADAFD IGSFDEEDTKGIKLLDCDGEVKMFPLVISERW QGEVTETVVEAWNADTDKIERARKAKQLGHEEDYALGKDCIM HGYMLKLGNPFLTQWQRRYFYLFPNRLEWRGEGESRQNLLTMEQ ILSVERTQIKDKKCILFFIKGGKQFVLQCESDPEVQWKKELNE TFKEAGRALRAPKHINRPRGGTUEDFEVSLCHRNSNGL  S955  1726  444  KREEFFLAWCPLRYFSAYESSPGTELREGGLGRSGGSFADCRR PANKQDVLSGWINLPVLQLTKDPLKTPGRLDHGTRTAFIHHREQ WKRCININRDWGLFGVLNEILANSEGLVFEWWKTASGKALALCR WASSLHGSLFPHISLRSEDLIABFAQVTINNSSCLRVFAWHPHT NKFAVALLDDSVRVYNASSTIVPSLKHRLQRNVASLAKKPLSAS VLAVACQSCILIWTLDFTSLSTRPSSGCAQVLSHPGHTPVTSLA WAPSGGRLLSASPVDAAIRWDVSTETCVPLEWFRGGCVTNLLW SPDGSKLLATTPSAVFRVWEAQMWTCERMFTLSGRCQTGCKSPD GSRLLFTVLGEPLIVSLSFPERCCEGKG\ALBVGSCQRLWQICL RQQYHQMVRRGLGERLTPWSGTPVGRWWLCL S956  1705  139  GVGWGGRARAMATVQEKAAALNLSALHSPAHRPFGFSVAQKFFGA TYWMSSIINTLQTQVEVKKRHRLKRHNDCFVGSEAVDVIFSHL IQNNYFGDVDIPRAKVVEVQALMKVFEAVPTKVFGKDKKPT FEDSSCSLYRPTTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWRHJCHONSTONESHVINSTALSPQVINEWWGEETIGRL LQLVDLFLLDSLLKQQEAVPKIPQFRQSTMNNSSNYLDRGILK AYSDSQEDEBLSAAIDCSGYLPDQMVVGISRSFPEQPDRTDLVK BLLFPAJGRYYSSGRFLINHLSQUFNEYBALGALLKHLKA US\VK\VK\LMAIQNGDPRDDAGYIVCQRIDQFDYSNNTEKTTKDE LLGLUKLLDFQNREEFFRLLYFMAVAANPSEFKLQKESDNRNVVK RIFSKAIVDNIKNLSKGKTDLLVLEI\MDHQMVFKIPGTLHKT VS\VK\LMAIQNGDPRDDAGYIVCQRIDQFDYSNNTEKTTKDE LLMLLKTLDEDGKLSAKEKKK\LLGQFYKCHPDIFIEHFGD  5957  1479  451  ELQVAVAMDTLDRVVKFKTKRAKRFLEKREPKLNENIKNAMLIK GGNANATYTKVLKDYVALKKFKYLYKKNITRPFEDDTSLEFF SKKSDCSLFMFGSHNKKPNNLVIGRMYDVLDMIELGIENFV SLKDIKNSKCPGBGTRWLTGRADDFVYLKKKNITRPFEDDTSLEFF SKKSDCSLFMFGSHNKRPNNLVIGRMYDVLDMIELGIENFV SLKDIKNSKCPGBGTVMLTFALDDLYKLSKLLDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE LSEMSPSLDLVLRRYTHLASGDLYKLKKNAISHD TFGTTTYGRIMMGXQDLJKLGYTKM\KGLKKRPABERITEDHEKKS KRIKKKLMBELSQPLLFHCVLLKRIIKGSIGSFL  ARALGMLLWFFRCQSTOPLLKKRIKKSGCRYYCCPWPAEGSACCRGIPF ARTASVLVGAPKANTSQDLIKGKGYYCCPWPAEGSACCRGIPF ARTASVLVGAPKANTSQDLIKGKGYYCCPWPAEGSACCRGIPF
RGHSPFRQHKTXDKHEIDRMILTUTWELDTFSPELKSLLEGIL ORDVSKRLCCHGGGSQEVKEHSFFKKUDWQHVYLQKYPPPLIPP RGEWNAADAPDIGSFDEEDTKGIKLLDCDQELYKMFPLVISERW CQEVTETVYEAVMADTDKIERRKRAKNKQLGHEEDVALGKDCIM HGYMLKLGNPFLTQWQRRYYFLPFNRLEWRGEGESRQNLLTMEQ ILSVEETQIKDKKCILFRIKGGKOFVLQCESDPEFVQWKKELNE TFKEAQRLERRAPKFLNKPRSGTTELPKPSLCHGNSNGL KREEPFLAVCPLRYSAYESSPOTTELREGGLCRSGOBFADCRR PANRQDVLSGWINLPVLQLTKDPLKTPGRLDHGTRTAFIHHREQ VWKRCINIHRUVGLEGULNEIANSEEEVFEWKTASGWALALCR WASSLHGSLPPHLSIKSEDLILAFBAQVTNUSSCCLEVRAWHPHT NKFAVALLDDSVEVVNASSTIVPSLKHRLQRWVASLAKKPLSAS VLAVACQSCILIWTLDFTSLSTRPSSGCAQVLSHPGHTPVTSLA WAPSGGRLLSAPFVDAAIRVWDVSTETCVPLPWFRGGCVTKLLW SPDGSKILAATPBAVFRWEAQMMTCERWFTLSGRCQTGCHSPD GSRLLFTVLGEPLIYSLSFPERCGEGKÇALEVOSQORLWQICL RQQYRHMWRRGLGERLTPWSGTFVGNWMLCL SQUGWRGARAMATTOEKAAMLISALHSPAHEPFGFSVAQKFFGA TYVWSSIINTLQTQVEVKERRHRLKRHNDCFVGSEAVDVIFSHL LQNNYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKDKKPT FEDSSCSLYRPTTIPNQDSGLGKENKLYSPARYADALFKSSDIR SASLEDLEWELSLKPANSPHVNISATPQVINEWQEETIGRL LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTWMSSNYLDRGILK AYSDSQEDEWLSAAIDCSBYLPQDMVVEISRSFPEQDBTDLVK ELLPDAIGRYYSSREPLLNHLSDVHNOIABLLUNGKTEIALEAT QLLLKLLDFORREFFRLLYPMAVAANPSEKLQKESDNRWVK RIFSKAIVDNKNLSKGKTDLLVLFL/NDHOKDVSTLADEAT QLLLKLLDFORREFFRELLYPMAVAANPSEKLQKESDNRWVK RIFSKAIVDNKNLSKGKTDLLVLFL/NDHOKDVSTLADEAT GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKPPNNLVIGRNYDVLDMIELGIENFV SLKDIKNSKCPBGTKYMLFTALGKLYFFSYKLLLKKSGCTETRIE LEEMGPSLDLVLRFTHLASDDLYKLSKMPKAKLPKKKNISHD TFGTTYGRIHMGKQDLSKLQTRAM/KGLKKRPABRITEDHEKKS KRIKKKLMELSQPLLFHCULKRIIKGSIGSFL ARALGHLUNFFRCQAFNLDVEKKLTKKSGFCTFGTBDE KRIKKKLMELSQPLLFHCULKRIIKGSIGSFL ARALGHVLWRFTRAGSACCRGIPP ARTASVLVGAPKANTSQPLIKWKSCKYFGKSYFGYAVDFHIPD ARTASVLVGAPKANTSQPLIKKEGSACYYYCFWPAEGSACCRGIPP ARTASVLVGAPKANTSQPLIKEGGAVYYCFWPAEGSACCRGIPP ARTASVLVGAPKANTSQPLIKEGGAVYYCFWPAEGSACCRGIPP
ORDVSKELGCHGGGSGEVKEHSFFKGVDWGHYYLQKYPPLJPP RGEVNAADAPDIGSFDEEDTKGIKLDCDGELYKNFPLVISERW OQEVTETVYEAVNADTDKIEARKRAKNKQLGHEEDYALGKDCIM HGYMLKLGNFILTQWGRRYFYLFPRNLEWRGEGSERGNLITMEQ LLSVEBFTQIKDKKCLIFFIKGGKGFVLQCESDPEPVQMKKELNE TFKEAGRLLRRAPKFLNKPRGGTVELPKPSLCHRNSNGL KREKEFFLAVCPLRYFSAYESSFGTELEKGGLCKSGGBFADCRR PANRQDVLSGWINLPVLQLTKDPLKTPGRLDHGTRTAFIHREQ VWKRCINIWRUVGLPGVLNEIANSEEVFEWVKTASGRALALCR WASSLHSSIPPHLSLRSEDLIAEFAQVTNWSSCCLRVFAWHPHT NKFAVALLDDSVRVYNASSTIVPSLKHRLQRNVASLAWKPLSAS VLAVACQSCILIWTLDFTSLSTTPSSGCAQVLSHBGHPPVTSLA WAPSGRLLSASPVDAAIRVWDVSTBTCVPLPWFRGGGVTNLW SPDGSKILATTPSAVFRWEAQMWTCERWFTLSGRCQTGCWSPD GSRLLFTVLGEPLIYSLSFPERGGEGKGALEVQSQCRMGICL RQQYVRGMWNRGIGERLTPWSGTPVGNVWLCL LQROYMGMVRRGIGERLTPWSGTPVGNVWLCL LQROYMGMVRRGIGERLTPWSGTPVGNVWLCL LQROYMGMVRRGIGERLTPWSGTPVGNVWLCL LQROYMGMVRRGIGERLTPWSGTPVGNVWLCL LQLVDLPFGDVDIPRAKVVRVCQALMDYKVPEAVPTKVFGKDKKFT FEDSSCSLYRFTTIPMODSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKPANSPHVNISATLSPAVYADALFKSSDIR LQLVDLPLLDSLLKQQEAVPKIPQPKRGSTMVNSNYLDRGILK AYSDSQEDEMLSAAIDCSSFLPDQMVVETSRSFPEQPDRTDLVK ELLPDAIGRYYSSREPLIANLSDVHNGIARLLVNGKTEIALEAT OLLLKLLDFONREFFRLLYFMAVAANPSEFKLQXESDNRMVVK RIFSKALVDNKNLSKKTDLLVLFLNMKTEIALEAT OLLLKLLDFONREFFRLLYFMAVAANPSEFKLQXESDNRMVVK RIFSKALVDNKNLSKKKTDLLVLFLNMKTEIALEAT OLLLKLLDFONREFFRLLYFMAVAANPSEFKLQXESDNRMVVK RIFSKALVDNKNLSKKKTDLLVLFLNMKTEIALEAT OLLLKLLDFONREFFRLLYFMAVAANPSEFKLQXESDNRMVVK RIFSKALVDNKNLSKKKTDLLVLFLNMKTEIALEAT OLLLKLLDFONREFFRLLYFMAVAANPSEFKLQXESDNRMVVK RIFSKALVDNKNLSKKKTDLLVLFLNMKTEIALEAT OLLLKLLDFONREFFRLLYFMAVAANPSEFKLQXESDNRMVVK RIFSKALVDNKNLSKKKTDLLVLFLNMKTEIALEAT OLLLKLLDFONREFFRLLYFMAVAANPSEFKLQXESDNRMVVK RIFSKALVDNKNLSKKKTDLLVLFLNMKKTEIALEAT OLLLKLLDFONREFFRLLYFMAVAANPSEFKLQXESDNRMVVK RIFSKALVDRKNLSKERFTLLYFMAVAANPSEFKLQXESDNRMVVK RIFSKALVDRKNKKCPGFORYPMLTRAKKRISLDDFFRC SKKSDCSLFWFGSHKKKRYNDLVJGRKKNKLKRHENDLIKRAMLIK GGNANATVTKVLKDVYALKKRYTGDFDVYTHVLDMLELGIENFY SKKSDCSLFWFGSHKKRKRRNNLVJGGRFDVYHVLDMIELGIENFY VSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKSGCGTPRIE LEEWSPSLDLVLRTHLASDDLYKLSKMKRKKKKRNISHD TFGTTYGRIHWQKQDLSKLTGRABRITEDH
ORDVSKELGCHGGGSGEVKEHSFFKGVDWGHYYLQKYPPLJPP RGEVNAADAPDIGSFDEEDTKGIKLDCDGELYKNFPLVISERW OQEVTETVYEAVNADTDKIEARKRAKNKQLGHEEDYALGKDCIM HGYMLKLGNFILTQWGRRYFYLFPRNLEWRGEGSERGNLITMEQ LLSVEBFTQIKDKKCLIFFIKGGKGFVLQCESDPEPVQMKKELNE TFKEAGRLLRRAPKFLNKPRGGTVELPKPSLCHRNSNGL KREKEFFLAVCPLRYFSAYESSFGTELEKGGLCKSGGBFADCRR PANRQDVLSGWINLPVLQLTKDPLKTPGRLDHGTRTAFIHREQ VWKRCINIWRUVGLPGVLNEIANSEEVFEWVKTASGRALALCR WASSLHSSIPPHLSLRSEDLIAEFAQVTNWSSCCLRVFAWHPHT NKFAVALLDDSVRVYNASSTIVPSLKHRLQRNVASLAWKPLSAS VLAVACQSCILIWTLDFTSLSTTPSSGCAQVLSHBGHPPVTSLA WAPSGRLLSASPVDAAIRVWDVSTBTCVPLPWFRGGGVTNLW SPDGSKILATTPSAVFRWEAQMWTCERWFTLSGRCQTGCWSPD GSRLLFTVLGEPLIYSLSFPERGGEGKGALEVQSQCRMGICL RQQYVRGMWNRGIGERLTPWSGTPVGNVWLCL LQROYMGMVRRGIGERLTPWSGTPVGNVWLCL LQROYMGMVRRGIGERLTPWSGTPVGNVWLCL LQROYMGMVRRGIGERLTPWSGTPVGNVWLCL LQROYMGMVRRGIGERLTPWSGTPVGNVWLCL LQLVDLPFGDVDIPRAKVVRVCQALMDYKVPEAVPTKVFGKDKKFT FEDSSCSLYRFTTIPMODSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKPANSPHVNISATLSPAVYADALFKSSDIR LQLVDLPLLDSLLKQQEAVPKIPQPKRGSTMVNSNYLDRGILK AYSDSQEDEMLSAAIDCSSFLPDQMVVETSRSFPEQPDRTDLVK ELLPDAIGRYYSSREPLIANLSDVHNGIARLLVNGKTEIALEAT OLLLKLLDFONREFFRLLYFMAVAANPSEFKLQXESDNRMVVK RIFSKALVDNKNLSKKTDLLVLFLNMKTEIALEAT OLLLKLLDFONREFFRLLYFMAVAANPSEFKLQXESDNRMVVK RIFSKALVDNKNLSKKKTDLLVLFLNMKTEIALEAT OLLLKLLDFONREFFRLLYFMAVAANPSEFKLQXESDNRMVVK RIFSKALVDNKNLSKKKTDLLVLFLNMKTEIALEAT OLLLKLLDFONREFFRLLYFMAVAANPSEFKLQXESDNRMVVK RIFSKALVDNKNLSKKKTDLLVLFLNMKTEIALEAT OLLLKLLDFONREFFRLLYFMAVAANPSEFKLQXESDNRMVVK RIFSKALVDNKNLSKKKTDLLVLFLNMKTEIALEAT OLLLKLLDFONREFFRLLYFMAVAANPSEFKLQXESDNRMVVK RIFSKALVDNKNLSKKKTDLLVLFLNMKTEIALEAT OLLLKLLDFONREFFRLLYFMAVAANPSEFKLQXESDNRMVVK RIFSKALVDNKNLSKKKTDLLVLFLNMKKTEIALEAT OLLLKLLDFONREFFRLLYFMAVAANPSEFKLQXESDNRMVVK RIFSKALVDRKNLSKERFTLLYFMAVAANPSEFKLQXESDNRMVVK RIFSKALVDRKNKKCPGFORYPMLTRAKKRISLDDFFRC SKKSDCSLFWFGSHKKKRYNDLVJGRKKNKLKRHENDLIKRAMLIK GGNANATVTKVLKDVYALKKRYTGDFDVYTHVLDMLELGIENFY SKKSDCSLFWFGSHKKRKRRNNLVJGGRFDVYHVLDMIELGIENFY VSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKSGCGTPRIE LEEWSPSLDLVLRTHLASDDLYKLSKMKRKKKKRNISHD TFGTTYGRIHWQKQDLSKLTGRABRITEDH
RGEWNAADAPDIGSPBEEDTKGIKLLDCDQELYKNFPLVISERW QQEVTETVYEAVNADTDKIEARKAKNKQLGHEEDYALGKDCIM HGYMLKLGNFFLTQWQRRYFYLFPRNEWRGEGESRQNLLTMEQ ILSVEFTQIKDKKCILFRIKGGKOFVLQCESDPEFVQWKKELNE TFKEAQRLERRAPKFLNKPRSGTVELPKPSLCHRNSNGL KREEFFLAVCPLRYPSAYESSPGTELRECGLCRSGQEFADCRR PANRQDVLSGWINLPVLQLTKDPLKTPGRLDHGTRTAPIHHREQ WKRCINIWRUVGLFGVLNEIANSECLVRYAGMHALLC WASSLHGSLPPHLSLRSEDLIAEFAQVTNWSSCCLRVPAWHPHT NKFAVALLDDSVRVYNASSTIVPSLKHRLQRRVASLAKKPLSAS VLAVACQSCILINTLDPTSLSTRSGCAQVLSHPGHTPVTSLA WAPSGGRLLSASPVDAAIRVWDVSTETCVPLPWFRGGGVTNLLW SPDGSKLILTTPSAVFRVWEAQMWTCERRPTLSGRCGTGCKSPD GSRLLFTVLGEPLIYSLSFPERSGEGAVLSHPGHTPVTSLA WAPSGGRLLSASPVDAAIRVWDVSTETCVPLPWFRGGGVTNLLW SPDGSKLILTTPSAVFRVWEAQMWTCERRPTLSGRCGTGCKSPD GSRLLFTVLGEPLIYSLSFPERGEGSKGALBEVGSQORLWQICL RQQYRHOMVRRGLGEBLITPRSGTPVGNVWLCL SYDGSKLITTPSAVFRVWEAQMWTCERRPTLSGRCTGCKSPD GSRLKFTVLCEPLIYSLSFPERGEGSKGALBEVGSQORLWQICL RQQYRHOMVRRGLGEBLITPRSGTPVGNVWLCL SYDGSKLITTPSAVFRVWEAQMWTCERRPTLSGRCTTGCKSPD GSRLKFTVLCEPLIYSLSFPERGEGSKGALBEVGSQORLWQICL RQQYRHOMVRRGLGEBLITPRSGTPVGNVWLCL SASLEDLWENLSLKPADAINSATLSPAHRPPFFSVAQKFFGA TYWSSIINTLQTVQVBVKKRRHRLKRHNDCFYGSEAVDVITSHL IQNNYFFGDVDIPRAKVVRVQQALMDYKVFEAVPTKVFGKDKKPT FEDSSCSLYRPTTIPNQDSQLJGKENKLYSPARYADALFKSSDIR AASSLEDLWENLSLKAPASPHVNISATLSPQVINEWQGETIGRL LQLUDLPLLISLLKQQBAVPKIPQFRGSTMMNSSNYLDRGILK AYSDSQEDEWLSAAIDCSEYLLDYFRAVANDSEFELQKESDNRMVVK RIFSKATUDNKNISKCKTDLLVFLLMDHQKDVFKIPGTLVHKI VS\VK\LMAIQNGRDPNRDAGYIYCORIDQRDYSNNTEKTTKDE LLNLKTLDEDSKLSAKEKKK,LLGQFYKCHDDIFIEHFGD  5957 1479 451 ELGWANADTILBEDSKLSAKEKKK,LLGQFYKCHDDIFIEHFGD SKKSCCSLFWFGSHNKKRPNNLVIGRWTUYHULMIELGIENFV SKKSCCSLFWFGSHNKRKRPNNLVIGRWTUYHULMIELGIENFV SKKSCCSLFWFGSHNKRKRPNNLVIGRWTUYHULMIELGIENFV SKKSCCSLFWFGSHNKRKRPNNLVIGRWTUYHULMIELGIENFV SKKSCCSLFWFGSHNKRKRPNNLVIGRWKRKKKLLKBLIDPFRG PTVSNIBLAGLEVVLHFTALNGKIYFRSYKLLLKKSGCRTFRIE LEEMGPSLDLVLRRTHLASDDLYKLKMNINDHIELGIENFV SKKSCLFGETKYMLIFAGDDFFVTEDYRRKSLLIDPFRG PTVSNIBLAGLEVULHFTALNGKIYFRSYKLLLKKSGCRTFRIE LEEMGPSLDLVLRRTHLASDDLYKLKSMKMPKALKPKKKKNISHD TFGTTYGRIMMGXQDLSKLGTRM\KGKKRKKKNISHD AAALGMLWFFSCACAVYCPWBAEGSAQCQCQIPP
QQEVTETVYRAVRADTOKIEARKRANIKQLGKEEDYALGKOCIM HGYMLKIGNFFLTQWQRRYFYLFPRRLEWRGEGESRQNLITMEQ ILSVEETQIKOKKCILFRIKGKQFVLQCESDPETVQKKKELNE TFKEAQRLLRAPKFLIKPRSGTVELPKPSLCHRNSNOL KREREFRLAVCPLRYFSAVESSPGTELRECGLCRSGQBFADCRR PANRQDVLSGWINLPVLQLTKOPLKTPGRLDHGTRTAFIHHREQ VWKRCINIWRDVGLFGYLNEIANSECLVEWFAWHPHT NKFAVALLDDSVRVYNASSTIVFSLKHRLQRRVASLAUKCR WASSLIGSLPPHLSLRSEDLIAEFAQVTNWSSCCLRVFAWHPHT NKFAVALLDDSVRVYNASSTIVFSLKHRLQRRVASLAUKCR WASSLIGSLPPHLSLRSEDLIAEFAQVTNSCLRVFAWHPHT NKFAVALLDDSVRVYNASSTIVFSLKHRLQRRVASLAUKCLSAS VLAVACQSCILIWTLDPTSLSTRPSSGCAQVLSHPGHPPVTSLA WAPSGGRLLSAS PVDAAIRVMVVSTETCVPLPWFRGGGVTNLLW SPDGSKILATTPSAVFRWEAQMWTCERRPTLSGRCQTGCMSPD GSRLLFTVLGEPLIYSLSFPERGGEKG ALEVQSQQRLWQICL RQQYRQMYRRGLGERLTPWSGTPVGNVWLCL SPDGSKILATTPSAVFRVEAQMWTCERRPTLSGRCQTGCMSPD GSRLLFTVLGEPLIYSLSFPERGGEKG ALEVQSQQRLWQICL RQQYRQMYRGLGERLTPWSGTPVGNVWLCL SPDGSKCLAYPTTIPNODSQLGKENKLYSPARYADALFKSSDIR INNYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKDKKPT FEDSSCSLYRPTTIPNODSQLGKENKLYSPARYADALFKSSDIR SASLEDLWERLSLKPANSPHVNISATLSPQVINEWQEETIGRL LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSNYLDRGILK AYSDSQEDEWLSAAIDCSSTLPDQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPLLNHLSDVINGIARLLVNGKTEILLEAT QLLLKLLDFONREFFRRLLYFMAVAANPSEFKLQKESDNRNVVK RIFSKALVDNKNLSKGKTDLLVLFLVMHQKDESLAERT QKIKKLMERGFRELLYFMAVAANPSEFKLQKESDNRNVVK RIFSKALVDNKNLSKGKTDLLVLFLVMHQKDESLGENFV SLKKDINNSKCPEGTKPMLIFAGDDPVTEDYRRKKTKNDE LLNLLKTLDEDSKLSAKEKKKLLGGFYKCHDPIFEGRIFF SKKSDCSLFWFGSHNKKRPNILVIGRMYDFALDMIELGIENFV SLKKDINNSKCPEGTKPMLIFAGDDPVTEDYRRKKSLLIDFFRG PTVSNIFLAGGLEVYLHFTALNGKIYFRSYKLLLKKSGCRTFRIE LSEMGPSLDLVLRRTHLASDDLYKLSKMMYKALKPKKKNLIDFFRG PTVSNIFLAGGLEVYLHFTALNGKIYFRSYKLLLKKSGCRTFRIE LSEMGPSLDLVLRRTHLASDDLYKLSKMMYKALKPKKKNLIDFFRG PTVSNIFLAGGLEVYLHFTALNGKIYFRSYKLLLKKSGCRTFRIE LSEMGPSLDLVLRRTHLASDDLYKLSKMMYKALKPKKKNLIDFFRG PTVSNIFLAGGLEVYLHFTALNGKIYFRSYKLLLKKSGCRTFRIE LSEMGPSLDLVLRRTHLASDDLYKLSKMMYKALKPKKKNLIDFTGTTTTGRIHMGKQDGLSKLGTRKM KGRLKRPAERITEDHEKKS KRIKKELMELSQPLLFFRCVLLKRIIKGSGSFL AAALGMLWFFPACQAFNLDVEKGRYYGPWPARGSAQCRQCQIFP
HGYMLKIGNPFLTOWQRRYFYLPNRLEWRGEGSERQNLLTMED  ILSVEETQIKDKKCJUFRIKGGKQFVLQCESDPEFVQWKKELNE TFKEAQRLLRRAPKFINKPRSGTVELPKPSLCHRNSRGL  5955  1726  444  KREREFRLAVCPLRYFSAYESSPOTELECGLCRSGGBFADCRR PANRQDVLSGWINLPVLQLTKDPLKTPGRLDHGTRTAFIHHREQ VWKRCINIWRUVGLFGVLNEIANSEERVFEWYKTASGWALALCR WASSLHGSLPPHLSLRSEDLIAEPAQVTNNSSCCLRVFAWHPHT NKFAVALLDDSVRVYNASSTIVPSLKHRLQRNVASLAWKPLSAS VLAVACQSCLLIWTLDETSLSTRPSGCAQVLSHPGHTPVTSLA WAPSGGRLLSASPVDAAIRVMDVSTETCVFLPWFRGGGVYNLLW SPOGSKILLATPSAVFRVWEAQWMTCEWPTLYSGRCQTGCWSPD GSRLLFTVLGEPLIYSLSFPERCGEGKG\ALBVQSQQRLWQICL RQQYRHQWVRRGLSERLTPWSGTPVGNWLCL RQQYRHQWVRRGLSERLTPWSGTPVGNWULCL RQQYRHQWVRRGLSERLTPWSGTPVGNWULCL RQQYRHQWVRRGLSERLTPWSGTPVGNWULCL RQQYRHGWVRRGLSERLTPWSGTPVGNWULCL RQQYRHGWVRRGLSERLTPWSGTPVGNWULCL RQQYRHGWVRRGLSERLTPWSGTPVGNWULCL RQQYRHGWVRRGLSERLTPWSGTPVGNWULCL RQQYRHGWVRRGLSHSTPVGSPRVWULCS RQYSKGAAMATVQEKAAALNLSALHSSPARPFGFSVAQKPFGA TYVWSSIINTLQTQVBVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKYFEAVPTXVFGKDKKPT PEDSSCSLYRFTITPRODSGVBRNKLYSPARYADALFKSDIR SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQLVDLPLLDSLLKQQEAVPKIPQFKRQSTMVNSSNYLDRGILK AYSDSQEDEWLSAAALOSERNKLYSPRAYDALFKSSDIR SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQLULLKLLDFQNREEFRRLLYFMAVAAAMPSEFKLKQKEDNRMVVK RIFSKAIVDMINLSKGKTUDLUVEL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPREDAGYIVCORIDQRDYSNNTEKTTKDE LLINLLKTLDEDSKLSAKEKKK\LLGGFYKCHPDIFIEHFGD SKKSDCSLFMFGSHNKRPNNLVIGRMYDYHVLDMIELGIENFV SLKNIKNSKCPEGTKYPMLIFADDFDVTEDYRRLKSLLIPFFRG PTVSNIRLAGLEYVLHFTALNGKTYFRSYKLLLKKSGCRTPRIE LSEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLAGTRN\KGLKKRPABRITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKRGSIGSFL  SAKTASUNGABCANTSCOPTURGGAVYYCOPAARGSAQCRQTPIPD ARTASVUNGAPKANTSCOPTURGGAVYYCOPAARGSAQCRQTPIPD ARTASVUNGAPKANTSCOPTURGGAVYYCOPAARGSAQCRQTPIPD ARTASVUNGAPKANTSCOPTURGGAVYYCOPAARGSAQCRQTPIPD ARTASVUNGAPKANTSCOPTURGGAVYYCOPAARGSAQCRQTPIPD ARTASVUNGAPKANTSCOPTURGGAVYYCOPAARGSAQCRQTPIPD
ILSVEETQIKDKKCILPRIKGGKOFVLQCESDPEPVOMKKELNE TFKEAQALLRRAPKFINKPRSGTVELPKPSLCHRNSNGL KREEFFILAVCPLEYPSAYESPOTELREGGLCRSGGSFADCRR PANRQDVLSGWINLPVLQLTKDPLKTPGRLDHGTRTAFIHHREQ VWKRCINIWRUVGLFGVLNEINASSEEVFEWVETASGWALALCR WASSLHGSLPPHLSLRSEDLIAEFAQVTNWSSCCLRVFAWHPHT NKFAVALLDDSVRVYNASSTIVPSLKHRLQRNVASLAWKPLSAS VLAVACQSCILIWTLDPTSLSTRPSSCAQVLSHPGHTPVTSLA WAPSGGRILASASPVDAAIRVMDVSTETCVPLPWFRGGGVTNLLW SPDGSKILATTPSAVFRVWEAQMWTCERWPTLSGRCQTGCWSPD GSRLLFTVLGEPLIYSLSFPERGEGGK\ALEVQSQRLWQICL RQQYTHQMVRRGLGERLTPWSGTPVGNVWLCL  5956  1705  139  GVGVRGARAMATVQEKAAALNLSALHSPAHRPPGFSVAQKPFGA TYVWSSIINTLQTQVBVKKRRHRLKRINDCFVGSEAVDVIPSHL IQNNYFGDVDIPRAKVVWVCQALMDYKVFEAVPTKVFGKOKKPT FEDSSCSLYRFTTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKQBAVEVQDLMDYKVFEAVPTKVFGKOKKPT FEDSSCSLYRFTTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKQBAVEVPQFKRGSTWNSNNYLDRGILK AYSDSQEDEWLSAAIDCSSYLPDQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPILNHISDVHNGIAELLVAGGEKVENPOKETIGRL AYSDSQEDEWLSAAIDCSSYLPDQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPILNHISDVHNGIAELLVAGKTEIALEAT QLLLKLLDFORREFFRELLYPMAVAANPSEFKLQKESDRNAVK RIFSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCGRIDQRDYSNNTEKTTKDE LLHILKTLDEDSKLSAKEKKLLGGFYKCHPDIFISEFFGD  5957  1479  451  ELQVAVAMDTLDRVVKPKTKRAXFFLEKREPKLNENIKNAMLIK GGNANATTTKVLKOVYALKKPYGGVIYKKNATTRFEDQTSLEFF SKKSDCSLFMFGSNKKKPPNILVIGRMYDVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFADGKTYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDLYKLSKMYLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFADGKTYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDLYKLSKMYLLMFKSGCRTPRIE LEEMGPSLDLVLRRTHLASDLYKLSKMKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPAERITEDHEKKS KRIKKKLMELSQPLLFHFCVLLKRIIKIGSIGSFL  AAALGMLLWFPACQAFNDLDVEKLTVYSG PKGSYFGYAVDFHIPD ARTASVUNGAPKANTLOPDIVEGGAVYYCPWPARGSAQCRQIPFP
ILSVEETQIKDKKCILPRIKGGKOFVLQCESDPEPVOMKKELNE TFKEAQALLRRAPKFINKPRSGTVELPKPSLCHRNSNGL KREEFFILAVCPLEYPSAYESPOTELREGGLCRSGGSFADCRR PANRQDVLSGWINLPVLQLTKDPLKTPGRLDHGTRTAFIHHREQ VWKRCINIWRUVGLFGVLNEINASSEEVFEWVETASGWALALCR WASSLHGSLPPHLSLRSEDLIAEFAQVTNWSSCCLRVFAWHPHT NKFAVALLDDSVRVYNASSTIVPSLKHRLQRNVASLAWKPLSAS VLAVACQSCILIWTLDPTSLSTRPSSCAQVLSHPGHTPVTSLA WAPSGGRILASASPVDAAIRVMDVSTETCVPLPWFRGGGVTNLLW SPDGSKILATTPSAVFRVWEAQMWTCERWPTLSGRCQTGCWSPD GSRLLFTVLGEPLIYSLSFPERGSEGK\ALEVQSQRLWQICL RQQYTHQMVRRGLGERLTPWSGTPVGNVWLCL  5956  1705  139  GVGVRGARAMATVQEKAAALNLSALHSPAHRPPGFSVAQKPFGA TYVWSSIINTLQTQVBVKKRRHRLKRINDCFVGSEAVDVIPSHL IQNNYFGDVDIPRAKVVWVCQALMDYKVFEAVPTKVFGKOKKPT FEDSSCSLYRFTTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKQBALVFQPFKRGTWNSNNYLDRGILK AYSDSQEDEWLSAAIDCSSYLPDQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPILNHSDVHNGIAELLVAGKTEIALEAT QLLLKLLDFORREFFRELLYPBAVAANPSEFKLQKESDRNVVK RIFSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\KKI VS\VK\LMAIQNGRDPNRDAGYIYCGRIDQRDYSNNTEKTTXDE LLNILKTLDEDSKLSAKEKKLLGGFYKCHPDIFISEFFGD  5957  1479  451  ELQVAVAMDTLDRVVKPKTKRAXFFLEKREPKLNENIKNAMLIK GGNANATTTKVLKOVYALKKPYGGLYKKKNITRFFEQOTSLEFF SKKSDCSLFMFGSNKKKPPNILVIGRMYDVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFADGRITYFSYKLLLKKSGCRTPRIE SKESDSLEMFGSNKKKPPNILVIGRMYDVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFADGRITYFSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDLYKLSKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPAERITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKIGSIGSFL  AAALGMLLWFPACQAFNDLDVEKLTVYSSPGYAVDFHIPD ARTASVUNGAPKANTSOPDIVEGGAVYYCPWPARGSAQCRQTPF
TFKEAQRLLRRAPKFLNKPRSGTVELPKPSLCHRNSNGL  5955  1726  444  KREREFRLÄVCPLRYPSÄYESSPGTLREGGLERSGGBFADCRR PANRQDVLSGNINLPVLQLTKOPLKTPGRLDHGTRTAFIHREG VWKRCINIWRDVGLPGVLNEIANSEEEVFEWVKTASGWALALCR WASSLHGSLPPHLSLRSEDLIAEPAQVTNWSSCCLRVPAWHPHT NKFAVALLDDSVRVYNASSTIVPSLKHRLQRNVASLAWKPLSAS VLAVACQSCILIWTLDPTSLSTRPSSGCAQVLSHPGHTPVTSLA WAPSGGRLLSASPVDAAIRVNDVSTETCVPLPWFRGGGVTNLLW SPDGSKILATTPSAVFRWEAQMWTCERNPTLSGRCQTGCWSPD GSRLLFTVLGEPLIYSLSFPERCGEGKG\ALBVQSQQRLWQICL RQQYRHQMYRRGLGERLTPWSGTPVONVMLCL  5956  1705  139  GVGWRGARAMATVQEKAAALNISALHSPAHRPPGFSVAQKFFGA TYVMSSIINTLQTQVGVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKOKKPT FEDSSCSLYRFTTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKPRNSPVNISATLSPQVINEVNQEETIGRL LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGILK AYSDSQEDEMLSAAIDCSFYLPDQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSRPBLNISATLSPQVINEVNQEETIGRL QLLKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSKKKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCORIDQRDYSNNTEKTTKDE LLNLKTLDEDSKLSAKEKK\LLQGFYKCHPDIFIEHFGD  5957  1479  451  ELQVAVAMDTLDRVVKPKRRAKRFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKYGVYYKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE LEEMSPSLDJULRRTHLASDDLYKLSMKMPKALKPKKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKLMELSQPLLFHCVLLKRI IKHQSIQSFL  5958  1 3138  AAALGMLLWFPACQAFNLDVEKLTVVSGPKGSYFGYAVDFHIPD ARTASVLVGAFKANTSQPDIVSGGAVYYCPWPABEGSAQCRQIPF
Total
PANRQDVLSGWINLPVLQLTKDPLKTPGRLDHGTRTAFIHHREQ VWKRCINTWRDVGLFGVLMEIANSEESUFAWTATASGMALALCR WASSLHGSLFPHLSIRSEDLIABFRQVTNWSSCCLRVFAWHPHT NKFAVALLDDSVRVYNASSTIVFSLKHRLQRNVASLAWKPLSAS VLAVACQSCILIWTLDPTSLSTRPSGGCAQVUSHPGHTPVTSLA WAPSGGRLLSASPVDAAIRVWDVSTETCVPLPWFRGGGVTNLLW SPDGSKLLATTTSAVPRVWBAQMMTCERWPTLSGRCQTGCWSPD GSRLLFTVLGPFLIYSLSFPERCGEGKG\ALBVQSQQRLWQICL RQQYRHQMVRRGLGERLTPWSGTPVGNVWLCL  S956  1705  139  GVGVKGARRMATVQEKAMAINLSALHSPAHRPBGFSVAQKPFGA TYVWSSIINTLQTQVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNXYFGDVDIPRAKVVRVCQAMDYKVFEAVPTKVFGKOKKPT FEDSSCSLYRFTTIPMOSQLGKENKLYSPARYADALFKSSDIR SASLEDLMENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQLVDLPFLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGILK AYSDSQEDEWLSAAIDCSPLPDQMVVEISRSFPEQPDRTDLVK ELLFPAIGRYYSSREPLLNHLSDVHNGIARLLVNGKTEIALEAT QLLLKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNEMVVK RIFSKAIVDNKNLSKCKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\WK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD  5957  1479  451  ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKJIKNSKCPBGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE LESMSPSLDLVLRRTHLASDDLYKLSMKMPKALKSKKISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKLMELSQPLLFHCVLLKKRIIKHQSIQSFL  4AALGMLLWFPACQAFRNLDVEKLTIKHQSIGSFL AAALGMLLWFPACQAFRNLDVEKLTVSGPKGSYFGYAVDFHIPD ARTASVLVGAPRANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
PANRQDVLSGWINLPVLQLTKDPLKTPGRLDHGTRTAFIHHREQ VWKRCINTWRDVGLFGVLMEIANSEESUFAWTATASGMALALCR WASSLHGSLFPHLSIRSEDLIABFRQVTNWSSCCLRVFAWHPHT NKFAVALLDDSVRVYNASSTIVFSLKHRLQRNVASLAWKPLSAS VLAVACQSCILIWTLDPTSLSTRPSGGCAQVUSHPGHTPVTSLA WAPSGGRLLSASPVDAAIRVWDVSTETCVPLPWFRGGGVTNLLW SPDGSKLLATTTSAVPRVWBAQMMTCERWPTLSGRCQTGCWSPD GSRLLFTVLGPFLIYSLSFPERCGEGKG\ALBVQSQQRLWQICL RQQYRHQMVRRGLGERLTPWSGTPVGNVWLCL  S956  1705  139  GVGVKGARRMATVQEKAMAINLSALHSPAHRPBGFSVAQKPFGA TYVWSSIINTLQTQVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNXYFGDVDIPRAKVVRVCQAMDYKVFEAVPTKVFGKOKKPT FEDSSCSLYRFTTIPMOSQLGKENKLYSPARYADALFKSSDIR SASLEDLMENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQLVDLPFLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGILK AYSDSQEDEWLSAAIDCSPLPDQMVVEISRSFPEQPDRTDLVK ELLFPAIGRYYSSREPLLNHLSDVHNGIARLLVNGKTEIALEAT QLLLKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNEMVVK RIFSKAIVDNKNLSKCKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\WK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD  5957  1479  451  ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKJIKNSKCPBGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE LESMSPSLDLVLRRTHLASDDLYKLSMKMPKALKSKKISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKLMELSQPLLFHCVLLKKRIIKHQSIQSFL  4AALGMLLWFPACQAFRNLDVEKLTIKHQSIGSFL AAALGMLLWFPACQAFRNLDVEKLTVSGPKGSYFGYAVDFHIPD ARTASVLVGAPRANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
VWKRCINIWRDVGLPGVLNEIANSEEVFEWVKTASGWALALCR WASSLHGSLPPHLSLRSEDLIABPAQVTNWSSCCLRVFAWHPHT NKFAVALLDDSVRVYNASSTIVPSLKHRLQRNVASLAWKPLSAS VLAVACQSCILIWTLDPTSLSTRPSSGCAQVLSHEGHTPVTSLA WAPSGGRLLSASPVDAAIRVMDVSTETCVPLPWFRGGGVTVNLLW SPDGSKILATTPSAVPRVWEAQMWTCERWPTLSGRCQTGCWSPD GSRLLFTVLGPPLIYSLSSPPERCGEGKG\ALBVQSQQRLWQICL RQQYRHQMVRRGLGERLTPWSGTPVGNVWLCL RQQYRHQMVRRGLGERLTPWSGTPVGNVWLCL S956 1705 139 GVGVVRGARRMATVQEKRAALNLSALHSPAHRPPGFSVAQKPFGA TYVWSSIINTLQTQVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNYYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKDKKPT FEDSSCSLYRPTTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKPANSPRVNISATLSPQVINEVWQEETIGRL LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSSYYLDRGILK AYSDSQEDEWLSAAIDCSEYLPDGMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPLINHLSDVHNGIARLLVNGKTEIALEAT QLLKKLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFI\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHRGD  5957 1479 451 ELQVAVAMDTLDRVVKPKTKRAXRFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVIYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPBGTKPMLIFRAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKTYFRSYKLLKKSGCRTPRIE LEEMSPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMGKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKLMELSQPLLFHCVLLKRIIKQSIQSFL  5958 1 3138 AAALGMLLWFPACQAFNLDVEKLTYVSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
WASSLHGSLPPHLSLRSEDLIAEFAQVTNWSSCCLRVFAWHPHT NKFAVALLDDSVRVYRASSTIVFSLKHRLQRNVASLAWKPLSAS VLAVACQSCILIWTLDPTSLSTRPSSGCAQVLSHPGHTPVTSLA WAPSGGRLLSASFVDAAIRVMDVSTETCVPLPWFRGGGVTNLLW SPDGSKILATTPSAVFRVWEAQMWTCERWFTLSGRQOTGVSPD GSRLLFTVIGPPLIYSISFPERGEGKG\ALEVQSQRLWQICL RQQYRHQMVRRGLGERITPWSGTPVGNVWLCL  5956  1705  139  GVGVRGARAMATVQEKAAALNLSALHSPAHRPPGFSVAQKFFGA TYVWSSIINTLQTQVEVKKRRRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVVRVCQALMDYKVFEAVPTKVFGKDKKPT FEDSSCSLYRFTIIPNODSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQUVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGILK AYSDSQEDEWLSAAIDCSEYLPDQMVVEISRSFFEQPDRTDLVK ELLFDAIGRYYSSREPLLNHLSDVHNGIARLLVNGKTEIALEAT QLLLKLLDFQNREEFFRLLYFMAVAANPSEKLQKESDNRMVVK RIFSKAIVDNKNLSKKKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCGRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGGFYKCHPDIFIEHFGD  5957  1479  451  ELQVAVAMDTLDRVVKPKTKRAKRFLEKEPEKNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLVKKKNITRFFEDOTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE LEEWSPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKPABRITEDHEKKS KRIKKLMELSQPLLFHCVLLKRIIKHQSIQSFL  5958  1 3138  AAALGMLLWFPACQAFNLDVEKLTVVSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
NKFAVALLDDSVRYYNASSTIVPSLKHRLQRNVASLAWKPLSAS VLAVACQSCILIWTLDFTSLSTRPSSGCAQVLSHPGHTPVTSLA WAPSGRLLSASPVDAAIRVWDVSTETCVPLPWFRGGGVTNLLW SPDGSKLLATTPSAVFRVWEAQMWTCERWFTLSGRCQTGCWSPD GSRLLFTVLGEPLIYSLSFPERCGEGKG\ALEVQSQQRLWQICL RQQYRHQMYRRGLGERLTPWSGTPVONVWLCL  5956  1705  139  GVGVRGARAMATVQEKAALNLSALHSPAHRPPGFSVAQKPFGA TYVWSSIINTLQTQVEVUKRRRIKKRHDCDFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKDKKPT FEDSSCSLYRFTTIPNQDSGLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTWVNSSNYLDRGILK AYSDSQEDWLSAAIDCSBYLPDQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPLLINHBDVHNGIARLLVNGKTETALEAT QLLLKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVFL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCORIDQRDYSNNTEKTTKDE LLNLKTLDEDSKLSAKEKKK\LLQFYKCHPDIFIEHFGD  5957  1479  451  ELQVAVAMDTLDRVVKPKTKRAKRFLEKRPFKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNILVIGRMYDTHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFGADDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKPPABRITEDHEKKS KRIKKLELSQPLLFTCVLLKRIIKHQSIQSFL  5958  1  3138  AAALGMLLWFPACQAFNLDVEGGAVYYCPWPAEGSAQCRQIPF
VLAVACQSCILIWTLDPTSLSTRPSSGCAQVLSHPGHTPVTSLA WAPSGGRLLSASPVDAAIRWDVSTETCVPLPHFREGGVTNLLW SPDGSKLLATTPSAVFRVWEAQMWTCERWPTLSGRCQTGCWSPD GSRLLFTVLGEPLIYSLSFPERCCEGKG\ALEVQSQQRLWQICL RQQYRHQMVRGLGERLTPWSGTPVGNVWLCL  S956  1705  139  GVGVRGARAMATVQEKAAAINLSALHSPAHRPPGFSVAQKPFGA TYVMSSIINTLQTQVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKDKKPT FEDSSCSLYRPTTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQLVDLPLLDSLLKQQEAVPKIPQFKRQSTMVNSSNYLDRGILK AYSDSQEDEWLSAAIDCSEYLPPQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPLLNHLSDVHNGIARLLVNGKTEIALEAT QLLLKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFI\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLKKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD  5957  1479  451  ELQVAVAMDTLDRVVKPKTKRAKFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKNNITRPFEDOTSLEFF SKKSDCSLEWFGSHNKKRPNILVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKTYFRSYKLLLKKSGCRTPRIE LSEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKLMELSQPLLFHCVLLKRIIKHQSIQSFL KRIKKLMELSQPLLFHCVLLKRIIKHQSIQSFL  5958  1 3138  AAALGMLLWFPACOAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
VLAVACQSCILIWTLDPTSLSTRPSSGCAQVLSHPGHTPVTSLA WAPSGGRLLSASPVDAAIRWDVSTETCVPLPHFREGGVTNLLW SPDGSKLLATTPSAVFRVWEAQMWTCERWPTLSGRCQTGCWSPD GSRLLFTVLGEPLIYSLSFPERCCEGKG\ALEVQSQQRLWQICL RQQYRHQMVRGLGERLTPWSGTPVGNVWLCL  S956  1705  139  GVGVRGARAMATVQEKAAAINLSALHSPAHRPPGFSVAQKPFGA TYVMSSIINTLQTQVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKDKKPT FEDSSCSLYRPTTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQLVDLPLLDSLLKQQEAVPKIPQFKRQSTMVNSSNYLDRGILK AYSDSQEDEWLSAAIDCSEYLPPQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPLLNHLSDVHNGIARLLVNGKTEIALEAT QLLLKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFI\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLKKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD  5957  1479  451  ELQVAVAMDTLDRVVKPKTKRAKFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKNNITRPFEDOTSLEFF SKKSDCSLEWFGSHNKKRPNILVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKTYFRSYKLLLKKSGCRTPRIE LSEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKLMELSQPLLFHCVLLKRIIKHQSIQSFL KRIKKLMELSQPLLFHCVLLKRIIKHQSIQSFL  5958  1 3138  AAALGMLLWFPACOAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
WAPSGRLLSAS PVDAAIRVMDVSTETCVPLPWFRGGGVTNLLW SPDGSKILATTPSAVFRVWEAQMMTCERMPTLSGRCQTGCWSPD GSRLLFTVLGEPLIYSLSFPERCGEGKG\ALEVQSQQRLWQICL RQQYRHQMVRRGLGERLTPWSGTPVGNVWLCL  5956 1705 139 GVGVRGARAMATVQEKAAALNLSALHSPAHRPPGFSVAQKPFGA TYVWSSIINTLQTQVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKDKKPT FEDSSCSLYRPTTIPNQDSQLGKENKLYSPARVADALFKSSDIR SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGILK AYSDSQEDEWLSAAIDCSBYLPPQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPLLNHLSDVHNGIARLLVNGKTEITALEAT QLLLKLLDFQNREEFFRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFI\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD  5957 1479 451 ELQVAVAMDTLDRVVKPKTKRAKFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLFWFGSHNKKRPNILVIGRMYDYHVLDMIELGIEBFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALINGKIYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL SAAALGMLLWFPACOAFNLDVEKLTVYSGFPGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
SPDGSKILATTPSAVFRVWEAQMWTCERWFTLSGRCQTGCWSPD GSRLIFTVLGEPLIYSLSFPERCGEGK ALBVQSQQRLWQICL RQQYRHQMVRRGLGERLTPWSGTPVGNVWLCL  5956 1705 139 GVGVRGARAMATVQEKAALNLSALHSPAHRPPGFSVAQKPFGA TYVWSSIINTLQTQVEVKKRHRLKRINDCFYGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKDKKPT FEDSSCSLYRFTTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGILK AYSDSQEDEMLSAAIDCSEYLPDQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPLLNHLSDVHNGIARLLVNGKTEIALEAT QLLLKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQDGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD  5957 1479 451 ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRAERITEDHEKKS KRIKKLMELSQPLLFHCVLLKRIIKHQSIQSFL FGTTYGRIHMQKQDLSKLQTRKM\KGLKKRAERITEDHEKKS KRIKKLMELSQPLLFHCVLLKRIIKHQSIQSFL SHIKKLMELSQPLLFHCVLLKRIIKHQSIQSFL ARALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
GSRLLFTVLGEPLIYSLSFPERCGEGKG\ALEVQSQQRLWQICL RQQYRMQMVRRGLGERLTPWSGTPVGNVWLCL SQTRMQMVRRGLGERLTPWSGTPVGNVWLCL GVGVRGARAMATVQEKAAALNLSALHSPAHRPPGFSVAQKPFGA TYVWSSIINTLQTQVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKDKKPT FEDSSCSLYRPTTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQLVDLPPLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGILK AYSDSQEDEWLSAAIDCSGYLPPDQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPLLNHLSDVHNGIARLLVNGKTEIALEAT QLLLKLLDFQNREEFRRLLYFMAVAANPSBFKLQKESDNRNVVK RIFSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD  5957 1479 451 ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITFPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCFBGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKKLMELSQPLLFFCVLLKRIIKHQSIQSFL  5958 1 3138 AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHTPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
RQQYRHQMVRRGLGERLTPWSGTPVGNVWLCL  5956  1705  139  GVGVRGARAMATVQEKAAALNLSALHSPAHRPPGFSVAQKPFGA TYVWSSIINTLQTQVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKDKKPT FEDSSCSLYRFTTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGILK AYSDSQEDEWLSAAIDCSEYLPDQMVVEISRSFFEQPDRTDLVK ELLFDAIGRYYSSREPLLNHLSDVHNGIARLLVNGKTEIALEAT QLLKKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKALVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD  5957  1479  451  ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTTKM\KGLKKRPABRITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL  5958  1  3138  AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
RQQYRHQMVRRGLGERLTPWSGTPVGNVWLCL  5956  1705  139  GVGVRGARAMATVQEKAAALNLSALHSPAHRPPGFSVAQKPFGA TYVWSSIINTLQTQVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKDKKPT FEDSSCSLYRFTTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGILK AYSDSQEDEWLSAAIDCSEYLPDQMVVEISRSFFEQPDRTDLVK ELLFDAIGRYYSSREPLLNHLSDVHNGIARLLVNGKTEIALEAT QLLKKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKALVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD  5957  1479  451  ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTTKM\KGLKKRPABRITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL  5958  1  3138  AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
S956 1705 139 GVGVRGARAMATVQEKAAALNLSALHSPAHRPPGFSVAQKPFGA TYVWSSIINTLQTQVEVKKRRHLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVYEAVPTKVFGKDKKPT FEDSSCSLYRFTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGILK AYSDSQEDEWLSAAIDCSEYLPDQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPLLNHLSDVHNGIAKLLVNGKTEIALEAT QLLLKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKAIVDNKNISKGKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD  5957 1479 451 ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLMENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL  5958 1 3138 AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
TYVWSSIINTLQTQVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKDKKPT FEDSSCSLYRFTTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQLVDLPLLDSLLKQQEAVPKIPQFKRQSTMVNSSNYLDRGILK AYSDSQEDEWLSAAIDCSEYLPPDQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPLLNHLSDVHNGIARLLVNGKTEIALEAT QLLLKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFI\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD  5957 1479 451 ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLNENIKNANLIK GGNANATTYKVLKDVYALKKPYGYLYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKTYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL S958 1 3138 AAALGMLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
IQNKYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKDKKPT FEDSSCSLYRPTTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGILK AYSDSQEDEWLSAAIDCSEYLPDQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPLLINHLSDVHNGIARLLVNGKTEIALEAT QLLLKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGGFYKCHPDIFIEHFGD  5957 1479 451 ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKTYFRSYKLLLKKSGCRTFRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKPABRITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL S958 1 3138 AAALGMLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
IQNKYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKDKKPT FEDSSCSLYRPTTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGILK AYSDSQEDEWLSAAIDCSEYLPDQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPLLINHLSDVHNGIARLLVNGKTEIALEAT QLLLKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGGFYKCHPDIFIEHFGD  5957 1479 451 ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKTYFRSYKLLLKKSGCRTFRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKPABRITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL S958 1 3138 AAALGMLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
FEDSSCSLYRFTTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMYNSSNYLDRGILK AYSDSQEDEWLSAAIDCSEYLPPQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPLLNHLSDVHNGIARLLVNGKTEIALEAT QLLLKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD  5957 1479 451 ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRFFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL S958 1 3138 AAALGMLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQLVDLPLLDSLLKQQEAVPKIPQFKRQSTMVNSSNYLDRGILK AYSDSQEDEWLSAAIDCSEYLPDOMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPLLNHLSDUHNGIARLLVNGKTEIALEAT QLLLKLLDFQNREEFFRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD  5957 1479 451 ELQVAVAMDTLDRVVKPKTKRAXRFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL 5958 1 3138 AAALGMLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGILK AYSDSQEDEWLSAAIDCSEYLPDQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPLINHLSDVHNGIARLLVNGKTEIALEAT QLLLKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD  5957 1479 451 ELQVAVAMDTLDRVVKPKTKRAXRFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE LEEMGPSLDVLRRTHLASDDLYKLSMKMPKAKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKPABRITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL  5958 1 3138 AAALGMLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
AYSDSQEDEWLSAAIDCSEYLPDQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPLLNHLSDVHNGIARLLVNGKTEIALEAT QLILKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD  5957 1479 451 ELQVAVAMDTLDRVVKPKTKRAKFFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKAKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKPABRITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
ELLFDAIGRYYSSREPLLNHLSDVHNGIARLLVNGKTEIALEAT QLLKKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFI\MDHQKDVFKIPGTI\HKI VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD  5957 1479 451 ELQVAVMDTLDRVVKPKTKRAKRFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVIYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKTYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKPABRITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIKHQSIQSFL  5958 1 3138 AAALGMLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
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GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKAKKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKPABRITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL S958 1 3138 AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALINGKTYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRTHLASDDLYKLSMKMPKALKPKKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL S958 1 3138 AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
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SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRTHLLASDDLYKLSMKMPKALKPKKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL S958 1 3138 AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
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DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP
LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP
EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA
NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ
ELVAGIPRGAONFGYVSIINSYDMTFIONFTGEQMASYFGYTVV
VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL
FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD
ORGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD
SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN
LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD
SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD
ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE
ABSTRACT AND A CONTRACT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF THE ASSESSMENT OF T
QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR
negegayeaelfvmipeeadyvgiernnkgfrplsceykmenvt
negegayeaelfvmipeeadyvgiernnkgfrplsceykmenvt

		Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted		(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	Glutamic Acid, Fernenylatanine, George inc,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	'	sequence	\=possible nucleotide insertion)
	sequence		
			EPHKEEBVGPLVEHIYELHNIGPSTISDTILEVGWPFSARDEFL
			LYIFHIQTLGPLQCQPNPNINPQDIKPAASPEDTPELSAFLRNS
•	į.		TIPHLVRKRDVHVVEFHRQSPAKILNCTNIECLQISCAVGRLEG
	1	1	GESAVLKVRSRLWAHTFLORKNDPYALASLVSFEVKKMPYTDQP
			AKLPEGSIAIKTSVIWATPNVSFSIPLWVIILAILLGLLVLAIL
			TLALWKCGFFDRARPPQEDMTDREQLTNDKTPEA
	ļ	ļ	
5959	1	1166	GTSGYAAQQLPSLLKEREFHLGTLNKVFASQWLNHRQVVCGTKC
			NTLFVVDVQTSQITKIPILKDREPGGVTQQGCGIHAIELNPSRT
		1	LLATGGDNPNSLAIYRLPTLDPVCVGDDGHKDWIFSIAWISDTM
			AVSGSRDGSMGLWEVTDDVLTKSDARHNVSRVPVYAHITHKALK
1	1		DIPKEDTNPDNCKVRALAFNNKNKELGAVSLDGYFHLWKAENTL
İ			SKLLSTKLPYCRENVCLAYGSEWSVYAVGSQAHVSFLDPRQPSY
1			
j	J	1	NVKSVCSRERGSGIRSVSFYEHIITVGTGQGSLLFYDIRAQRFL
			EERLSACYGSKPRLAGENLKLTTG\KGWLNHDETWRNYFSDIDF
<b>!</b>		1	FPNAVYTHCYDSSGTKLFVAGGPLPSGLHGNYAGLWS
5960	2853	870	FVWSDGGPRPRRGPAVGAGAAHLSDPWAMTPGTANRATNPLNKE
] 5,00	2033	1	LDWASINGFCEQLNEDFEGPPLATRLLAHKIQSPQEWEAIQALT
I		1	VLETCMKSCGKRFHDEVGKFRFLNELIKVVSPKYLGSRTSEKVK
l	ł	1	
		1	NKILELLYSWTVGLPEEVKIAEAYQMLKKQG\IVKSDPKLPDDT
l	1		TFPLPPPRPKNVIFEDEEKSKMLARLLKSSHPEDLRAANKLIKE
l			MVQEDQKRMEKISKRVNAIEEVNNNVKLLTEMVMSHSQGGAAAG
i	· I		SSEDL\MKEL\YQRCERMRPTLFPTGRVDTEDND\EALAEILQA
		ļ	NDNLTOVINLYKOLVRGEEVNGDATAGSIPGSTSALLDLSGLDL
1	1		PPAGTTYPAMPTRPGEQASPEQPSASVSLLDDELMSLGLSDPTP
1	i	1	PSGPSLDGTGWNSFQSSDATEPPAPALAQAPSMESRPPAQTSLP
ł	ì	1	ASSGLDDLDLLGKTLLQQSLPPESQQVRWEKQQPTPRLTLRDLQ
l .	1		NKSSSCSSPSSSATSLLHTVSPEPPRPPQQPVPTELSLASITVP
1			LESIKPSNILPVTVYDQHGFRILFHFARDPLPGRSDVLVVVVSM
ŀ	1	1	LSTAPOPIRNIVFQSAVPKVMKVKLQPPSGTELPAFNPIVHPSA
i	j		ITOVLLLANPOKEKVRLRYKLTPTMGDQTYNEMGDVDQFPPPET
	1		WGSL
5961	198	3147	SGEPRPEPGNMATCIGEKIEDFKVGNLLGKGSFAGVYRAESIHT
ł			GLEVAIKMIDKKAMYKAGMVQRVQNEVKIHCQLKHPSILELYNY
1	ļ	i	FEDSNYVYLVLEMCHNGEMNRYLKNRVKPFSENEARHFMHQIIT
	1	1	GMLYLHSHGILHRDLTLSNLLLTRNMNIKIADFGLATQLKMPHE
1	}	]	KHYTLCGTPNYISPEIATRSAHGLESDVWSLGCMFYTLLIGRPP
			FDTDTVKNTLNKVVLADYEMPTFLSIEAKDLIHQLLRRNPADRL
1	i	(	
1	i		SLSSVLDHPFMSRNSSTKSKDLGTVEDSIDSGHATISTAITASS
1			STSISGSLFDKRRLLIGQPLPNKMTVFPKNKSSTDFSSSGDGNS
	100	1	FYTQWGNQETSNSGRGRVIQDAEERPHSRYLRRAYSSDRSGTSN
1		į	SQSQAKTYTMERCHSAEMLSVSKRSGGGENEERYSPTDNNANIF
1	1	<b>+</b>	NFFKEKTSSSSGSFERPDNNQALSNHLCPGKTPFPFADPTPQTE
i	1		TVQQWFGNLQINAHLRKTTEYDSISPNRDFQGHPDLQKDTSKNA
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	}	1	WTDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPEIIQQECVF
	1	1	GSDPLSEQSKTRGMEPPWGYQNRTLRSITSPLVAHRLKPIRQKT
1			KKAVVSILDSEEVCVELVKEYASQEYVKEVLQISSDGNTITIYY
	1		PNGG\RGFPLA\DRPPSPT\DNISR\YSF\DNLPEKYWRKYQYA
	1	1	SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVWFYDGVKI
i	1		HKTEDFIQVIEKTGKSYTLKSESEVNSLKEEIKMYMDHANBGHR
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			ICLALESIISEEERKTRSAPFFPIIIGRKPGSTSSPKALSPPPS
			VDSNYPTRDRASFNRMVMHSAASPTQAPILNPSMVTNEGLGLTT
			TASGTDISSNSLKDCLPKSAQLLKSVFVKNVGWATQ\LTSGAVW
1			VQFNDGSQLVVQAGVSSISYTSPNGQ\TTR\YGENEKLPDYIKQ
			KLOCLSSILLMFSNPTPNFH
5962	20	2447	RVCSSSASTASQAVMADAWEEIRRLAADFQRAQFAEATQRLSER
1			NCIEIVNKLIAQKQLEVVHTLDGKEYITPAQISKEMRDELHVRG
1			GRVNIVDLQQVINVDLIHIENRIGDIIKSEKHVQLVLGQLIDEN
1	)	1	YLDRLAEEVNDKLQESGQVTISELCKTYDLPGNFLTQALTQRLG
1			RIISGHIDLDNRGVIFTEAFVARHKARIRGLFSAITRPTAVNSL
	]		ISKYGFQEQLLYSVLEELVNSGRLRGTVVGGRQDKAVFVPDIYS
1	1	i	RTQSTWVDSFFRQNGYLEFDALSRLGIPDAVSYIKKRYKTTQLL
ŀ			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
I D	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1 1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
		Beduence	Codon, /=possible nucleotide delection,
	sequence		\=possible nucleotide insertion)
1 1			PLKAACVGQGLVDQVEASVEEAISSGTWVDIAPLLPTSLSVEDA
1			AILLQQVMRAFSKQASTVVFSDTVVVSEKF\INDCTELFRELMH
1 1			QKAEKEMKNNPVHLITEEDLKQISTLESVSTSKKDKKDERRRKA
1 1			TEGSGSMRGGGGGNAREYKIKKVKKKGRKDDDSDDESQSSHTGK
			KKPEISFMFQDEIEDFLRKHIQDAPEEFISELAEYLIKPLNKTY
			LEVVRSVFMSSTTSASGTGRKRTIKDLQEEVSNLYNNIRLFEKG
1 1			MKFFADDTQAALTKHLLKSVCTDITNLIFNFLASDLMMAVDDPA
1 1			AITSEIRKKILSKLSEETKVALTKLHNSLNEKSIEDFISCLDSA
1 1		}	AEACDIMVKRGDKKRERQILFOHROALAEQLKVTEDPALILHLT
1 1			SVLLFQFSTHSMLHAPGRCVPQIIAFLNSKIPEDQHALLVKYQG
1 1			LVVKQLVSQSKKTGQGDYPLNNELDKEQEDVASTTRKELQELSS
; [			SIKDLVLKSRKSSVTER
5963	62	1130	PWNPQDFPGNRGLMG\QKGEIGPP\GQQGKKGAPGMP\GLMGSN
3303	₩.	1130	
1 1			GSPGQPGTPGSKGSKGEPGIQGMPGASGLKGEPGATGSPGEPGY
		,	MGLPGIQGKKGDKGNQGEKGIQGQKGENGRQGIPGQQGIQGHHG
<b>l</b>			AKGERGEKGEPGVRGAIGSKGESGVDGLMGPAGPKGQPGDPGPQ
1			GPPGLDGKPGREFSEQFIRQVCTDVIRAQLPVLLQSGRIRNCDH
1			CLSQHGSPGIPGPPGPIGPEGPRGLPGLPGRDGVPGLVGVPGRP
i 1			GVRGLKGLPGRNGEKGSQGFGYPGEQGPPGPPGPEGPPGISKEG
1 1			PPGDPGLPGKDGDHGKPGIQGQPGPPGICDPSLCFSVIARRDPF
			RKGPNY
5964	3	2147	SCRTRGRLSPLQPREAGSSRGSRARSEPPRPGGMEEACQVQTTK
1			RGDPHELRNIFLQYASTEVDGERYMTPEDFVQRYLGLYNDPNSN
1			PKIVQLLAGVADQTKDGLISYQEFLAFESVLCAPDSMFIVAFOL
			FDKSGNGEVTFENVKEIFGQTIIHHHIPFNWDCEFIRLHFGHNR
1			KKHLNYTEFTQFLQELQLEHARQAFALKDKSKSGMISGLDFSDI
l i			MVTIRSHMLTPFVEENLVSAAGGSISHQVSFSYFNAFNSLLNNM
1			ELVRKIYSTLAGTRKDAEVTKEEFAQSAIRYGQATPLEIDILYQ
1			LADLYNASGRLTLADIERIAPLAEGALPYNLAELOROOSPGLGR
1			PIWLQIAESAYRFTLGSVAGAVGATAVYPIDLVKTRMONORGSG
1 1			SVVGELMYKNSFDCFKKVLRYEGFFGLYRGLIPQLIGVAPEKAI
l i			KLTVNDFVRDKFTRRDGSVPLPAEVLAGGCAGGSQVIFTNPLEI
			VKIRLQVAGEITTGPRVSALNVLRDLGIFGLYKGAKACFLRDIP
1			FSAIYFPVYAHCKLLLADENGHVGGLNLLAAGAMAG\VPAASLV
1 1			
1			TPADVIKTRLQVAARAGQTTYSGVIDCFRKIL\REEGPSAFWKG
1 1			TAARVFRSSPQFG\VTLVTYELLQRGFYIDFGGLKPAGSEPTPK
1			SRIADLPPANPDHIGGYRLATATFAGIENKFGLYLPKFKSPSVA
			VVQPKAAVAATQ
5965	1	1498	MVTWLYRFLPTSNMAAKLRSLLPPDLRLQFWLHARLQKCFLSRG
1			CGSYCAGAKASPLPGKMAMGLMCGRRELLRLLQSGRRVHSVAGP
1			SQWLGKPLTTRLLFPAAPCCCRPHYLFLAASGPRSLSTSAISFA
1			EVQVQAPPVVAATPSPTAVPEVASGETADVVQTAAEQSFAELGL
1			GSYTPVGLIQNLLEFMHVDLGLPWWGAIAACTVFARCLIFPLIV
			TGQREAARIHNHLPEIQKFSSRIREAKLAGDHIEYYKASSEMAL
1			YQKKHGIKLYKPLILPVTQAPIFISFFIALREMANLPVPSLQTG
			GLWWFQDLTVSDPIYILPLAVTATMWAVLELGAETGVQSSDLQW
1			MRNVIRMMPLITLPITMHFPTAVFMYWLSSNLFSLVQVSCLRIP
1 1			AVRTVLKIPORVVHDLDKLPPREGFLESFKKGWKNAEMTROLRE
1			REQRMRNQLELAARGPLRQTFTHNPLLQPGKDNPPNIPSS\SSS
			SSKPKSKYPWHDTLG
5966	102	1925	
3500	102	1925	RSKQVMARLTKRRQADTKAIQHLWAAIEIIRNQKQIANIDRITK
] ]			YMSRVHGMHPKETTRQLSLAVKDGLIVETLTVGCKGSKAGIEQE
1			GYWLPGDEIDWETENHDWYCFBCHLPGEVLICDLCFRVYHSKCL
1 1			SDEFRLRDSSSPWQCPVCRSIKKKNTNKQEMGTYLRFIVSRMKE
			RAIDLNKKGKDNKHPMYRRLVHSAVDVPTIQEKVNEGKYRSYEE
1			FKADAQLLLHNTVIFYGADSEQADIARMLYKDTCHEL\DELQLC
]			KNCFYLANARPDNWFCYPCIPNHELDWAKMKGFGFWPAKVMQKE
1 1			DNQVDVRFFGHHHQRAWIPSENIQDITVNIHRLHVKRSMGWKKA
1			CDELELHQRFLREGRFWKSKNEDRGEEEAESSISSTSNEQLKVT
			CEPRAKKGRRNQSVEPKKEEPEPETEAVSSSOEIPTMPOPIEKV
			CEPRAKKGRRNQSVEPKKEEPEPETEAVSSSQEIPTMPQPIEKV SVSTQTKKLSASSPRMLHRSTQTTNDGVCQSMCHDKYTKIFNDF

Deginning   nuclectide   location   cortesponding   to first   anino acid   residue of   residue of   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   anino acid   residue of   anino acid   anino acid   residue of   anino acid   residue of   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Notation   location   corresponding   to first   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   s	_			(A-Alanina C-Cystaina D-Assault Asid E
location   corresponding   to first   amino acid   amino acid   casidue of   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amin			-	Clubaria Acid E-Dhanel-lander C Clubaria
to first amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid am	Mo.			U-Wighiding T Including W Israel
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amino acid residue of amino acid sequence codon, /=possible nucleotide deletion Northypophan, Y=yfyrosine, X=uknkovm, *=stop Codon, /=possible nucleotide deletion Northypophan, Y=yfyrosine, X=uknkovm, *=stop EMDRKCKOVERKCEEPEVERIAIDULSTOKKOVENOV EERAMYHCCMITSYCSIKCOCDHWIAERKHTCRER SROWMARAITKERGADTHACHGUMANATEI ITBROKGTANIORITK YMSKUHGHDEKETTROLSLAVEDGLIVSTITUTGCKOSKAGIEGE GYHLPOED INDETENBUNGPEPCKLEGOVILTOLLCEPTYVISTOK ERAMYHCCMITSYCSIKCOCDHWIAERKHTCRER RADIAINKAGKONKHEPTRACHGUMANATEI TURGKOTANIORITK YMSKUHGHDEKETTROLSLAVEDGLIVSTITUTGCKOSKAGIEGE GYHLPOED INDETENBUNGPEPCKLEGOVILTOLLCEPTYVISTOK ERAMYHCCMITSYCSIKCOCDHWIAERKHTCRER RADIAINKAGKONKHEPTRACHGUMANATEI TURGKOTANIORITK YMSKUHGHDEKETTROLSLAVEDGLIVSTITUTGCKOSKAGIEGE GYHLPOED INDETENBUNGPEPCKLEGOVILTOLLCEPTYVISTOK ERADAGLLLHINTUTFYGADSGADIARHLYKOTCHELIDELGU NGCPULANARPDHMCTGCPERMELDWARMGGFGFPAAVKHKKA CDELLANGEPIRGCREWERVESADVETTUTGCKOSKAGATEGE ERAMYHCCMITSYSTOKOCHOCHTUTTYFGADSGADIARHLYKOTCHELIDELGU NGCPULANARPDHMCTGCPENTHELDWARMGGFGFPAAVKHKKA CDELLANGEPIRGCREWERVESADVETTYFTOKOCHOCHTUTTYFGADSGADIARHLYKOTCHELIDELGU NGCPULANARPDHMCTGCPENTHELDWARMAGGFGFPAAVKHKKA CDELLANGEPIRGCREWERVERADERGAVKAVANNOG GEMARKCKURASSGANERNENTOTTOMOCHOCHCENTYRT HOURS SANTOTKKASSGANERNENTYTOMOCHOCHCENTYRT HOURS SANTOTKKASSGANERNENTYTOMOCHOCHCENTYRT HOURS SANTOTKKASSGANERNENTYTOMOCHOCHCENTYRT HOURS EMAMTACCHTUTTYFGADSGADIARHLYKOTCHCH ERAMYHCCMITSYCSIKCOCHOCHCHTUTTYRGKAGADATA VERPENGANTAGANARANARA SANTOTHACHACHACHACHACHACHACHACHACHACHACHACHACH				
reaidue of amino acid sequence  ##Tryptophan, Y=Tyrosine, X=Unknown, *=stop codon, deposible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide insertion)  ### MORKCROVERCREFVEIRILATORIKOLISOTEKKOMCYNE EMDRKCROVERCREFVEIRILATORIKOLISOTEKKOMCYNE EMDRKCROVERCREFVEIRILATORIKOLISOTEKKOMCYNE EEAWHYDCHONTSYSCIS LAVOCALUSTITYOCKOSKAGIEGE GYMLPOBEIDMETENBOWCPECLLEGEVILIOLICERYTYISCK SEAGHIGE GYMLPOBEIDMETENBOWCPECLLEGEVILIOLICERYTYISCK SEAGHIGE GYMLPOBEIDMETENBOWCPECLLEGEVILIOLICERYTYISCK SEAGHIGE GYMLPOBEIDMETENBOWCPECLLEGEVILIOLICERYTYISCK SEAGHIGE GYMLPOBEIDMETENBOWCPECLLEGEVILIOLICERYTYISCK SEAGHIGE GYMLPOBEIDMETENBOWCPECLLEGEVILIOLICERYTYISCK SEAGHIGE GYMLPOBEIDMETENBOWCPECLLEGEVILIOLICERYTYISCKE RAIDLAKKGKONKHPWERILVESAVOVETIGEKNOBERYSSYEE FRADAQLLIANTIVITYEOLISCKENGTYSEVEE FRADAQLLIANTIVITYEOLISCKENGTYSEVEE FRADAQLIANTIVITYEOLISCKENGTYSEVEE FRADAQLIANTIVITYEOLISCKENGTYSEVEE FRADAGLIANTIVITYEOLISCHENGTYSEVEE FRADAGLIANTIVITYEOLISCHENGTYSEVEE FRADAGLIANTIVITYEOLISCHENGTYSEVEE FRADAGLIANTIVITYEOLISCHENGTYSEVEE FRADAGLIANTIVITYEOLISCHENGTYSEVEE FRADAGLIANTIVITYEOLISCHENGTYSEVEE FRADAGLIANTIVITYEOLISCHENGTYSEVEE FRADAGLIANTIVITYEOLISCHENGTYSEVEE FRADAGLIANTIVITYEOLISCHENGTYSEVEE FRADAGLIANTIVITYEOLISCHENGTYSEVEE FRADAGLIANTIVITYEOLISCHENGTYSEVEE FRADAGLIANTIVITYEOLISCHENGTYSEVEE FRADAGLIANTIVITYEOLISCHENGTYSEVEE FRADAGLIANTIVITYEOLISCHENGTYSEVE FRADAGLIANTIVITYEOLISCHENGTYSEVE FRADAGRIANTIVITYEOLISCHENGTYSEVE FRADAGRIANTIVITYEOLISCHENGTYSEVE FRADAGRIANTIVITYEOLISCHENGTYSEVE FRADAGRIANTIVITYEOLISCHENGTYSE FRADAGRIANTIVITYEOLISCHENGTYSE FRADAGRIANTIVITYEOLISCHENGT FRADAGRIANTIVITYEOLISCHENGT FRADAGRIANTIVITYEOLISCHENGT FRADAGRIANTIVITYEOLISCHENGT FRADAGRIANTIVITYEOLISCHENGT FRADAGRIANTIVITYEOLISCHENGT FRADAGRIANTIVITYEOLISCHENGT FRADAGRIANTIVITYEOLISCHENGT FRADAGRIANTIVITYEOLISCHENGT FRADAGRIANTIVITYEOLISCHENGT FRADAGRIANTIVITYEOLISCHENGT FRADAGRIANTIVITYEOLISCHENGT FRADAGRIANTIVITYEOLISCHENGT FRADAGRIANTIVITYEOLISCHENGT FRADAGRIANTIVITYEOLISCHENGT FRADAGRIANTIVIT	İ			
amino acid sequence    Codon, /=possible nucleotide deletion,	1			S=Serine, T=Threonine, V=Valine,
Sequence   Veposable nucleotide insertion		I .	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
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ENNLPWSYVPYVILPCBEIFMKKHYKREKPLQPVWSGYPOPKL  LEHRPTOLLTIPPWLLDIVSGTYPNEBLIGHIYQPLNLTIGYTV FAVGN/HFLESAEEFFMRGYRVHYYIFTDNPAMYPGVPLGPHRL LSSIPIQGHSHWEETSMRARETISGHIAKRAHREVDYLFCLUVD MYFRNPWGPETIGGUVAAIHESYTAVPRQOFFYERRKYSTAFVA DSEGDFYYGGAVFGGOVARVYEFTRGCHAAILADKANGIMAARR EESHLMRHFISNKPSKVLSPPYLMDDRKPQPPSLKLIRFSTLDK DISCLRS  5969 1126 503 DVGFNIKRKCDLDVFLESPRKPSGRRDAAPEKQRTIAANKCLC TGVREGEPPS/TTSGKVKEAGRDFTYLIVVLEGISITGGFYTI FKSLFSSSSPSKIYGRALEKCRSHPEVIGVFGESVKGYGFVTRR GRRQHVRFTEYVKDGLKHTCVKFYYEGSPGKOGTGVAQVKENP GSGSVDFRYIFVEISYPRRTIIEDNRSQDD  5970 316 4712 SQDNIGHRLLGKHGWKLGQGIGKSLGGRTDFIFVWYDVMGMG RMMELDVAEDATERRVLEWEEDTELRGKYKDYVMSKATA KALEDLRANFYCELCDKQYGKHQEFDNHINSYDHAHKQRLKDLK QREFARNVSSRSRKDEKKQEKALRALHHLBAGRKQAECAFGSGP MFKPTTVAVDEEGGEDDKDESATNSGTGATASCGLGSFSTDKG GPFTAVQIINTTGLAQAPGLASGGISFGIKNLGTPLQKLGSVF SFAKKAPVKLSSIASVKOHAEBGTEEDGTKPDEKSSDQLGKV GDSGSSSNLDGKKEDEDPQDGGSLASTLSKLKRMKREEGAGATE PEYYHYIPPAHCKVKNFFPLLFMRASSQMDODNTTHPKNAPES KKGSSFKYSCIKAAASQGAEKTVSSGGKNEDFOKTSNSKRTSLATPA GKSSGGSKHFTGGTPFVLSKUSSTSNSKRTSLATPA GKSSGGEKHFTGFPFPVLSKUSSTALQWPSELLIFTKAAPFSIS SYSCNPLYFDFKLSRNKDARTKGTEKPKDIGSSSKOHLQGLDFGE PNKSKEVGGBKIVRSSGGRNAPASGSACSGLNQEFGGSHAB GKSSGGSFKFSCIKAASAGGAEKTVSSGGRNAPASGSACSGLNQEFGGSHAB FPRRRRAQDDSQTSLESHSGVSETQMCSSISKSKHSLATPA GKSSGGEKFFKTCIKAAASGAGEKTVSSGRNAPASGSACSGLNQEFGGSHAB FPRRRRAQDDSQTSLESHSGVSETQMCSGSSKODHOGGRIH KGELPPSSCGRRAGTKRSSRSHRRSKRSKRSKRSSSSSSSSSSSSSSSSSSSSS	3,000	"	1200	PDVGVCTCAOACETVDTPGRQQGVFTGPQRPGSEPDTPARGQPRPP
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RMMELDYAEDATERRVLEVEKEDTEELRQKYKDYVDKEKAIA KALEDLRANFYCELCDKQYQKHQEFDNHINSYDHAHKQRLKDLK QREFARRVSSRSRKDEKKQEKALRRIHELAEQRKQAECAPGSGP MFKPTTVAVDEEGGEDDKDESATNSGTGATASCGLGSEFSTDKG GPFTAVQITNTTGLAQAPGLASQGISFGIKNNLGTPLQKLGVSF SFAKKAPVKLESIASVFKDHAEEGTSEDGTKPDEKSSDQGLQKV GDSDGSSNLDGKKEDEDPQDGGSLASTLSKLKRMKREEGAGATE PEYYHYIPPAHCKVKPNFPFLLFMRASEQMDGDNTTHPKNAPES KKGSSPKPKSCIKAAASQGAEKTVSEVSEQPKETSMTEPSEPGS KAEAKKALGGDVSDQSLESHSQKVSETQMCESNSSKETSLATPA GKESQEGFKHPTGPFFPVLSKDESTALQWPSELLIFTKAEPSIS YSCNPLYFDFKLSRNKDARTKGTEKPKDIGSSSKDHLQGLDPGE PNKSKEVGGEKIVRSSGGRMDAPASGSACSGLNKQEPGGSHGSE TEDTGRSLPSKKERSGKSHRHKKKKKKKSKHKKHKADTEEK SSKAESGEKSKKRKKKRKKKKKKSAPADSRGPKEPPGGSGPA PPRRRRAQDDSQRRSLPAEGSSGKKDEGGGSSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSSHRSQPSSCDEDSDDASSHRLHQ KSPSQYSEEEEEDSGSEHSRSRSSRSRRHSKRSKRSYSSSS DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHDSDDSDYAS SKHRSKHKYSSSDDDYSLGSQSRSRSRSHTRERSRSRGRSRS SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGR KKSWGHESPEERHSGRRDFIRSKIVRSQSSHYRRSGRGFGFGFKK MCSWGHESPEERHSGRRDFIRSKIVRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPGGYFGFKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEGQEGSETEEGPP GSSDALFGHOPF) SEETTGFLLDPPPEESKSGBVTADHPVAPLG	5070	336	4732	
KALEDLRANFYCELCDKQYQKHQEFDNHINSYDHAHKQRLKDLK QREFARNVSSRSRKDEKKQEKALRRIHBILAEQRKQAECAPGSGP MFKPTTVAVDEEGGEDDKDESATNSGTGATASCGLGSEFSTDKG GFPTAVQITNTTGLAQAPGLASQGISFGIKNNLGTPLQKLGVSF SFAKKAPVKLESIASVFKDHAEEGTSEDGTKPDEKSSDQGLQKV GDSDGSSNLDGKKEDEDPQDGGSLASTLSKLKRMKREEGAGATE PEYYHYIPPAHCKVKPNFPFLLFMRASEQMDGDNTTHPKNAPES KKGSSPKPKSCIKAAASQGAEKTVSEVSEQPKETSMTEPSEPGS KAEAKKALGGDVSDQSLESHSQKVSETQMCESNSSKETSLATPA GKESQEGFKHPTGPFFPVLSKDBSTALQMPSELLIFTKAEPSIS YSCNPLYFDFKLSRNKDARTKGTEKPDIGSSSKDHLQGLDPGE PNKSKEVGGEK IVRSSGGRMDAPASGSACSGLNKQEPGGSHGSE TEDTGRSLPSKKERSGKSHRHKKKKHKKSSHKRKHKADTEEK SSKAESGEKSKKKKKKRKKKKKKKKKKKKKKHKADTEEK SSKAESGEKSKKKKKKRKKKKSAPADSERGPKPEPPGSGSPA PPRRRRAQDDSQRRSIPAEEGSGKNDEGGGSSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSSGKSDEDSDDASSHRLHQ KSPSQYSEEEEEEDSGEHSRSRSGRRHSSKRSSSSSS DASSDQSCYSRQRSYSDDSYDYSDRSRRHSKRSHDSDDSDYAS SKHRSKRKKYSSSDDDYSLSCSQSRSRSRSHTHERSRSGRSRS SSCSRSSKRRSRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGR KSSWGHESPEERHSGRRDFIRSKIYRSQSPHYPRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEGEGEGEFPP GSSDALFGHOPP\SEETTGPLLDPPPEESKSGBVTADHPVAPLG PPAHFDCYLGDPTISHNYLPPDSDGNTLESLDSSSGPOPVESSL	39,0	316	4/12	
QREFARNVSSRSRKDEKKQEKALRRLHBLAEQRKQAECAPGSGP MFKPTTVAVDEEGGEDDKDESATNSGTGATASCGLGSEFSTDKG GPFTAVQITNTTGLAQAPGLASQGISFGIKNNLGTPLQKLGVSF SFAKKAPVKLESIASVFKDHAEEGTSEDGTKPDEKSSDQGLQKV GDSDGSSNLDGKKEDEDPQDGGGLASTLSKLKRMKREEGAGATE PEYYHYIPPAHCKVKPNFPFLLFMRASEQMDGDNTTHPKNAPES KKGSSPKPKSCIKAAASQGAEKTVSEVSEQPKETSMTEPSEPGS KAEAKKALGGDVSDQSLESHSQKVSETQMCESNSSKETSLATPA GKESQEGFKHPTGPFFPVLSKDBSTALQWPSELLIFTKAEPSIS YSCNPLYFDFKLSRNKDARTKGTEKPKDIGSSSKDHLQGLDPGE PNKSKEVGGEKIVRSSGGMDAPASGSACSGLNKQEPGGSHGSE TEDTGRSLPSKKERSGKSHRHKKKKKKHKKSSKHKKKHKADTEEK SSKAESGEKSKKKKKKKKKKKKKKKSAPADSERGPKPEPPGSGSPA PPRRRRAQDDSQRSSLPAEEGSGKNDEGGGGSSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDSDDASSHRLHQ KSPSQYSEEEEEDSGSEHSRSRSRSGRRHSKRSSRSSSS DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHDSDDSDYAS SKHRSKRHKYSSSDDDYSLSCSQSRSRSRSHTRERSRRSRSS SSCSRSKKRRSRSTTAHSWQRSRSYSRDRSRSTTSPSQRSGR KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKLQSRKVERKPSVSEEVQATENKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEEGEQESETEEGPP GSSDALFGHOFP\SEETIGPLLDPPPEESKSGRVTADHPVAPLG PPAHFDCYLGDPTISHNYLPPDSDGNTLESLDSSSQPGVESSL				
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SFAKKAPVKLESIASVFKDHAEEGTSEDGTKPDEKSSDQGLQKV GDSDGSSNLDGKKEDEDPQDGGSLASTLSKLKRMKREEGAGATE PEYYHYIPPAHCKVKPNFPFLLFMRASEQMDGDNTTHPKNAPES KKGSSPKPKSCIKAAASQGAEKTVSEVSEQPKETSMTEPSEPGS KAEAKKALGGDVSDQSLESHSQKVSETQMCESNSSKETSLATPA GKESQEGPKHPTGPFFPVLSKDESTALQWPSELLIFTKAEPSIS YSCNPLYFDFKLSRNKDARTKGTEKPKDIGSSSKDHLQGLDPGE PNKSKEVGGEKIVRSSGGMDAPASGSACSGLNKQEPGGSHGSE TEDTGRSLPSKKERSGKSHRHKKKKKHKSSKHKRKHKADTEEK SSKAESGEKSKKRKKRKKKKNKSSAPADSERGPKPEPPGSGSPA PPRRRRAQDDSQRRSLPAEEGSSGKKDEGGGSSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSSRSQPSSGDEDSDDASSHRLHQ KSPSQYSEEEEEEDSGSHSRSRSRSGRRHSSHRSSRSYSSSS DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHDSDDSDYAS SKHRSKRHKYSSSDDDYSLSCSQSRSRSRSHTRERSRSRGRSRS SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGR KRSWGHESPEERHSGRDFIRSKTYRSQSPHYPRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTALLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEEQQSETEEGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGEVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL	1			
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KAEAKKALGGDVSDQSLESHSQKVSETQMCESNSSKETSLATPA GKESQEGFKHPTGPFFPVLSKDESTALQWPSELLIFTKAEPSIS YSCNPLYFDFKLSRNKDAFKGTEKPKDIGSSSKDHLQGLDPGE PNKSKEVGGEKIVRSSGGRMDAPASGSACSGLNKQEPGGSHGSE TEDTGRSLPSKKERSGKSHRHKKKKKHKKSSKHKRKHKADTEEK SSKAESGEKSKKRKRKKKKKSSAPADSERGPKPEPPGSGSPA PPRRRRAQDDSQRRSLPAEGSSGKKDEGGGGSSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDDDASSHRLHQ KSPSQYSEEEEEEDGSEHSRSRRSGRHSSKRSSRSYSSSS DASSDQSCYSRQRSYSDDBYSDYSDRSRRHSKRSKRSYSSSS SKHSKRHKYSSSDDDYSLSCSQSRSRSRSHTKERSRRGRSS SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATKFNKKCEESGLERGEEQGSETEEGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGRVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL	1			PEYYHYIPPAHCKVKPNFPFLLFMRASEQMDGDNTTHPKNAPES
KAEAKKALGGDVSDQSLESHSQKVSETQMCESNSSKETSLATPA GKESQEGPKHPTGPFFPVLSKDESTALQWPSELLIFTKAEPSIS YSCNPLYFDFKLSRNKDAFKGTEKPKDIGSSSKDHLQGLDPGE PNKSKEVGGEKIVRSSGGMDAPASGSACSGLNKQEPGGSHGSE TEDTGRSLPSKKERSGKSHRHKKKKHKKSSKHKRKHKADTEEK SSKAESGEKSKKRKKRKKKKKSSAPADSERGPKPEPPGSGSPA PPRRRRAQDDSQRRSLPAEGSSGKKDEGGGGSSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDDDASSHRLHQ KSPSQYSEEEEEEDSGSEHSRSRSRSGRRHSSKRSSRSSSSS DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHDSDDSPYAS SKHRSKRHKYSSSDDDYSLSCSQSRSRSRSHTHERSRSRGRSS SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEBQEGSETEEGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGRVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL	1			KKGSSPKPKSCIKAAASQGAEKTVSEVSEQPKETSMTEPSEPGS
GKESQEGKHPTGPFFPVLSKDESTALQWPSELLIFTKAEPSIS YSCNPLYFDFKLSRNKDARTKGTEKPKDIGSSSKDHLQGLDPGE PNKSKEVGGEKIVRSSGGRMDAPASGSACSGLNKQEPGGSHGSE TEDTGRSLPSKKERSGKSHRHKKKKKKKSSKHKRKHKADTEEK SSKAESGEKSKKRKRKKKKNSSAPADSERGPKPEPPGSGSPA PPRRRRAQDDSQRRSLPAEGSSGKKDEGGGGSSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSSHRSQPSSCDEDSDDASSHRLHQ KSPSQYSEEEEEDSGSEHSRSRSRSGRSHSSKRSYSSSS DASSDQSCYSRQRSYSDDSYSDRSRRHSKRSSRSYSSSS SKHSKRHKYSSSDDDYSLSCSQSRSRSRSHTRERSRSRGRSS SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRTTRSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPSKLKDPPQYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEBQEGSETEEGPP GSSDALFGHQFF\SEETTGPLLDPPPEESKSGRVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL	1	ĺ	1	
YSCNPLYFDFKLSRNKDARTKGTEKPKDIGSSSKDHLQGLDPGE PNKSKEVGGEKIVRSSGGMDAPASGSACSGLNKQEPGSHGSE TEDTGRSLFSKKERSGKSHRHKKKKHKKSSKHKRKHKADTEEK SSKAESGEKSKKRKKKKKKKKSAPADSERGPKPEPPGSGSPA PPRRRRAQDDSQRRSLPAEGSSGKKDEGGGSSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDSDASSHRLHQ KSPSQYSEEEEEEDSGEHSRSRSRSGRRHSSKRSSRSSSS DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHDSDDSDYAS SKHRSKRHKYSSSDDDYSLSCSQSRSRSHSKRSHRSRSRSRS SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKTYRSQSPHYPRSGRGEGFGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATKKPNKKCEESGLERGEEQQSETEEGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGEVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL	1			
PNKSKEVGGEKIVRSSGGMDAPASGSACSGLNKQEPGGSHGSE TEDTGRSLFSKKERSGKSHRHKKKKHKKSSKHKRKHKADTEEK SSKAESGEKSKKRKKKKKKKKKKKHKKSSKHKRKHKADTEEK SSKAESGEKSKKRKKKKKKKKKKKSKAPADSERGPKPEPPGSGSPA PPRRRRAQDDSQRRSLPAEGSSGKKDEGGGSSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDSDDASSHRLHQ KSPSQYSEEEEEEDSGSEHSRSRSRSGRRHSSKRSYSSSS DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHDSDDSDYAS SKHRSKRHKYSSSDDDYSLSCSQSRSRSRSHTRERSRSRGRSRS SKHRSKRHKYSSSDDDYSLSCSQSRSRSRSHTRERSRSRGRSRS SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKTYRSQSPHYPRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEEQQSETEEGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGRVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL	i			
TEDTGRSLPSKKERSGKSHRHKKKKKKKKKKKKKKKADTEEK SSKAESGEKSKKRKKKKKKKKKKKKKKKKKKKKKKKKADTEEK SSKAESGEKSKKRKKKKKKKKKKKKKKKKKKEPEPPGSGSPA PPRRRRAQDDSQRRSLPAEGSSGKKDEGGGGSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDDASSHRLHQ KSPSQYSEEEEEEDSGSEHSRSRSRSGRHSSHRSSRSYSSSS DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHDSDDSDYAS SKHRSKRHKYSSSDDDYSLSCSQSRSRSRHTKERSRSGRSRS SKHRSKRHKYSSSDDDYSLSCSQSRSRSRSHTRERSRSGRSRS SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKIVRSQSPHYPRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPPLIGKLPATRKPNKKCEESGLERGEEQQSETEEGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGRVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL				
SSKAESGEKSKKRKKKKKKKSSAPADSERGPKPEPPGSGSPA PPRRRRAQDDSQRRSLPAEGSSGKKDEGGGGSSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDSDASSHRLHQ KSPSQYSEEEEEDGSEHSRSRSGRRHSSHRSSRRSYSSSS DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHDSDDSDYAS SKHRSKRHKYSSSDDDYSLSCSGSRSRSRSHTTERSRSGRSRS SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRTSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEGQSETEEGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGRVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL	1	]		
PPRRRRAQDDSQRRSLPAEEGSSGKKDEGGGSSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDDDASSHRLHQ KSPSQYSEEEEEDGSEEHSRSRSRSGRHSSKRSSRSSSSS DASSDQSCYSQRSGPUSSDYSDYSDRSRRHSKRSRRSYSSSS SKHSKRHKYSSSDDDYSLSCSQSRSRSRSHTRERSRSRGRSS SKHSKRHKYSSSDDDYSLSCSQSRSRSRSHTRERSRSRGRSRS SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRTTSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPSKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEEGQSETEEGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGRVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL		į į		
KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDSDDASSHRLHQ KSPSQYSEEEEEEDSGSEHSRSRSRSGRRHSSHRSSRSYSSSS DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHDSDDSDYAS SKHRSKRHKYSSSDDDYSLSCSQSRSRSRSHTERSRSRGRSRS SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRSTTRSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGERQESGEPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGEVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL	1			
KSPSQYSEEEEEBDSGSEHSRSRSGRRHSSHRSSRSYSSSS DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHDSDDSDYAS SKHRSKRHKYSSSDDDYSLSCSQSRSRSRSHTRERSRSRSRS SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRSTTRSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYPRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGERQEGSETEBGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGEVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL				
DASSDQSCYSRQRSYSDDSYSDRSRRHSKRSHDSDDSDYAS SKHRSKRHKYSSSDDDYSLSCSQSRSRSRSHTRERSRSRGRSRS SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYBRSGRGEGFCKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPECKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEEQCETEEGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGEVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL	1			
SKHRSKRHKYSSSDDDYSLSCSQSRSRSRSHTRERSRSRGRSRS SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYPRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEKNSVTAALLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPPLIGKLPATRKPNKKCEESGLERGEEGQEGETEEGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGBVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL	1			
SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEEGEGFPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGBVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL	1			
KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEEQEQSETEEGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGEVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL	1		İ	
DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEEQEQSETEEGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGEVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL				SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGSR
DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEEQEQSETEEGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGEVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL				
EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEBQEQSETEEGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGBVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL	]			
LGNKPVLPLIGKLPATRKPNKKCEESGLERGEEQEQSETEEGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGBVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL		!		
GSSDALFGHQFP\SEETTGPLLDPPPEESKSGEVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL				· · · · · · · · · · · · · · · · · · ·
PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL			ı	
		l		
DPTAPULBHIPS TAPPSGUPSTESTUGAEDA \SLAPLESQPITF				
<u>-</u>	L	<u></u>		DETAFFUBRIES TAPPS OUPSIES TUGAEUA SLAPLES OPITE

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
1 .	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	sequence	bequence	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TDEEMERYCKIOONNOOULOOLLAWORD
1			TPEEMEKYSKLQQAAQQHIQQQLLAKQVKAFPASAALAPATPAL QPIHIQQPATASATSITTVQHAILQHHAAAAAAAIGIHPHPHPQ
		ŀ	PLAQVHHIPQPHLTPISLSHLTHSIIPGHPATFLASHPIHIIPA
1			SAIHPGPPTFHPVPHAALYPTLLAPRPAAAAATALHLHPLLHPI
1			FSGODLOHPPSHGT
5971	53	2149	SFLYFVGVDMDNPIGNWDGRFDGVQLCSFACVESTILLHINDII
1			PESVTQERRPPKLAFMSRGVGDKGSSSHNKPKATGSTSDPGNRN
1			RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTD
[			FDRSSPPLQPPPVNSLTTENRFHSLPFSLTKMPNTNGSIGHSPL
I			SLSAQSVMEELNTAPVQESPPLAMPPGNSHGLEVGSLAEVKENP
i			PFYGVIRWIGOPPGLNEVLAGLELEDECAG\CTDGTF/REGTRY
	1		FTCALKKALFVKLKSCRPDSRFASLQPVSNQIERCNSLAIWEAY
			LSEVVEENTPTQKWEKEGLEIMIG\KKKGIQGHYNSCYLDSTLF
			CLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRIYG
1			YVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHHILRV
			EPLLKIRSAGQKVQDCYFYQIFMEKNEKVGVPTIOOLLEWSFIN
1			SNLKFAEAPSCLIIQMPRFGKDFKLFKKIFPSLELNITDLLEDT
1			PROCRICGGLAMYECRECYDDPDISAGKIKOFCKTCNTOVHLHP
1	}		KRLNHKYNPVSLPKDLPDWDWRHGCIPCONMELFAVLCIETSHY
			VAFVKYGKDDSAWLFFDSMADRDGGQNGFNIPQVTPCPEVGEYL
5972	- 440		KMSLEDLHSLDSRRIQGCARRLLCDAIYVPCTQSPTMSLYK
39/2	440	1761	ILLAGSPSPRDQCSQRQSSGGDKELVTRGCTFSTAVVSPSAMTQ
] ]	ļ		EPFREELAYDRMPTLERGRQDPASYAPDAKPSDLQLSKRLPPCF
1 . 1			SHKTWVFSVLMGSCLLVTSGFSLYLGNVFPAEMDYLRCAAGSCI
		•	PSAIVSFTVSRRNANVIPNFQILFVSTFAVTTTCLIWFGCKLVL
i			NPSAININFNLILLLLELLMAATVIIAARSSEEDCKKKKGSMS
			DSANILDEVPFPARVLKSYSVVEVIAGISAVLGGIIALNVDDSV
1 1	1		SGPHLSVTFFWILVACFPSAIASHVAAECPNKCLVEVLIAISSL
1			TSPLLFTASGYLSFSIMRIVEMFKDYPPAIKPSYDVLLLLLLLV LLLQA/GPQHGHRHPVRALQGQCKAAGCILGHPERPAGAPGWGG
1 1			GQEPPEGVRQGESLESRRGANGPVTPRRGNRVAAPSLAPGMETH
!			NP
5973	65	· 2007	NGDGKDLFGHIWAWRSNGIISNFRRSPHAGMAEDEPDAKSPKTG
			GRAPPGGAEAGEPTTLLQRLRGTISKAVQNKVEGILQDVQKFSD
i l			NDKLYLYLQLPSGPTTGDKSSEPSTLSNEEYMYAYRWIRNHLEE
			HTDTCLPKQSVYDAYRKYCESLACCRPLSTANFGKIIREIFPDI
1 1			KARRLGGRGQSKYCYSGIRRKTLVSMPPLPGLDLKGSESPEMGP
			EVTPAPRDELVEAACALTCDWAERILKRSFSSIVEVARFLLQQH
			LISARSAHAHVLKAMGLAEEDEHAPRERSSKPKNGLENPEGGAH
l i			KKPERLAQPPKDLEARTGAGPLARGERKKSVVESSAPGANNLOV
			NALVARLPLLLPRAPRSLIPPIPVSPPILAPRLSSGALKVATLP
1			LSSRAGAPPAAVPIINMILPTVPALPGPGPGPGRAPPGGLTOPR
l i			GTENREVGIGGDQGPHDKGVKRTAEVPVSEASGOAPPAKAAKOD
l i			I EDTASDAKRKRGRPLKKSGGSGERNSTPLKSAAAMESAQSSRL
1			PWETWGSGGEGNSAGGAERPGPMGEARKGAVLAQG\QGDGTVSX
1			GGRGPGSQHTKEAEDKIPLVPSKVSVIKGSRSQKEAFPLAKGEV
5974			DTAPQGNKDLKEHVLQSSLSQEHKDPKATPP
3974	4293	2200	LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK\BID
			LESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIVKNRR
- 1	J	J	TV\ASIKNDPPS\RDNRVVGSARARPSQFPEQFSSAQQNGSV\S
		İ	DISPVQAAKKEFGPPSRRKSNCVKEVEKLQEKREKRRLQQQELR
			EKRAQDVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDEHRIC
			VCVRKRPLNKKETQMKDLDVITIPSKDVVMVHEPKQKVDLTRYL
		1	ENQTFRFDYAFDDSAPNEMVYRFTARPLVETIFERGMATCFAYG
1	1	İ	QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKPNYKK
	Ì		LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVVGLQE REVKCVEDVLKLIDIGNSCRTSGQTSANAHSSRSHAVFQIILRR
1		i	KEVKCVEDVLKLIDIGNSCRTSGQTSANAHSSRSHAVFQIILRR KGKLHGKFSLIDLAGNERGADTSSADRQTRLEGAEINKSLLALK
1			ECIRALGRNKPHTPFRASKLTQVLRDSFIGENSRTCMIATISPG
ł			MASCENTLINTLRYANRVKELTVDPTAAGDVRPIMHHPPNQI\DD
			LETQWGVGSSPQRDDLKLLCEQNEEEVSPQLFTFHEAVSQMVEM

SEQ Predicted   Predicted end   Amino acid segment containing signal pep   (A=Alanine, C=Cysteine, D=Aspartic Acid, NO: nucleotide   location   corresponding   to first   amino acid   residue of   amino acid   sequence   S=Serine, T=Threonine, V=Valine,   P=Proline, Q=Glutamine, R=Arginine,   S=Serine, T=Threonine, V=Valine,   W=Tryptophan, Y=Tyrosine, X=Unknown, *=S   Codon, /=possible nucleotide deletion,   P=Possible nucleotide deletion,   P=Sofible nucleotide insertion   EEQVVEDHRAVFQESIRWLEDEKALLEMTEEVDYDVDSYA   AILEQKIDILTELRDKVKSFRAALQEEQASKQINPKRPR   LESIFSLNP, UDL VPDGEIEPSP \ ETPPPPASSAKVNKIV   TV\ASIKNDPPS\RDNRVVGSARARPSQFPEQFSSAQQNG   DISPVQAAKKEFQPPSRRKSNCVKEVEKLQEKREKRRLQQ   EKRAQDVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDE   VCVRKRPLNKKETQMKDLDVITIPSKDVVMVHEPKQKVDL   ENGTFRFDYAFDDSAPNEMYYRFTARPLVETIFERGMATC   QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKP   LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVV   REVKCVEDVLKLIDIGNSCRTSGQTSANAHSSRSHAVFOI	E=  TOLE  AL  EID  KNRR  EV\S  QELR  HRIC  IRYL  FAYG  NYKK
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence Codon, /=possible nucleotide deletion, /=possible nucleotide insertion)  5975  4293  2200  LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK LESIFSLNP\DL\VPDGEIEPSP\ETPPPASSAKVNKIV TV\ASIKNDPPS\RDNRVVGSARARPSQFPEQFSSAQONG EKRAQDVDATNPNYEIMCMITGFRGSLDYRPLTTAPPIDE CYCVPRRPLNKEFTQMTGSAPPATCA QCGSKGIYALAARDVFIMLKKP LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVV	TQLE AL VEID KNRR EV\S QELR HRIC IRYL FAYG
location corresponding to first amino acid residue of amino acid sequence  2200  L=Leucine, M=Methionine, N=Asparagine, Alegaration L=Leucine, M=Methionine, N=Asparagine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=S Codon, /=possible nucleotide deletion, L=Leucine, M=Methionine, N=Asparagine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=S Codon, /=possible nucleotide deletion, L=Leucine, M=Methionine, N=Asparagine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=S Codon, /=possible nucleotide deletion, L=possible nucleotide insertion) EEQVVEDHRAVYQESIRWLEDEKALLEMTEEVDYDVDSYA AILEQKIDILIELRDKVKKSFRAALQEEEQASKQINPKRPR LESIFSLIP\DL\VPDGEIBPSP\ETPPPPASSAKVNKIV TV\ASIKNDPPS\RDNRVVGSARARPSQFPEQFSSAQONG DISPVQAAKKEFGPPSRRKSNCVKEVEKLQEKREKRRLQQ EKRAQDVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDE VCVVRKRPLNKKETQMKDLDVITIPSKDVWVHEPKQKVDU ENQTFRFDYAFDDSAPNEMVYRFTARPLVETIFERGMATC QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKP LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVV	TOLE AL VEID KNRR EV\S DELR HRIC IRYL FAYG
corresponding to first amino acid residue of amino acid residue of amino acid sequence  5 2 200  1 2 200  1 2 200  1 2 200  1 2 200  1 2 200  1 2 200  1 2 200  1 2 200  1 2 200  1 2 200  1 2 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 2	TOLE AL VEID KNRR SV\S QELR HRIC TRYL FAYG
corresponding to first amino acid residue of amino acid residue of amino acid sequence  5 2 200  1 2 200  1 2 200  1 2 200  1 2 200  1 2 200  1 2 200  1 2 200  1 2 200  1 2 200  1 2 200  1 2 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 200  1 3 2	TOLE AL VEID KNRR SV\S QELR HRIC TRYL FAYG
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amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=S (Codon, /=possible nucleotide deletion, Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence	TOLE AL VEID KNRR SV\S QELR HRIC TRYL FAYG
residue of amino acid sequence  amino acid sequence    Codon, /=possible nucleotide deletion,   EDVVEDHRAVPQESIRWLEDEKALLEMTEEVDYDVDSYA	TOLE AL VEID KNRR SV\S QELR HRIC TRYL FAYG
amino acid sequence Codon, /=possible nucleotide deletion,    =possible nucleotide insertion    EEQVVEDHRAVYQESIRWLEDEKALLEMTEEVDYDVDSYA     AlleQKIDILTELRDKVKSFRAALQEEEQASKQINPKRPR     S975   4293   2200   LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK     LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK     LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK     LGLGMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK     LGLGMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK     LGLGMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK     LGLGMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK     LGLGMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK     LGLGMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK     LGLGMHTTSGRIHQAMVTSTARPLVETIFERGMATC     QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKP     LGLGVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVV	TOLE AL VEID KNRR SV\S QELR HRIC TRYL FAYG
sequence \ \=possible nucleotide insertion\)  EEQVVEDHRAVPQESIRWLEDEKALLEMTEEVDYDVDSYA AILEQKIDILTBLRDKVKSFRAALQEEEQASKQINPKRPR 5975 4293 2200 LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK LESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIV TV\ASIKNDPPS\RDNRVVGSARARPSQFPEQFSSAQQNG DISPVQAAKKEFGPPSRRKSNCVKEVBKLQEKREKRRLQQ EKRAQDVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDE VCVRKRPLNKKETQMKDLDVITIPSKDVVMVHEPKQKVDL ENQTFRFDYAFDDSAPNEMYYRFTARPLVETIFERGMATC QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKP LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVV	AL VEID KNRR SV\S QELR HRIC TRYL FAYG NYKK
EEQVVEDHRAVPQESIRWLEDEKALLEMTEEVDYDVDSYA AILEQKIDILTELRDKVKSFRAALQEEEQASKQINPKRPR 5975 4293 2200 LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKĞK LESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIV TV\ASIKNDPPS\RDNRVVGSARAPPSQFPEQFSSAQQNG DISPVQAAKKEPGPPSRKSNCVKEVBKLQEKREKRRLQQ EKRAQDVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDE VCVKKRPLNKKETQMKDLDVITIPSKDVVMVHEPKQKVDL ENQTFRFDYAFDDSAPNEMYYRFTARPLVETIFERGMATC QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKP LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVV	AL VEID KNRR SV\S QELR HRIC TRYL FAYG NYKK
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LESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIV TV\ASIKNDPPS\RDNRVVGSARARPSQFPEQFSSAQQNG DISPVQAAKKEFGPPSRRKSNCVKEVBKLQEKREKRRLQQ EKRAQDVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDE VCVRKRPLNKKETQMKDLDVITIPSKDVVMVHEPKQKVDL ENQTFRFDYAFDDSAPNEMYYRFTARPLVETIFERGMATC QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKP LBLQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVV	KNRR SV\S QELR HRIC TRYL FAYG
TV\ASIKNDPPS\RDNRVVGSARARPSQFPEQFSSAQONG DISPVQAAKKEFGPPSRRKSNCVKEVBKLQEKREKRRLQQ EKRAQDVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDE VCVRKRPLNKETQMKDLDVITIPSKDVVMVHEPKQKVDU ENQTFRFDYAFDDSAPNEMVYRFTARPLVETIFERGMATC QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKP LBLQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVV	SV\S QELR HRIC TRYL FAYG NYKK
DISPVQAAKKEFGPPSRRKSNCVKEVBKLQEKREKRRLQQ EKRAQDVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDE VCVRKRPLNKKETQMKDLDVITIPSKDVVMVHEPKQKVDL ENQTFRFDYAFDDSAPNEMVYRFTARPLVETIFERGMATC QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKP LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVV	DELR HRIC TRYL FAYG NYKK
DISPVQAAKKEFGPPSRRKSNCVKEVBKLQEKREKRRLQQ EKRAQDVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDE VCVRKRPLNKKETQMKDLDVITIPSKDVVMVHEPKQKVDL ENQTFRFDYAFDDSAPNEMVYRFTARPLVETIFERGMATC QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKP LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVV	DELR HRIC TRYL FAYG NYKK
EKRAQDVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDE VCVRKRPLNKKETQMKDLDVITIPSKDVVMVHEPKQKVDL ENQTFRFDYAFDDSAPNEMVYRFTARPLVETIFERGMATC QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKP LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVV	HRIC TRYL FAYG NYKK
VCVRKRPLNKKETQMKDLDVITIPSKDVVMVHEPKQKVDL ENQTFRFDYAFDDSAPNEMVYRFTARPLVETIFERGMATC QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKP LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVV	TRYL FAYG NYKK
ENQTFRFDYAFDDSAPNEMVYRFTARPLVETIFERGMATC QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKP LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVV	FAYG NYKK
QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKP LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVV	<b>NYKK</b>
LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVV	
LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVV	
KGKLHGKFSLIDLAGNERGADTSSADRQTRLEGAEINKSL	
ECIRALGRNKPHTPFRASKLTQVLRDSFIGENSRTCMIAT	
MASCENTLNTLRYANRVKELTVDPTAAGDVRPIMHHPPNQ	I/DD
LETQWGVGSSPQRDDLKLLCEQNEEEVSPQLFTFHEAVSQ	MYEM
EEQVVEDHRAVFQESIRWLEDEXALLEMTEEVDYDVDSYA	
AILEQKIDILTELRDKVKSFRAALQEEEQASKQINPKRPR	
5976 20 2949 VHHLHLTRVSVVVNLDIILRIAQQMGIKTLNLVLG\LKRA	•
PEVSWMEVKDPNMKGAMLTNTGKYAIPTIDA\EAYAIGKK	
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	FKNE
TGYTKRLRKQLPSPPPPIPPRPLIQRNLQPLMRSFISRQ	ODPL
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ATVSISVHSEKSDOPFRDSDNKILPAAALASEHSKGTSSI	
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APPLSREEFYREQRRLKEEEKKKSKLDEFTNDFAKELMEY	KKIO
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RSHSRSYSRSPPYPRRGRGKSRNYRSRSRSHGYHRSRSRS	
RYHSRSRSPQAFRGQSPNKRNVPQGETEREYFNRYREVPP	
KAYYGRSVDFRDPFEKERYREWERKYREWYBKYYKGYAAG	-
PSANRENFSPERFLPLNIRNSPFTRGRREDYVGGQSHRSR	NIGS
NYPEKLSARDGHNQKDNTKSKEKESENAPGDGKGNKHKKH	≀KRR
KGEESEGFLNPELLETSRKSREPTGVEENKTDSLFVLPSR	DAT
PVRDEPMDAESITFKSVSEKDKRERDKPKAKGDKTKRKND	VASE
SKKENIVKPAKGPQEKVDG\DVRDLLDLNL\QLKKPKEET	
TILNHHLPLRRMKKSL\EPP\EKLTLNQQK\TPRNKTSQR	
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EGLFQRCQIRKANN	
5977 1363 TLEDRGQVLSHFQCLSLHSINHILHPGAGVAAGPATGW/R	
PVLKESKFKETGVITPEEFVAAGDHLVHHCPTWQWATGEE	
AYLPTGKQFLVTKNVPCYKRCKQMBYSDELEAIIEEDDGD	
DTYHNTGITGITEAVKEITLENKDNIRLQDCSALCEEEED	3DEG
EAADMEEYEESGLLETDRATLDTRKIVEACKAKTDAGGED.	/ILO
TRTYDLYITYDKYYOTPRLWLFGYDBOROPLTVEHMYEDI.	_
VKKTVTIENHPHLPPPPMCSVHPCRHAEVMKKIIETVAEG	
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5978 160 3213 RDGARRWGGCQSPLTWAPGFYRRFDLATSGRRLRGQTAEP. RPRREPEAMDEQSVESIAEVFRCFICMEKLRDARLCPHCS	KLCC DTLQ
5978 160 3213 RDGARRWGGCQSPLTWAPGFYRRFDLATSGRRLRGQTAEP. RPRREPEAMDEQSVESIABVFRCFICMEKLRDARLCPHCS FSCIRRWLTEQRAQCPHCRAPLQLRELVNCRWAEEVTQQL LCSLTKHEENEKDKCENHHEKLSVFCWTCKKCICHQCALW	KLCC OTLQ EGMH
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5978 160 3213 RDGARRWGGCQSPLTWAPGFYRRFDLATSGRRLRGQTAEP. RPRREPEAMDEQSVESIAEVFRCFICMEKLRDARLCPHCS: FSCIRRWLTEQRAQCPHCRAPLQLRELVNCRWAEEVTQQLL LCSLTKHEENEKKCENHHEKLSVFCWTCKKCICHQCALW GGHTFKPLAEIYEQHVTKVNEEVAKLRRRLMELISLVQEV: EAVRNAKDERVREIRNAVEMMIARLDTQLKNKLITLMGQK QETELLESLLQEVEHQLRSCSKSELISKSSEILMMFQQVH	CLCC OTLQ GGMH ERNV TSLT CKPM
5978 160 3213 RDGARRWGGCQSPLTWAPGFYRRFDLATSGRRLRGQTAEP. RPRREPEAMDEQSVESIAEVFRCFICMEKLRDARLCPHCS FSCIRRWLTEQRAQCPHCRAPLQLRELVNCRWABEVTQQL LCSLTKHEENEKDKCENHHEKLSVFCWTCKKCICHQCALW GGHTFKPLAEIYBQHVTKVNEEVAKLRRRLMELISLVQEV EAVKNAKDERVRBIRNAVEMMIARLDTQLKNKLITLMGQK QETELLESLLQEVEHQLRSCSKSELISKSSEILMMFQQVH ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPV	KLCC OTLQ GGMH ERNV TSLT RKPM KSPP KEYR
5978 160 3213 RDGARRWGGCQSPLTWAPGFYRRFDLATSGRRLRGQTAEP. RPRREPEAMDEQSVESIABVFRCFICMEKLRDARLCPHCS: FSCIRRWLTEQRAQCPHCRAPLQLRELVNCRWAEEVTQQL: LCSLTKHEENEKDKCENHHEKLSVFCVTCKKCICHQCALW: GGHTFKPLAEITYBQHVTKVNEEVAKLRRRLMELISLVQEV EAVRNAKDERVRBIRNAVEMMIARLDTQLKNKLITLMGQK: QETELLESLLQEVEHQLRSCSKSELISKSSEILMMFQQVH: ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPV LQVSGLCWRLKVYPDGNGVVRGYYLSVFLELSAGLPETSK VEMVHQSCNDPTKNIIREFASDFEVGBCWGYNRFFRLDLL	KLCC OTLQ GGMH ERNV TSLT KKPM KSPP KEYR
5978 160 3213 RDGARRWGGCQSPLTWAPGFYRRFDLATSGRRLRGQTAEP. RPRREPEAMDEQSVESIABVFRCFICMEKLRDARLCPHCS: FSCIRRWLTEQRAQCPHCRAPLQLRELVNCRWAEEVTQQL: LCSLTKHEENEKDKCENHHEKLSVFCWTCKKCICHQCALW GGHTFKPLAEIYEQHVTKVNEEVAKLRRRLMELISLVQEV: EAVRNAKDERVRBIRNAVEMMIARLDTQLKNKLITLMGQK QETELLESLLQEVEHQLRSCSKSELISKSSEILMMFQQVH ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPV LQVSGLCWRLKVYPDGNGVVRGYYLSVFLELSAGLPETSK	KLCC OTLQ GGMH ERNV ISLT RKPM (SPP VEYR ANEG VIQQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine.
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
1 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
J	sequence		\=possible nucleotide insertion)
1 1			CSDMLLER\GPYSAS\VREAKEDEEDEEKIQNEDYHHELSDGDL
1 1			DLDLVYEDEVNQLDGSSSSASSTATSNTEENDIDEETMSGENDV
			EYNNMELEEGELMEDAAAAGPAGSSHGYVGSSSRISRRTHLCSA
]			ATSSLLDIDPLILIHLLDLKDRSSIENLWGLQPRPPASLLQPTA SYSRKDKDQRKQQAMWRVPSDLKMLKRLKTQMAEVRCMKTDVKN
1 1			TLSEIKSSSAASGDMQTSLFSADQAALAACGTENSGRLQDLGME
			LLAKSSVANCYIRNSTNKKSNSPKPARSSVAGSLSLRRAVDPGE
1 1			NSRSKGDCQTLSEGSPGSSQSGSRHSSPRALIHGSIGDILPKTE
1 1			DRQCKALDSDAVVVAVFSGLPAVEKRRKMVTLGANAKGGHLEGL
			QMTDLENNSETGELQPVLPEGASAAPEEGMSSDSDIECDTENEE
1 1			QEEHTSVGGFHDSFMVMTQPPDEDTHSSFPDGEQIGPEDLSFNT
			DENSGR
5979	212	3665	LPDMTMYLWLKLLAFGFAFLDTEVFVTGQSPTPSPTDAYLNASE
			TTTLSPSGSAVISTTTIATTPSKPTCDEKYANITVDYLYNKETK
1			LFTAKLNVNENVECGNNTCTNNEVHNLTECKNASVSISHNSCTA
1 1			PDKTLILDVPPGVEKVPVHCCS\QVEQPDSTIWLKWKNIETSTC
			DTQNITYRFQCGNMIFDNKEIKLENLEPEHEYKCDSEILYNSHK
1 1			FTNASKIIKTDFGSPGEPQIIFCRSEAAHQGVITWNPPQRSFHN FTLCYIKETEKDCLNLDKNLIKYDLQNLKPYTKYVLSLHAYIIA
			KVQRNGSAAMCHFTTKSAPPSQVWNMTVSMTSDNSMHVKCRPPR
1 1			DRNGPHERYHLEVEAGNTLVRNESHKNCDFRVKDLQYSTDYTFK
1			AYFHNGDYPGEPFILHHSTSYNSKALIAFLAPLIIVTSIALLVV
1	i		LYKIYDLHKKRSCNLDEQQELVERDDEKQLMNVEPIHADILLET
1 1			YKRKIADEGRLFLAEFQSIPRVFSKFPIKEARKPFNONKNRYVD
1			ILPYDYNRVELSEINGDAGSNYINASYIDGFKEPRKYIAAOGPR
1 1			DETVDDFWRMIWEQKATVIVMVTRCEEGNRNKCAEYWPSMEEGT
			RAPGECCCKDLTKHKRCP\DYIIQKLNIVNKKBKATGREVTHIO
1 [			FTSWPDHGVPEDPHLLLKLRRRVNAFSNFFSGPIVVHCSAGVGR
1			TGTYIGIDAMLEGLEAENKVDVYGYVVKLRRQRCLMVQVEAQYI
1			LIHQALVEYNQFGETEVNLSELHPYLHNMKKRDPPSEPSPLEAE
i . I			FQRLPSYRSWRTQHIGNQE\ENKSKNRNSNVIPYDYNRVPLKHE
1 1			LEMSKESEHDSDESSDDDSDSEEPSKYINASFIMSYWKP\EVMI AAQGPLKETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQYWG
1 1		•	EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQ
			YTNWSVEQLPABPKELISMIQVVKQKLPQKNSSBGNKHHKSTPL
1			LIHCRDGSQQTGIFCALLNLLESAETEEVVDIFQVVKALRKARP
			GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQRDKIEFDNEVD
	ļ	Í	KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP
-			ASPALNQGS
5980	3	2363	DAWGCKLRRLRPTYGTQTRVSLALPGQYELVHTLVAHQGNWETI
			PEEDLEVQENNEDAAHDLTELEVIMHHALLOEVDVVVAPCOGLR
	]		PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSFP
]	İ		VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN
	!		CGAPGODTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN
			LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMN IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP
			VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL
			ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR
			MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK
			SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK
		ł	DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVYLCDN
		Ì	WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG
			SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLOIAL
			DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA
		1	MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK
			LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG
5981	1		DPLKRPLLGIVQPMLQGIMNRLCKS\NSEQPNRGLDDST
3331	- 1	2519	GRRHSAAMERPWGAADGLSRWPHGLGLLLLQLLPPSTLSQDRL
}			DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP
			G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV ILVLTTFHVPLVIMTFGQSKLYRSEDYGKNFKDITDLINNTFIR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.7.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
<b>!</b>	sequence		\=possible nucleotide insertion)
<b>—</b>			TEFGMAIGPENSGKVVLTAEVSGGSRGGRIFRSSDFAKNFVOTD
			LPFHPLTQMMYSPQNSDYLLALSTENGLWVSKNFGGKWEEIHKA
		]	VCLAKWGSDNTIFFTTYANGSCKADLGALELWRTSDLGKSFKTI
			GVKIYSFGLGGRFLFASVMADKDTTRRIHVSTDQGDTWSMAQLP
			SVGQEQFYSILAANDDMVFMHVDEPGDTGFGTIFTSDDRGIVYS
			KSLDRHLYTTTGGETDFTNVTSLRGVYITSVLSEDNSIQTMITF
			DQGGRWTHLRKPENSECDATAKNKNECSLHIHASYSISOKLNVP
]			MAPLSEPNAVGIVIAHGSVGDAISVMVPDVYISDDGGYSWTKML
1	1		EGPHYYTILDSGGIIVAIEHSSRPINVIKFSTDEGQCWQTYTFT
			RDPIYFTGLASEPGARSMNISIWGFTESFLTSQWVSYTIDFKDI
1	}		LERNCEEKDYTIWLAHSTDPEDYEDGCILGYKEOFLRLRKSSVC
[			QNGRDYVVTKQPSICLCSLEDFLCDFGYYRPENDSKCVEQPELK
			GHDLEFCLYGREEHLTTNGYRKIPGDKCQGGVNPVREVKDLKKK
	- 3		CTSNFLSPEKQNSKSNSVPIILAIVGLMLVTVVAGVLIVKKYVC
			GGRFLVHLYSVLQQH\AEA\NGVDGVDALDTASHTNKSGYHDDS
			DEDLLE
5982	56	2316	ATRPPRGSSWCRQFSRTASAAPGRSNMLRIPVRKALVGLSKSPK
1			GCVRTTATAASNLIEVFVDGQSVMVEPGTTVLQACEKVGMQIPR
1		[	FCYHERLSVAGNCRMCLVEIEKAPKVVAACAMPVMKGWNILTNS
			EKSKKAREGVMEFLLANHPLDCPICDQGGECDLQDQSMMFGNDR
			SRFLEGKRAVEDKNIGPLVKTIMTRCIQCTRCIRFASEIAGVDD
			LGTTGRGNDMQVGTYIEKMFMSELSGNIIDICPVGALTSKPYAF
			TARPWETRKTESIDVMDAVGSNIVVSTRTGEVMRILPRMHEDIN
			EEWISDKTRFAYDGLKRQRLTEPMVRNEKGLLTYTSWEDALSRV
]	Į		AGMLQSFQGKDVAAIAGGLVDAEALVALKDLLNRVDSDTLCTEK
ł		l	VFPTAGAGTDLRSNYLLNTTIAGVEEADVVLLVGTNPRFEAPLF
			NARIRKSWLHNDLKVALIGSPVDLTYTYDHLGDSPKILQDIASG
			SHPFSQVLKEAKKPMVVLGSSALQRNDGAAILAAVSSIAQKIRM
			TSGVTGDWKVMNILHRIASQVAALDLGYKPGVEAIRKNPPKVLF
			LLGADGGCITRQDLPKDCFIIYQGHHGDVGAPIADVILPGAAYT
			EKSATYVNTEGRAQQTKVAVTPPGLAREDWKIIRALSEIAGMTL
		ł	PYDTL\DQVRNRLEEVSPNLVRYDDIEG\ANYFQQANELSKLVN
			QQLLADPLVPPQLTMKDFYMTDSISRASQTMAKCVKAVTEGAQA
			VEEPSIC
5983	248	1763	EARGDGGRRHRASGRRAGRGEP\AGLKSQGQRAVPKRAVARGG
			RQ\YSAAIALLEPAGSEIADDLSILYSNRAACYLKEGNCSGCIQ
		!	DCNRALELHPFSMKPLLRRAMAYETLEQYGKAYVDYKTVLQIDC
]			GLQLANDSVNRLSRILMELDGPNWREKLSLIPAVPASVPLQAWH
			PAKEMISKQAGDSSSHRQQGITDEKTFKALKEEGNQCVNDKNYK
			DALSKYSECLKINNKECAIYTNRALCYLKLCQFEEAKQDCDQAL
			QLADGNVKAFYRRALAHKGLKNYQKSLIDLNKVILLDPSIIEAK MELBEVTRLLNLKDKTAPFNKEKERRKIEIQEVNEGKEEPGRPA
			GEVSTGCLASEKGGKSSRSPEDPEKLPIAKPNNAYEFGQIINAL
!		i	OPACIOCHMODICOGROSICOPER DE L'ARPRINAI EL GOLL MAL
			STRKNERACAHITA ITTA DENI DARET CARET DODDRET I I TOGE TORE
			STRKDKEACAHLLAITAPKDLPMFLSNKLEGDTFLLLIQSLKNN
			LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDL
5984	755	1193	LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDL SDTPNNHFTLBDIQALKRQYEL
5984	755	1193	LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDL SDTPNNHFTLBDIQALKRQYEL SSVCMACTYVSNLGKKQRSVSFLASGLMRVSTGPELRLHHSFVL
5984	755	1193	LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDL SDTPNNHFTLBDIQALKRQYEL SSVCMACTYVSNLGKKQRSVSFLASGLMRVSTGPELRLHHSFVL TGDVGRRICRLLVGLFTKGDTSSKRVHPFSPGPCFLLCDLARVG
5984	755	1193	LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDL SDTPNNHFTLBDIQALKRQYEL SSVCMACTYVSNLGKKQRSVSFLASGLMRVSTGPELRLHHSFVL TGDVGRRICRLLVGLFTKGDTSSKRVHPFSPGPCFLLCDLARVG SSPKINVSPFYQN\QTSTQRSCTVFVWQRCSLVGPFQVTVFTMY
			LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDL SDTPNNHFTLBDIQALKRQYEL SSVCMACTYVSNLGKKQRSVSFLASGLMRVSTGPELRLHHSFVL TGDVGRRICRLLVGLFTKGDTSSKRVHPFSPGPCFLLCDLARVG SSPKINVSPFYQN\QTSTQRSCTVFVWQRCSLVGPFQVTVFTMY FHHSLRSISRFSSG
5984	755	1193	LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDL SDTPNNHFTLBDIQALKRQYEL SSVCMACTYVSNLGKKQRSVSFLASGLMRVSTGPELRLHHSFVL TGDVGRRICRLLVGLFTKGDTSSKRVHPFSPGPCFLLCDLARVG SSPKINVSPFYQN\QTSTQRSCTVFVWQRCSLVGPFQVTVFTMY FHHSLRSISRFSSG RRVARPGTAEPAKARRTVRRGRARRDLAGAERKAGVSERGDSGR
			LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDL SDTPNNHFTLBDIQALKRQYEL SSVCMACTYVSNLGKKQRSVSFLASGLMRVSTGPELRLHHSPVL TGDVGRRICRLLVGLFTKGDTSSKRVHPFSPGPCFLLCDLARVG SSPKINVSPFYQN\QTSTQRSCTVFVWQRCSLVGPFQVTVFTMY FHHSLRSISRFSSG RRVARPGTAEPAKARRTVRRGRARRDLAGAERKAGVSERGDSGR RRPNPSIPSAAAGMSHIQIPPGLTELLQGYTVEVLRQQPPDLVE
			LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDL SDTPNNHFTLBDIQALKRQYEL SSVCMACTYVSNLGKKQRSVSFLASGLMRVSTGPELRLHHSFVL TGDVGRRICRLLVGLTTKGDTSSKRVHPFSPGPCFLLCDLARVG SSPKINVSPFYQN\QTSTQRSCTVFVWQRCSLVGPFQVTVFTMY FHHSLRSISRFSSG RRVARPGTAEPAKARRTVRRGRARRDLAGAERKAGVSERGDSGR RRPNPSIPSAAACMSHIQIPPGLTELLQGYTVEVLRQQPPDLVE FAVEYFTRLREARAPASVLPAATPRQSLGHPPPEPGPDRVADAK
			LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDL SDTPNNHFTLBDIQALKRQYEL SSVCMACTYVSNLGKKQRSVSFLASGLMRVSTGPELRLHHSFVL TGDVGRRICRLLVGLFTKGDTSSKRVHPFSPGEGFLLCDLARVG SSPKINVSPFYQN\QTSTQRSCTVFVWQRCSLVGPFQVTVFTMY FHHSLRSISRFSSG RRVARPGTAEPAKARRTVRRGRARRDLAGAERKAGVSERGDSGR RRPNPSIPSAAAGMSHIQIPPGLTELLQGYTVEVLRQQPPDLVE FAVEYFTRLREARAPASVLPAATPRQSLGHPPPEPGPDRVADAK GDSESEEDEDLEVPVPSRFNRRVSVCAETYNPDEEEEDTDPRVI
			LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDL SDTPNNHFTLBDIQALKRQYEL SSVCMACTYVSNLGKKQRSVSFLASGLMRVSTGPELRLHHSFVL TGDVGRRICRLLVGLFTKGDTSSKRVHPFSPGPCFLLCDLARVG SSPKINVSPFYQN\CYTSTORSCTVFVWQRCSLVGPFQVTVFTMY FHHSLRSISRFSSG RRVARPGTAEPAKARRTVRRGRARRDLAGAERKAGVSERGDSGR RRPNPSIPSAAAGMSHIQIPPGLTELLQGYTVEVLRQQPPDLVE FAVEYFTRLREARAPASVLPAATPRQSLGHPPPEPGPDRVADAK GDSESEEDEDLEVPVPSRFNRRVSVCAETYNPDEEEEDTDPRVI HPKTDEQRCRLQEACKDILLFKNLDQEQLSQVLDAMFERIVKAD
			LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDL SDTPNNHFTLBDIQALKRQYEL SSVCMACTYVSNLGKKQRSVSFLASGLMRVSTGPELRLHHSFVL TGDVGRRICRLLVGLFTKGDTSSKRVHPFSPGPCFLLCDLARVG SSPKINVSPFYQN\QTSTQRSCTVFVWQRCSLVGPFQVTVFTMY FHHSLRSISRFSSG RRVARPGTAEPAKARRTVRRGRARRDLAGAERKAGVSERGDSGR RRPNPSIPSAAAGMSHIQIPPGLTELLQGYTVEVLRQQPPDLVE FAVEYFTRLREARAPASVLPAATPRQSLGHPPPEPGPDRVADAK GDSESEEDEDLEVPVPSRFNRRVSVCAETYNPDEBEEDTDPRVI HPKTDEQRCRLQEACKDILLFKNLDQEQLSQVLDAMFERIVKAD EHVIDQGDDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFG
			LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDL SDTPNNHFTLBDIQALKRQYEL SSVCMACTYVSNLGKKQRSVSFLASGLMRVSTGFELRLHHSFVL TGDVGRRICRLLVGLFTKGDTSSKRVHPFSPGPCFLLCDLARVG SSPKINVSPFYQN\QTSTQRSCTVFVWQRCSLVGPFQVTVFTMY FHHSLRSISRFSSG RRVARPGTAEFAKARRTVRRGRARRDLAGAERKAGVSERGDSGR RRPNPSIPSAAAGMSHIQIPPGLTELLQGYTVEVLRQQPPDLVE FAVEYFTRLREARAFASVLPAATFRQSLGHPPPEPGPDRVADAK GDSESEEDEDLEVPVPSRFNRVSVCAETYNPDEBEEDTDPRVI HPKTDEQRCRLQEACKDILLFKNLDQEQLSQVLDAMFERIVKAD EHVIDQGDDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFG ELALMYNTPRAATIVATSEGSLWGLDRVTFRRIIVKNNAKKRKM
			LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDL SDTPNNHFTLBDIQALKRQYEL SSVCMACTYVSNLGKKQRSVSFLASGLMRVSTGPELRLHHSPVL TGDVGRRICRLLVGLFTKGDTSSKRVHPFSPGPCFLLCDLARVG SSPKINVSPFYQN\QTSTQRSCTVFVWQRCSLVGPFQVTVFTMY FHHSLRSISRFSSG RRVARPGTAEPAKARRTVRRGRARRDLAGAERKAGVSERGDSGR RRPNPSIPSAAAGMSHIQIPPGLTELLQGYTVEVLRQQPPDLVE FAVEYFTRLREARAPASVLPAATPRQSLGHPPPEPGPDRVADAK GDSESEEDEDLEVPVPSRFNRRVSVCAETYNPDEBEEDTDPRVI HPKTDEQRCRLQEACKDILLFKNLDQEQLSQVLDAMFERIVKAD EHVIDQGDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFG ELALMYNTPRAATIVATSEGSLWCLDRVTFRRIIVKNNAKKRKM FESFIESVPLLKSLEVSERMKIVDVIGEKIYKR/DGERIITQGE
			LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDL SDTPNNHFTLBDIQALKRQYEL SSVCMACTYVSNLGKKQRSVSFLASGLMRVSTGFELRLHHSFVL TGDVGRRICRLLVGLFTKGDTSSKRVHPFSPGPCFLLCDLARVG SSPKINVSPFYQN\QTSTQRSCTVFVWQRCSLVGPFQVTVFTMY FHHSLRSISRFSSG RRVARPGTAEPAKARRTVRRGRARRDLAGAERKAGVSERGDSGR RRPNPSIPSAAAGMSHIQIPPGLTELLQGYTVEVLRQQPPDLVE FAVEYFTRLREARAPASVLPAATPRQSLGHPPPEPGPDRVADAK GDSESEEDEDLEVPVPSRFNRRVSVCAETYNPDEBEEDTDPRVI HPKTDEQRCRLQEACKDILLFKNLDQEQLSQVLDAMFERIVKAD EHVIDQGDDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFG ELALMYNTPRAATIVATSEGSLWGLDRVTFRRIIVKNNAKKRKM FESFIESVPLLKSLEVSERMKIVDVIGBKIYKR/DGERIITQGE K\ADSFYIIESGEVSILIRSRTKSNKDGGNQEVELARCHKGQYF
			LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDL SDTPNNHFTLBDIQALKRQYEL SSVCMACTYVSNLGKKQRSVSFLASGLMRVSTGPELRLHHSPVL TGDVGRRICRLLVGLFTKGDTSSKRVHPFSPGPCFLLCDLARVG SSPKINVSPFYQN\QTSTQRSCTVFVWQRCSLVGPFQVTVFTMY FHHSLRSISRFSSG RRVARPGTAEPAKARRTVRRGRARRDLAGAERKAGVSERGDSGR RRPNPSIPSAAAGMSHIQIPPGLTELLQGYTVEVLRQQPPDLVE FAVEYFTRLREARAPASVLPAATPRQSLGHPPPEPGPDRVADAK GDSESEEDEDLEVPVPSRFNRRVSVCAETYNPDEBEEDTDPRVI HPKTDEQRCRLQEACKDILLFKNLDQEQLSQVLDAMFERIVKAD EHVIDQGDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFG ELALMYNTPRAATIVATSEGSLWCLDRVTFRRIIVKNNAKKRKM FESFIESVPLLKSLEVSERMKIVDVIGEKIYKR/DGERIITQGE

670	T 8 37 -5-2	1 50 32 24 2 3 2 2	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
ĺ	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
5986	1806	484	\=possible nucleotide insertion)
7,500	1000	1 404	DAWKSTSLTFHWKLWGRHRGRRRGLAHPKNHLSPQQGGATPQVP
			SPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPPVPSGPPMEED
			GLRWTPKSPLDPDSGLLSCTLPNGFGGQSGPEGERSLAPPDASI
	1		LISNVCSIGDHVAQELFQGSDLGMAEEAERPGEK\AGQHSPLRE
1		}	EHVTCVQSILDEFLQT\YGSLIPLSTDEVVEKLEDIFQQEFSTP
			SRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYG
i	}		QNWLNDQVMNMYGDLVMDTVPEK\VHFFNSFFY\DKLRTKGYDG VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQ
ł	1	ł	PTI NDDCDYHIA WYL CAEAUWYDD DEUGGWGWGWGWGWGWGWGWGWGWGWGWGWGWGWGWGWGWG
			RTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNN
			DSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL TV
5987	1806	484	DAWKSTSLTFHWKLWGRHRGRRRGLAHPKNHLSPQQGGATPQVP
-507		704	
			SPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPPVPSGPPMEED GLRWTPKSPLDPDSGLLSCTLPNGFGGOSGPEGERSLAPPDASI
	[		
1	1		LISNVCSIGDHVAQELFQGSDLGMAEEAERPGEK\AGQHSPLRE EHVTCVQSILDEFLQT\YGSLIPLSTDEVVEKLEDIFQQEFSTP
			SRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYG
			QNWLNDQVMNMYGDLVMDTVPEK\VHFFNSFFY\DKLRTKGYDG
			VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQ
1	ļ		RTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNN
			DSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL
-			TV
5988	1292	410	FKKYFLSFLGLLESSHSRDRIHNLVLMFLLATHNLVWWFTCRFQ
	,		RLDCIYLNAGIMPNPQLNIKALLFGLFS\ABGLLTQGDKITADG
ļ			LQEVFETDVFGHFILIRELEPLLCHSDNPSQLIWTSSRNARKSN
	,		FSLEDFQHSKGKEPYSSSKYATDLLSVALNRNFNQQGLYSNVAC
			PGTALTNLTYGILPPFIWTLLMPAILLLRFFANAFTLTPYNGTE
			ALVWLFHQKPESLNPLIKYLSATTGFGRNYIMTQKMDLDEDTAE
ĺ			KFYQKLLELEKHIRVTIQKTDNQARLSGSCL
5989	194	2610	AMDFPQHSQHVLEQLNQQRQLGLLCDCTFVVDGVHFKAHKAVLA
		•	ACSEYFKMLFVDQKDVVHLDISNAAGLGQVLEFMYTAKLSLSPE
			NVDDVL\AVATFLQMQDIITACHALKSLAEPATSPGGNARALAT
ł			EGGDKRAKEEKVATSTLSRLEQAGRSTPIGPSRDLKEERGGQAQ
	i		SAASGAEQTEKADAPREPPPVELKPDPTSGMAAAEAEAALSESS
			EQEMEVEPARKGEEEQKEQEEQEEGAGPAEVKEEGSQLENGEA
			PEENENEESAGTDSGQELGSEARGLRSGTYGDRTESKAYGSVIH
•			KCEDCGKEFTHTGNFKRHIRIHTGEKPFSCRECSKAFSDPAACK
			AHEKTHSPLKPYGCEECGKSYRLISLLNLRKKRHSGEARYRCED
]			CGKLFTTSGNLKRHQLVHSGEKPYQCDYCGRSFSDPTSKMRHLE
			THDTDKEHKCPHCDKKFNQVGNLKAHLKIHIADGPLKCRECGKO
1			FTTSGNLKRHLRIHSGEKPYVCIHCQRQFADPGALQRHVRIHTG
			EKPCQCVMCGKAFTQASSLIAHVRQHTGEKPYVCERCGKRFVOS
'	i.		SQLANHIRHHDNIRPHKCSVCSKAFVNVGDLSKHIIIHTGEKPY
	·		LCDKCGRGFNRVDNLRSHVKTVHQGKAGIKILEPEEGSEVSVVT
			VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLKAEISKA
			VKQVQEEDPNTHILYACDSCGDKFLDANSLAQHVRIHTAQALVM
			FQTDADFYQQYGPGGTWPAGQVLQAGELVFRPRDGAEGQPALAE
			TSPTAPECPPPAE
5990	2	4700	FGPGPDSGGGARGSGWGSRSQAPYGTLGAVSGGEQVLLHEEAGD
			SGFVSLSRLGPSLRDKDLEMEELMLQDETLLGTMQSYMDASLIS
	·		LIEDFGSLGEVEMSLPDPSWDFSPPSFLETSSPKLPSWRPPRSR
			PRWGQSPPPQQRSDGEEEEEVASFSGQILAGELDNCVSSIPDFP
		1	MHLACPEBEDKATAAEMAVPAAGDESISSLSELVRAMHPYCLPN
			LTHLASLEDELQEQPDDLTLPEGCVVLEIVGQAATAGDDLEIPV
			VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL
			CSEKEGLSLNSEEKLDSACLLKPREVVEPVVPKEPONPPANAAP
			GSQRARKGRKKKSKEQPAACVEGYARRLRSSSRGQSTVGTEVTS
			QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAAALENSSPKN
			LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS
	İ		PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA
			EPVLINPVLADSAAVDPAVVPISDNLPPVDAVPSGPAPVDLALV

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NO.   nucleotide   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   correspondi	- 1			
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amino acid residue of amino acid sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  seq	1		amino acid	P=Proline, Q=Glutamine, R=Arginine,
menio acid dequence amino acid dequence dequence amino acid dequence codom, *possible nuclectide deletion) Apposible nuclectide insertion) Deventure province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province province provinc	- 1			S=Serine, T=Threonine, V=Valine,
amino acid aequence   Sequence	ļ.			
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DPVNNLTPVDPVILVSRPTIDERGAVSSALGGSAFOLLVESSE  LDPPKTIT IPEVKEVVDSLAKIEGGTSATTHEARPRILSLESFERR  RQQQAETERSSQPPTGKWPSLPPTGLADIPCLVIPPAPAR  KYALQASPPTHELICLUPVUSPSASSPEPPVSKWASSPTEVO  PSQBMPLLARPSSPVQSVSPAVPTPSSSSPEPPVSKWASSSPTEVO  RYDLOPSDPLISAMSPVQSVSPAVPTPSSSSEPPVSKWASSSPTEVO  CLPPPTVPLVSGTPGALAVPPTCSVPHAPPPAPVSYSSPSTY  GPLOMOGROGOGRAPPKSTVPPPEDPAPASTVSPSYSSPSTY  GPLOMOGROGOGRAPPKSTVPPPEDPAPASTVSPVPSSSTSTY  GPLOMOGROGOGRAPPKSTVPPPEDPAPASTVSPSSPSTEY  KREUDATKAVPTERGSSTVEKDAVHADLASHRCYTYSSFSTEYPKSAVTYSSPSSTATA  KREUDATKAVPTERGSTVEKDAVHADLASKSSTSTPTSTVSKYPAVRAVROSTORTAP  KREUDATKAVPTERGSTVEKDAVHADLASKSSTSTAVEKDAVHADLASKSSSTSTPTSTTAVSTVARVAVRSKOPTSTAVEKTORTAP  KREUDATKAVPTERGSTVEKDAVHADLASKSSTSTAVEKDAVHADLASKSSSTSTPTSTAVARVAVRSKOPTSTAVEKTORTAP  RVHVSSALVOSSPOMTATAVSTVEKDAVHADLASKSSTSTAVERGOGTAPADGLAAV  AVSLLAKARSPSTAGGSTLKSEGVTVEKDAVHADLASKTSTAVEKTORTAPADGLA  GRISGOVET POGKREDIBLÖRGAREKAVANGLIFFATAFOLIKAVEKTORTA  RVHVSSGDEDVCVVSKSTPPKK\MPALLIFFATSSKAVKRKGODI  TIKPVLSLAPASPPCTIANTTPRESAKORSSKORTKYKAKAGASPSSC  GROGORGONNSKVSGGNATTSRASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	3	amino acid	sequence	
LDPPKTI I PEVKEVUDSLAKISGTSATTHEARPRILSLSEYRRM ROGOGRETERS DEPPTOKADIFELLIPPADAM KYALAGSPETPLEICLUPUNGSPAS SEREPPYSKEVAS SPIEDV PSORMLLAR RSPOTEVOS VSPANT PPSSKSALIPPADGGGMPE LPPPPLOPSULAR RSPOTEVOS VSPANT PPSSKSALIPPADGGGMPE LPPPPLOPSULAR RSPOTEVOS VSPANT PPSSKSALIPPADGGAMPE LPPPPLOPSULAR RSPOTEVOS VSPANT PPSSKSALIPPADGAMPAVS YSSTCTY GPLAWGEGGGIAPPE STVEPPEL PASS IGRAVPOT NESSECTIF GPENNI-PLISARPIJSGLFORGATOTS TYVEVKEV PASS PHER HEVSALVOS POMALACVS RGEVTY VSEPAS PERL KRETOSTEPRE KPPLPATKAVPTPRGSTVPKLPANHARLEKUS FLPTPETOGSS DVOATISE IG IERAGUS VSERAKKE OPPADGIAN GNSGGVLT 100 KRETLDRIANHARLEKUS FLPTPETOGSS DVOATISE IG IERAGUS LISEUGE VERSAKKE OPPADGIAN GNSGGVLT 100 KRETLDRIANHARLEKUS FLPTPETOGSS RVHVGSCONDIY CVSSTTPKK (MPALLIPPETOS TRANSVAKUS GONGGOVET 100 KRETLDRIANHARLEKUS FLPTPETOGSS RVHVGSCONDIY CVSSTTPKK (MPALLIPPETOS TRANSVAKUS GONGGOVET 100 KRETLDRIANHARLEKUS FLPTPETOGSS GNOGGONS SEVSSOS SSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	1	sequence		
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FRMLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPEC RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRI RH  5994  394  1934  AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWPI PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLI LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKG HNEATGKSSWWMLNPEGGKSGKAPRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSFVGHFAKWGGSPCSRNREEADMWTT FRPRSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSG SLFSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPADVIMTQVI PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTI SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNFEPDP		İ	1	
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RH  5994  394  1934  AGEVQLHVWIRGMRIQPQ/KAAATIDLDPDFEPQSRPRSCTWPI PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQATESAPEKRLT LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKG HNEATGKSSWWMLNPEGGKSGKAPRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPADVLMTQVI PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLKAPGPSSLVPTI SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMT MENLECDMDNIISDLMDEGEGLDFNFEPDP		1		The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
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PRPETANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKT HNEATGKSSWWMLNPEGGKSGKAPRRAASMDSSSKLLRGRSK PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPADVLMTQVI PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTI SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMT MENLECDMDNIISDLMDEGEGLDFNFEPDP			:	
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PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKT HNEATGKSSWWMLNPEGGKSGKAPRRRAASMDSSSKLLRGRSKI PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSACEGCFSSSQALEALLTSDTPPPPADVLMTQVT PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTT SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMT MENLECDMDNIISDLMDEGEGLDFNFEPDP				PRPEIANOPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG
LAQIYEMMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKO HNEATGKSSWMMLNPEGGKSGKAPRRRASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSACEGCFSSSQALEALLTSDTPPPPADVLMTQVI PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTI SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMMT				
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SLFSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPADVLMTQVI PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLKAPGPSSLVPTI SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMM MENLECDMDNIISDLMDEGEGLDFNFEPDP	[			LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS
PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLBAPGPSSLVPTI SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMM MENLECDMDNIISDLMDEGEGLDFNFEPDP	1			SLFSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPADVLMTQVD
SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMM MENLECDMDNIISDLMDEGEGLDFNFEPDP	[			
MENLECDMDNI ISDLMDEGEGLDFNFEPDP	1			
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5995 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGI	l .			
	5995	2	2437	RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR
				GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAAA
	1	Į.		AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNQSL
			1	CSVGSLSDKEVETPEKKQNDQRNRKRKAEPYETSQGKGTPRGHK
COVORDON TO A DESIGNATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T	1	1		

	1 5 37 -5 3	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NU:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
			Codon, /=possible nucleotide deletion,
	amino acid	sequence	
	sequence		\=possible nucleotide insertion)
		ļ	ISDYFERRVEQPLYGLDGSAAKEATEEQSALPTLMSVMLAKPRL
			DTEQLAQRGAGLCFTFVSAQQNSPSSTGSGNTEHSCSSQKQISI
			QHRQT\QSDLTIEKISALENSKNSDLEKKEGRIDDLLRANCDLR
			RQI\DEQQKMLEKYK\ERLNRCFDNEPRNFLIEKSKQEKMACRD
			KSMQDRLRLGHFTTVRHGASFTEQWTDGYAFQNLIKQQERINSQ
			REEIERORKMLAKRKPPAMGQAPPATNEQKQRKSKTNGAENETL
			TLAEYHEQEEIFKLRLGHLKKEEAEIQAELERLERVRNLHIREL
		ļ	KRIHNEDNSQFKDHPTLNDRYLLLHLLGRGGFSEVYKAFDLTEQ
	i		RYVAVKIHQLNKNWRDEKKENYHKHACREYRIHKELDHPRIVKL
			YDYFSLDTDSFCTVLEYCEGNDLDFYLKQHKLMSEKEARSIIMQ
			IVNALKYLNEIKPPIIHYDLKPGNILLVNGTACGEIKITDFGLS
			KIMDDDSYNSVDGMBLTSQGAGTYWYLPPECFVVGKEPPKISNK
			VDVWSVGVIFYOCLYGRKPFGHNOSOODILOENTILKATEVOFP
			PKPVVTPEAKAFIRRCLAYRKEDRIDVQQLACDPYLLPHIRKSV
			STSSPAGAAIASTSGASNNSSSN
5996	1612	981	DOOACLLGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
2236	1012	301	LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
			AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
			FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
			FFSIFTWSLTAALAVRRPKDLSFQEEYSTLPP\ASAQP
5997	1612	981	DQQACLLGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB
			LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
			AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
	1		FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
	1		FFS1FTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP
5998	1612	981	DQQACLLGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
			LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
			AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
			FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNBGTDASPGRPSPFS
		1	FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP
5999	2	1790	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP
3333	_		GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG
			ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG
		}	LLOAKLOLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS
			OVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG
			ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD
	1		FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS
			_
			KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE
			QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE
			EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI
			LFRQQKHLSDAIVEVEEALIQIHDPBLRKLLNPTTADLRFADYL
			VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV
			LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK
			TA\MSSWLSTFTTSTSQSLTEPPDEKP
6000	101	1561	TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL
			DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR
			KAEELIQQEHADQAEIRSLVTWGNYAWVYYHMGRLSDVQIYVDK
			VKHVCEKFSSPYRIESPELDCEEGWTRLKCGGNQNERAKVCFEK
1			ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD
j		1	NOYLKVLLALKLHKMREEGEEEGEGEK\LVEEALEKAPG\VTDV
ļ			LRSAA\KFYRGKDEPDKAIELLKKALEYIP\NNAYLHCQIGCCY
			RAKVFOVMNLRENGMYGKRKLLELIGHAVAHLKKADEANDNLFR
]	1	1	VCSILASLHALADOYEDAEYYFQKEFSKELTPVAKQLLHLRYGN
1			FOLYOMKCEDKAIHHFIEGVKINQKSREKEKMKDKLQKIAKMRL
ļ		1	
	1		SKNGADSEALHVLAFLQELNEKMQQADEDSERGLESGSLIPSAS
i		1	SWNGE
6001	176	1038	AFAHSPSRGHRHTHIHTPRHTPRCTMAESHLQSSLITASQFFEI
6001	176	1038	WLHFDADGSGYLEGKELQNLIQELQQARKKAGLELSPEMKTFVD
6001	176	1038	_ · · · · · · · · · · · · · · · · · · ·

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
í	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
-	sequence	•	\=possible nucleotide insertion)
		<del> </del>	LKLFDSNNDGKLELTEMARLLPVQENFLLKFQGIKMCGKEFNKA
			FELYDQDGNGYIDENELDALLKDLCEKNKQDLDINNITTYKKNI
		1	MALSDGGKLYRTDLALILCAGDN
6002	977	81	LAPPGGGLHIPPRTPLSHSRPPPSHHAPHPSPLPLPPADLHPHS
			SMAQRSDLLELDCQLTRDRVVVVSHDENLCRQSGLNRDVGSLDF
			EDLPLYKEKLEVYFSPGHFAHGSDRRMVRLEDLFQRFPRTPMSV
1	j	į .	EIKGKNEELIREQ/VLVRRYDRNEITIWASEKSSVMKKCKAANP
1		i	EMPLSFTISRGFWVLLSYYLGLLPFIPIPEKFFFCFLPNIINRT
1			YFPFSCSCLNQLLAVVSKWLIMRKSLIRHLEERGVQVVFWCLNE
			ESDFEAAFSVGATGVITDYPTALRHYLDNHGPAARTS
6003	140	4098	GKLRAFRGMRRLICKRICDYKSFDDEESVDGNRPSSAASAFKVP
1			APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA
1			FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKKIR
l			SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACITVA
i .			HLSTVLGNKFDHGAEAIVPTLFNLVPNSAKVMATSGCAAIRFII
			RHTHVPRLIPLITSNCTSKSVPVRRRSFEFLDLLLQEWQTHSLE
			RHAAVLVETIKKGIHDADAEARVEARKTYMGLRNHFPGEAETLY
			NSLEPSYOKSLOTYLKSSGSVASLPQSDRSSSSSQESLNRPFSS
1			KWSTANPSTVAGRVSAGSSKASSLPGSLQRSRSDIDVNAAAGAK
İ			AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGRV
			RAKLSAPLAGMGNAKADSRGRSRTKMVSQSQPGSRSGSPGRVLT
			TTALSTVSSGVQRVLVNSASAQKRSKIPRSQGCSREASPSRLSV
			ARSSRIPRPSVSQGCSREASRESSRDTSPVRSFQPLASRHHSRS
1			TGALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLNTGSDVEEA
I i			VADALLLGDIRTKKKPARRYESYGMHSDDDANSDASSACSERS
1 1			YSSRNGSIPTYMRQT\EDV\AEVLNRCASSNWSERKEGLLGLQN
İ I			LLKNORTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDFI
1			QVHKDDLQDWLFVLLTQLLKKMGADLLGSVQAKVQKALDVTRES
			FPNDLQFNILMRFTVDQTQTPSLKVKVAILKYIETLAKQMDPGD
1 1			FINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFBLNTPE
			FTMLLGALPKTFQDGATKLLHNHLRNTGNGTQSSMGSPLTRPTP
1 1			RSPANWSSPLTSPTNTSQNTLSPSAFDYDTENMNSEDIYSSLRG
1 1			VTEAIQNFSFRSQEDMNEPLKRDSKKDDGDSMCGGPG\MSDPRA
			GGDATDSSQTAL\DNKASLLHSMPTHSSPRSRDYNPYNYSDSIS
	,		PFNKSALKEAMFDDDADQFPDDLSLDHSDLVABLLKELSNHNER
			VEERKIALYELMKLTQEBSFSVWDEHFKTILLLLLETLGDKEPT
1			IRALALKVLREILRHQPARFKNYAELTVMKTLEAHKDPHKEVVR
1			SAEEAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKMQT
			KVIERVSKETLNLLLPEIMPGLIQGYDNSESSVRKACVFCLVAV
			HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS
			GQS
6004	140	4098	GKLRAFRGMRRLICKRICDYKSFDDEESVDGNRPSSAASAFKVP
			APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA
			FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDORANALKKIR
1 1			SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACITVA
			HLSTVLGNKFDHGAEAIVPTLFNLVPNSAKVMATSGCAAIRFII
			RHTHVPRLIPLITSNCTSKSVPVRRRSFEFLDLLLQEWQTHSLE
	1		RHAAVLVETIKKGIHDADAEARVEARKTYMGLRNHFPGEAETLY
1 1			NSLEPSYQKSLQTYLKSSGSVASLPQSDRSSSSSQESLNRPFSS
1 1			KWSTANPSTVAGRVSAGSSKASSLPGSLQRSRSDIDVNAAAGAK
1 1			AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGRV
]			RAKLSAPLAGMGNAKADSRGRSRTKMVSQSQPGSRSGSPGRVLT
	Ì	ļ	TTALSTVSSGVQRVLVNSASAQKRSKIPRSQGCSRRASPSRLSV
	.		ARSSRIPRPSVSQGCSREASRESSRDTSPVRSFQPLASRHHSRS
			TGALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLNTGSDVEEA
J - }			VADALLIGDIRTKKKPARRYESYGMHSDDDANSDASSACSERS
[	1		YSSRNGSIPTYMRQT\EDV\ABVLNRCASSNWSERKEGLLGLQN
	1	İ	LLKNORTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDFI
	ŀ		QVHKDDLQDWLFVLLTQLLKKMGADLLGSVQAKVQKALDVTRES
	1		FPNDLQFNILMRFTVDQTQTPSLKVKVAILKYIETLAKQMDPGD
			PINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFELNTPE
			TOTAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MANUAL MAN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding		
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			FTMLLGALPKTFQDGATKLLHNHLRNTGNGTQSSMGSPLTRPTP
	<b>!</b>	1	RSPANWSSPLTSPTNTSQNTLSPSAFDYDTENMNSEDIYSSLRG
ļ	1	ļ	VTEAIONFSFRSQEDMNEPLKRDSKKDDGDSMCGGPG\M9DPRA
Ì			GGDATDSSQTAL\DNKASLLHSMPTHSSPRSRDYNPYNYSDSIS
			PFNKSALKEAMFDDDADQFPDDLSLDHSDLVAELLKELSNHNER
1	1	1	VEERKIALYELMKLTQEESFSVWDEHFKTILLLLLETLGDKEPT
			IRALALKVLREILRHOPARFKNYAELTVMKTLEAHKDPHKEVVR
1			SAEEAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKMQT
	1	4	, , , , , , , , , , , , , , , , , , , ,
		<b>,</b>	KVIERVSKETLNLLLPEIMPGLIQGYDNSESSVRKACVFCLVAV
1			HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS
1			GQS
6005	133	5955	RSSGRRQEQLGQFPGRERKGMASGLGSPSPCSAGSEEEDMDALL
1			NNSLPPPHPENEEDPEEDLSETETPKLKKKKKPKKPRDPKIPKS
1		1	KRQKKERMLLCRQLGDSSGEGPEFVEEEEEVALRSDSEGSDYTP
1		1	GKKKKKKLGPKKEKKSKSKRKEEEEEDDDDDDDSKEPKSSAQLL
ļ		1	BDWGMEDIDHVFSEEDYRTLTNYKAFSQFVRPLIAAKNPKIAVS
Ì		Ī	KMMMVLGAKWREFSTNNPFKGSSGASVAAAAAAAVAVVESMVTA
1			TEVAPPPPPVEVPIRKAKTKEGKGPNARRKPKGSPRVPDAKKPK
1		ļ	PKKVAPLKIKLGGFGSKRKRSSSEDDDLDVESDFDDASINSYSV
ł		1	SDGSTSRSSRSRKKLRTTKKKKKKGEEEVTAVDGYETDHQDYCEV
1			COOGGEIILCDTCPRAYHMVCLDPDMEKAPEGKWSCPHCEKEGI
l	1	1	OWEAKEDNSEGEEILBEVGGDLEEEDDHHMEFCRVCKDGGELLC
1		1	
			CDTCPSSYHIHCLNPPLPEIPNGEWLCPRCTCPALKGKVQKILI
		ł	WKWGQPPSPTPVPRPPDADPNTPSPKPLEGRPERQFFVKWQGMS
1		j	YWHCSWVSELQLELHC\QVMFRNYQRKNDMDEPPSGDFGGDEEK
ı			S\RKRKNKDPKFAEMBERFYRYGIKPEW\MMIHRILNHSVDKKG
1		1	HVHYLIKWRDLPYDQASWESEDVEIQDYDLFKQSYWNHRELMRG
			EEGRPGKKLKKVKLRKLERPPETPTVDPTVKYERQPEYLDATGG
			TLHPYQMEGLNWLRFSWAQGTDTILADEMGLGKTVQTAVFLYSL
1 .		1	YKEGHSKGPFLVSAPLSTIIN\WEREFEMWAPDMYV\VTYVGDK
		i	DSRAIIRENEFS\FEDNAIRGGKKASRMKKEASVKFHVLLTSYE
		1	LITIDMAILGSIDWACLIVDEAHRLKNNQSKFFRVLNGYSLQHK
}	}	1	LLLTGTPLONNLEELFHLLNFLTPERFHNLEGPLEEFADIAKED
	1	1	QIKKLHDMLG\PHMLRRLKADVFKNMPSKTELIV\RVELSPM\Q
1			KKYYK\YILHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNHPY
			LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLOKMLKNLKEGGH
l			RVLIFSQMTKMLDLLEDFLEHEGYKYERIDGGITGNMRQEAIDR
	1	1	FNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQ
		1	AFSRAHRIGONKKVMIYRFVTRASVEERITOVAKKKMMLTHLVV
			RPGLGSKTGSMSKQELDDILKFGTEELFKDEATDGGGDNKEGED
			SSVIHYDDKAIERLLDRNQDETEDTELQGMNEYLSSFKVAQYVV
1			
			REEEMGEEEEVEREIIKQEESVDFDYWEKLLRHHYEQQQEDLAR
			NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEEGDE
			DFDERSEAPRRPSRKGLRNDKDKPLPPLLARVGGNIEVLGFNAR
1			QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVSLF
		}	MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKKVQ
			EFEHVNGRWSMPELAEVEENKKMSQPGSPSPKTPTPSTPGDTQP
			NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIECT
1	i		QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKGKG
	1		AADVEKVEEKSAIDLTPIVVEDKEEKKEEEEKKEVMLQNGETPK
1			DLNDEKOKKNIKORFMFNIADGGFTELHSLWONEERAATVTKKT
1			YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKGEM
ł	1		NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDPSH
			PSMALNTRFAEVECLAESHOHLSKESMAGNKPANAVLHKVLKQL
			EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP
	<b></b>	ļ	EPTPQQVAQQQ
6006	1	965	DNDFLRNTVHRHBPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC
			GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAAVS
1			ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKVGV
1			CRVDPRGKPCETVFQRLSYNGQSSVVRCRPLTGRTHQIRVHLQF
			LGHPILNDPIYNSVAWGPSRGRGGYIPKTNEELLRDLVAEHQAK

0.00	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ			(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	
NO:	nucleotide	location	Glutamic Acid, F≈Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid		Codon, /=possible nucleotide deletion,
1		sequence	\=possible nucleotide insertion)
	sequence		
_			QSLDVLDLCEGDLSPGLTDSTAPSSELGKDDLEELAAAA\QKME
	]		EVAEAAPQELDTIALASEKAVETDVMNQ\RQT\TLCRVPAGATG
i	1	Į	SLAPRPCDVPTCPTL
6007	3	2351	HELGOVEYVFTDKTGTLTENEMOFRECSINGMKYQEINGRLVPE
8007	1		GPTPDSSEGNLSYLSSLSHLNNLSHLTTSSSFRTSPENETELIK
]	į	1	
1	1	ł	EHDLFFKAVSLCHTVQINNVQTDCTGDGPWQSNLAPSQLEYYAS
}			SPDEKALVEAAARIGIVFIGNSEETMEVKTLGKLERYKLLHILE
1		1	FDSDRRRMSVIVQAPSGEKLLFAKGAESSILPKCIGGEIEKTRI
Į.			HVDEFALKGLRTLCIAYRKFTSKEYEEIDKRIFEARTALQQR\E
		į	EKLAAVFOFIEKDLILLGATAVEDRLODKVRETIEALRMAGIKV
			WVLTGDKHETAVSVSLSCGHFHRTMNILELINQKSDSBCAEQLR
1			OLARRITEDHVIOHGLVVDGTSLSLALREHEKLFMEVCRNCSAV
1			[ = · · · ·
1	1	1	LCCRMAPLQKAKVIRLIKISPEKPITLAVGDGANDVSMIQEAHV
		1	GIGIMGKEGRQAARNSDYAIARFKFLSKLLFVHGHFYYIRIATL
1		1	VQYFFYKNVCFITPQFLYQFYCLFSQQTLYDSVYLTLY\NICFT
		1	SLPILIYSLLEQHVDPHVLQNKPTLYRDISKNRLLSIKTFLYWT
		[	ILGFSHAFIFFFGSYLLIGKDTSLLGNGQMFGNWTFGTLVFTVM
	1	1	VITVTVKMALETHFWTWINHLVTWGSIIFYFVFSLFYGGILWPF
			LGSONMYFVFIQLLSSGSAWFAIILMVVTCLFLDIIKKVFDRHL
l .		1	HPTSTEKAQLTETNAGIKCLDSMCCFPEGEAACASVGRMLERVI
			·-
			GRCSPTHISRSWSASDPFYTNDRSILTLSTMDSSTC
6008	4554	1089	AGVRRAGARRGPGRALPAGATAVPPPSARRRRRCPAPEHAGPAR
		1	ASRPSQETMFQLPVNNLGSLRKARKTVKKILSDIGLEYCKEHIE
1		1	DFKQFEPNDFYLKNTTWEDVGLWDPSLTKNQDYRTKPFCCSACP
1	1	1	FSSKFFSAYKSHFRNVHSEDFENRILLNCPYCTFNADKKTLETH
			IKIFHAPNASAPSSSLSTFKDKNKNDGLKPKQADSVEQAVYYCK
1	}		KCTYRDPLYEIVRKHIYRBHFQHVAAPYIAKAGEKSLNGAVPLG
			SNAREESSIHCKRCLFMPKSYEALVOHVIEDHERIGYQVTAMIG
1	1		
		1	HTNVVVPRSKPLMLIAPKPQDKKSMGLPPRIGSLASGNV\RSLP
1	i		SQQMVNRLSIPKPNLNSTGVNMMSSVHLQQNNYGVKSVGQGYSV
i			GQSMRLGLGGNAPVSIPQQSQSVKQLLPSGNGRSYGLGSEQRSQ
İ		Į.	APARYSLQSANASSLSSGQLKSPSLSQSQASRVLGQSSSKPAAA
ł	l .	1	ATGPPPGNTSSTQKWKICTICNELFPENVYSVHFEKEHKAEKVP
-	1		AVANYIMKIHNFTSKCLYCNRYLPTDTLLNHMLIHGLSCPYCRS
	1	Į.	TFNDVEKMAAHMRNVHIDEEMGPKTDSTLSFDLTLQQGSHTNIH
1	1		LLVTTYNLRDAPAESVAYHAONNPPVPPKPOPKVQEKADIPVKS
1			
			SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERHQVIQ
1			TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLVHCRGVGKTQN
1	1		GQDKTNAPSRLNQSPSLAPVKRTYEQMEFPLLKKRKLDDDSDSP
1			SFFEEKPEEPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPYP
i		}	TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL
			LGFNMKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN
		1	LGKEDDSSSDSFENLEEESNESGSPFDPVFEVEPKISNDNPEEH
			VLKVIPEDASESEEKLDOKEDGSKYETIHLTEEPTKLMHNASDS
			EVDODDVVEWKDGASPSESGPGSOOVSDFEDNTCEMKPGTWSDE
1		1	7
1			SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD
			QSQWKNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP
			MHGSLAGVKLSSQQA
6009	4272	1534	CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC
1			HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW
i			EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG
		1	RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL
i			NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG
1		i	1
1	İ		NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA
	1	1	VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL
1		1	FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP
i			I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN
ł			AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG
		1	DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP
j	ļ	1	RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT
1			
		<u> </u>	RDLLRGGDRGHVVVIVLCRLGSLVGGLGTDBLLWFGGR*LIIIG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	0042000	\=possible nucleotide insertion)
			I**RGRLSGEWGCGLGRGELFQVSIGIGVSIVHIGOGDHEVLGG
			AGLVERGALHATGQGVEALVQQLLDVGPAGALGLCDGAALFOGP
1 1			GRVGQLPAEGLQVCITLVAQWRMHDGRELGGAEWPWQALHGAAI
			CGVGGAILLKALSQYFLKGG*RLWCARGQ*PVKKRQRRWRG*TR
			R*NGLTIHCFN*LI*GAVCCRLVILRWCGLLEVHGVYGT*IHCL
ļ			GSFPGRLWP*PFISQERPNGHCQWEFRLAVPSWKCRWSRWRVRG
1			TWRYGNPLLNLL*GAWLGGAACGGQQGGPLSTWQACTGPGQAAF
			LPPFQGACRPRTQRCRTWVCPIAWRQLLAYTRD
6010	1	3533	IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM
			AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD
			PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA
			TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL
ł			VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS
<b>i</b>			IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP
			PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC
			IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP
			IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM
			TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK
1			EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG
ł			TFVDYQTTVVKYSKALAVTAQEMMTKSVTNPEELGGLASQMTSD
i			YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\
			ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI
			TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA
1			KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA
			SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM
			YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ
1			ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE
			DVIATANLSRKAVSDMLTACKQASFHPDVSDEVRTRALRFGTEC
			TLGYLDLLEHVLVILQKPTPELKQQLAAFSKRVAGAVTELIQAA
1			EAMKGTEWVDPEDPTVIAETELLGAAASIEAAAKKLEQLKPRAK
			PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAQGK
ļ			VGSIPANAADDGQWSQGLISAARMVAAATSSLCEAANASVQGHA
1			SEEKLISSAKQVAASTAQLLVACKVKADQDSEAMRRLQAAGNAV
1			KRASDNLVRAAQKAAFGKADDDDVVVKTKFVGGIAQIIAAQEEM
			LKKERELEEARKKLAQIRQQQYKFLPTELREDEG
6011	446	1835	LLQPAMRKSPGLSDCLWAWILLLSTLTGRSYGQPSLQDELKDNT
			TVFTRILDRLLDGYDNRLRPGLGERVTEVKTDIFVTSFGPVSDH
1			DMEYTIDVFFRQSWKDERLKFKGPMTVLRLNNLMASKIWTPDTF
			FHNGKKSVAHNMTMPNKLLRITEDGTLLYTMRLTVR\AECPMAF
			GRDFPM\D\AHACPLKFGSYAYTRAEVVYEWTREPARSVVVAED
			GSRLNQYDLLGQTVDSGIVQSSTGEYVVMTTHFHLKRKIGYFVI
			QTYLPCIMTVILSQVSFWLNRESVPARTVFGVTTVLTMTTLSIS ARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRGYA
			WDGKSVVPEKPKKVKDPLIKKNNTYAPTATSYTPNLARGDPGLA
]			TIAKSATIEPKEVKPETKPPEPKKTFNSVSKIDRLSRIAFPLLF
			GIFNLVYWATYLNREPQLKAPTPHO
6012	351	5013	PAELFQSFAIWHKELYDWRLGPWNQCQPVISKSLEKPLECIKGE
	]	2013	EGIQVREIACIQKDKDIPAEDIICEYFEPKPLLEQACLIPCOOD
			CIVSEFSAWSECSKTCGSGLQHRTRHVVAPPQFGGSGCPNLTEF
		'	QVCQSSPCEAEELRYSLHVGPWSTCSMPHSRQVRQARRRGKNKE
}			REKDRSKGVKDPEARELIKKKRNRNRQNRQENKYWDIQIGYQTR
			EVMCINKTGKAADLSFCQQEKLPMTFQSCVITKECQVSEWSEWS
			PCSKTCHDMVSPAGTRVRTRTIRQFPIGSEKECPEFEEKEPCLS
	İ		QGDGVVPCATYGWRTTEWTECRVDPLLSQQDKRRGNQTALCGGG
			IQTREVYCVQANENLLSQLSTHKNKEASKPMDLKLCTGPIPNTT
		,	QLCHIPCPTECEVSPWSAWGPCTYENCNDQQGKKGFKLRKRRIT
			NEPTGGSGVTGNCPHLLEAIPCEEPACYDWKAVRLGDCEPDNGK
			BCGPGTQVQEVVCINSDGEEVDRQLCRDAIFPIPVACDAPCPKD
1			
1			CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRCP NSSALOEVRSCNEHPCTVVHWOTGPWGOCIRDTSVSSENTTTTW
			CVLSTWSTWSSCSHTCSGKITEGKQIRARSILAYAGEEGGIRCP NSSALQEVRSCNEHPCTVYHWQTGPWGQCIEDTSVSSFNTTTTW NGEASCSVGMQTRKVICVRVNVGQVGPKKCPESLRPETVRPCLL

	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning		Glutamic Acid, F-Phenylalanine, G-Glycine,
NO:	nucleotide	location	
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
<del></del>	<del>                                     </del>		PCKKDCIVTPYSDWTSCPS\SCKEGDSSIRKQSRHRVIIQLPAN
1	1		GGRDCTDPLYEEKACEAPQACQSYRW\KTHKW\HRCQ\LVP\WS
1	}	1	VQQDSP\GAQEGCGPGRQARAITCRKQDGGQAGIHECLQYAGPV
1			PALTOACQIPCODDCQLTSWSKFSSCNGDCGAVRTRKRTLVGKS
		İ	KKKEKCKNSHLYPLIETOYCPCDKYNAOPVGNWSDCILPEGKVE
1	1	İ	-
1			VLLGMKVQGDIKECGQGYRYQAMACYDQNGRLVETSRCNSHGYI
1	}	1	EEACIIPCPSDCKLSEWSNWSRCSKSCGSGVKVRSKWLREKPYN
1	<b>\$</b>		GGRPCPKLDHVNQAQVYEVVPCHSDCNQYLWVTEPWSICKVTFV
	1	l	NMRENCGEGVQTRKVRCMQNTADGPSEHVEDYLCDPEEMPLGSR
}	1		VCKLPCPEDCVISEWGPWTQCVLPCNQSSFRQRSADPIRQPADE
	1	1	GRSCPNAVEKEPCNLNKNCYHYDYNVTDWSTCQLSEKAVCGNGI
	1		KTRMLDCVRSDGKSVDLKYCEALGLEKNWQMNTSCMVECPVNCQ
1	İ		LSDWSPWSECSQTCGLTGKMIRRRTVTQPFQGDGRPCPSLMDQS
1	1	1	KPCPVKPCYRWQYGQWSPCQVQEAQCGEGTRTRNISCVVSDGSA
1	1		DDFSKVVDBEFCADIBLIIDGNKNMVLEBSCSQPCPGDCYLKDW
1			SSWSLCOLTCVNGEDLGFGGIQVRSRPVIIQELENQHLCPEQML
1			ETKSCYDGQCYEYKWMASAWKGSSRTVWCQRSDGINVTGGCLVM
	1		SOPDADRSCNPPCSQPHSYCSETKTCHCEEGYTEVMSSNSTLEQ
		ŀ	1
		1	CTLIPVVVLPTMEDKRGDVKTSRAVHPTQPSSNPAGRGRTWFLQ
ĺ			PFGPDGRLKTWYYGVAAGAFVLLIFIVSMIYLACKKPKKPQRRQ
1			NNRLKPLTLAYDGDADM
6013	1161	710	GAFIAGVPVQPVLIRYPNSLDTTSWAWRGPGVLKVLWLTASQPC
ł			SIVDVEFLPVYHPSPEESRDPTLYANNVQRVMAQALGIPATECE
j			FVGSLPVIVVGRLKVALEPQL/WGTGKSASEGWAVRWLCGRWGR
ļ			ARPESNDQPGRVCQAATAL
6014	2857	613	EAVAGGMEKSRMNLPKGPDTLCPDKDEFMKEDFDVDHFVSDCRK
0011	1 203.		RVQLEELRDDLELYYKLLKTAMVELINKDYADF\VNLSTNLVGM
	ŀ	l	DKALNOLSVPLGQLREEVLSLRSSVSEGIRAVDERMSKQEDIRK
	1		KKMCVLRLIQVIRSVEKIEKILNSQSSKETSALEASSPLLTGQI
		1	
	1		LERIATEFNQLQFHACQSK\GMPLLDKVRPRIAGITAMLQQSLE
l l			GLLLEGLQTSDVDIIRHCLRTYATIDKTRDAEALVGQVLVKPYI
	1	1	DEVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS
1	1		EKGNTVPGYDFLVNSVWPQIVQGLEEKLPSLFNPGNPDAFHEKY
	1	1	TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYFQI
}	i	i	RFREIAGSLEAALTDVLEDAPAESPYCLLASHRTWSSLRRCWSD
		1	EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKE
	1	1	IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV
1	1		ADLDKLQEQLPELLEIIKPKLEMIGFKNFSSISAALEDSQSSFS
1	1		ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKEVPTTAS
1			SYVDSALKPLFQLQSGHKDKLKQAIIQQWLEGTLSESTHKYYET
1		1	VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL
1			OLALDVEYLGEQIQKLGLQASDIKSFSALAELVAAAKDQATAEQ
			p
		I	
6015	13	2237	AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC
1		1	VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN
			RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY
	İ	i	GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT
1			HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR
			EGIEEEDQEEDKNIVVDDITEQKPBPQDDGKSTESDVKADGDSK
1		1	GSEEVDSHCKKALSHKELYERARELLVSYEEEQFTVLEKFRYLP
			KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT
i	}		FEOLAALQIEYEENVDLNDVLVPKPFSQFWQPLLRGLHSQNFTQ
		1	ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRF
1	1		SAGOWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPOLLRII
l	1		
i			F\KAMGQGLQDE\EQEKLLRICSIYTQSGENSLVQEGSEASPIG
			KSPYTLDSLYWSVKPASSSFGSEAKAQQQEEQGSVNDVKBEEKE
			EKEVLPDQVEEEEENDDQBEEEEDEDDEDDEEBDRMEVGPFSTG
			QESPTAENARLLAQKRGALQGSAWQVSSEDVRWDTFP\LGRMPR
			SRPRTPAELMLENYDTHVIFWTKPVL\EQRLEPSTCK\TDTLGL
,	1		\SCGVGS\GNCSNSSSSNFRGAFLLRARGSLH\GL\KTGLQLF
6016	. 13	2237	AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC
		<del></del>	

0.00	1 5 3/ 3	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted		
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		1	
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
İ	sequence	•	\=possible nucleotide insertion)
<u> </u>	20420000		VKGKGSLPLSAHGIVVAWLSRAEWDOVTVYLFCDDHKLORYALN
	1	1	RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY
	f	ł	GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT
1	Į.	i	HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR
į.			EGIEEEDQEEDKNIVVDDITEQKPEPQDDGKSTESDVKADGDSK
1			
ļ		Ì	GSEEVDSHCKKALSHKELYERARELLVSYEEEQFTVLEKFRYLP
1	ì		KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT
J	ļ		FEQLAALQIEYEENVDLNDVLVPKPFSQFWQPLLRGLHSQNFTQ
1	ļ		ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRF
ì	1	1	SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPOLLRII
1	ł	1	
1	1	1	F\KAMGQGLQDE\EQEKLLRICSIYTQSGENSLVQEGSEASPIG
1		1	KSPYTLDSLYWSVKPASSSFGSEAKAQQQEEQGSVNDVKEEEKE
1		ĺ	EKEVLPDQVEEEERNDDQEEBEEDEDDBDDEEEDRMEVGPFSTG
1		1	QESPTAENARLLAQKRGALQGSAWQVSSEDVRWDTFP\LGRMPR
		1	SRPRTPAELMLENYDTHVIFWTKPVL\EQRLEPSTCK\TDTLGL
1	1	1	\SCGVGS\GNCSNSSSSNFRGAFLLEARGSLH\GL\KTGLQLF
	1	7750	l
6017	203	3469	SHQEIEQNSAMAPRKRGGRGISFIFCCFRNNDHPEITYRLRNDS
1			NFALQTMEPALPMPPVEELDVMFSELVDELDLTDKHREAMFALP
	·	ì	AEKKWQIYCSKKKDQEENKGATSWPEFYIDQLNSMAARKSLLAL
1	1	ł.	EKEEEEERSKTIESLKTALRTKPMRFVTRFIDLDGLSCILNFLK
1	1		TMDYETSESRIHTSLIGCIKALMNNSQGRAHVLAHSESINVIAQ
		1	SLSTENIKTKVAVLEILGAVCLVPGGHKKVLOAMLHYOKYASER
İ			
	1		TRFQTLINDLDKSTGRYRDEVSLKTAIMSFINAVLSQGAGVESL
1	1		DFRLHLRYE\FLMLGIHPVMDKLRKHENSTLDRHLDFFEMLRNE
İ			DELEFAKRFELVHIDTKSATQMFELTRKRLTHSEAYPHFMSILH
		1	HCLQMPYKRSGNTVQYWLLLDRIIQQIVIQNDKGQDPDSTPLEN
	1		FNIKNVVRMLVNENEVKOWKEQABKMRKEHNBLOOKLBKKEREC
			DAKTQEKEEMMQTLNKMKEKLEKETTEHKQVKQQVADLTAQLHE
-		!	
			LSRRAVCASIPGGPSPGAPGGPFPSSVPGSLLPPPPPPPPLPGGM
	1	i	LPPPPPPLPPGGPPPPPGPPPLGAIMPPPGAPMGLALKKKSIPQ
İ	1	1	PTNALKSFNWSKLPENKLEGTVWTEIDDTKVFKILDLEDLERTF
	1		SAYQRQQDFFVNSNSKQKEADAIDDTLSSKLKVKELSVIDGRRA
1	1		QNCNILLSRLKLSNDEIKRAILTMDEQEDLPKDMLEQLLKFVPE
	i	1	KSDIDLLEEHKHELDRMAKADRFLFEMSRINHYQQRLQSLYFKK
	1		KFAERVAEVKPKVEAIRSGSEEVFRSGALKOLLEVVLAFGNYMN
	1	ľ	
			KGQRGNAYGFKISSLNKIADTKSSIDKNITLLHYLITIVENKYP
	1	1	SVLNLNEELRDIPQAAKVNMTELDKEISTLRSGLKAVETELEYQ
1			KSQPPQPGDKFVSVVSQFITVASFSFSDVEDLLAEAKDLFTKAV
	1		KHFGEEAGKIQPDEFFGIFDQFLQAVSEAKQENENMRKKKEEEE
	1		RRARMEAQLKEQRERERKMRKAKENSEESGEFDDLVSALRSGEV
	1		FDKDLSKLKRNRKRITNOMTDSSRERPITKLNF
	<del> </del>	1 25-2	I
6018	13	2510	TISQSGGIRRRREAVWFEVVNMDFSRLHMYSPPQCVPENTGYTY
1			ALSSSYSSDALDFETEHKLDPVFDSPRMSRRSLRLATTACTLGD
1	1	1	GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINHVSRQV
1			TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD
1			GDLKGGNKAAIOGNGDVGAGAATGHNGFFCSNCNMLSERKDVLT
[			AHPAAPGPVSRVYSRDRNOKCDDCKGKRHLDAHPGRAGTLWHIW
			1
1			ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF
1			WWLGIGWYQFVTLISWLNVFLLTRCLRNICKFLVLLIPLFLLLG
1			LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ
1			PLOGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLOK
1			LOARVDOMEGGAAGPSASVRDAVGOPPRETDFMAFHOEHEVRMS
		1	
1			HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL
ł			ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED
ì			QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV
l			TKOLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSODKTG
1	1		MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR
I			
i			VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL
1			SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF
L			QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK
6019	2	1066	TPNDREPPPQRPPSSRRASHLAQEITSAASLGDQTQILGSLTTA
	<del></del>	<u> </u>	<u> </u>

SEO	Predicted	Predicted end	Doming pold compart and
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
I NO:	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			PVITSAIRSMPGISSQILTNAQGQVIGTLPWVVNSASVAAPAPA
1			QSLQVQAVTPQLLLNAQGQVIATLASSPLPPPVAVRK\PSTPES
	1		
	ľ		LLKSEVQPIKPTPTVPQPAVVIASPAPAAKPSASAPIPITCSET
			PTVSQLVSKPHTPSLDEDGINLEEIREFAKNFKIRRLSLGLTQT
1			QVGQALTATEGPAYSQSAICRFEKLDITPKSAQKLKPVLEKWLN
ł			EAELRNQEGQQNLMEFVGGEPSKKRKRRTSFTPQAIEALNAYFE
1			KNPLPTGQEITEIAKELNYDREVVRVWFCNRRQTLKNTSKLNVF
			QIP
6020	4953	549	EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW
1			AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI
1			QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTOI
	1		RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE
1	1		EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
			GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE
i	İ		
			GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF
1	1		FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP
1			GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR
I	1		AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD
!	1		LTQTASSTAGAMEELQDQEGWBYASLIGWKFHWKQRSSDTFRRR
			RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA
ĺ	1		TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP
			YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ
	1		NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW
			HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP
			QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGGERV
1	1		ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVIDHRO
	<b>[</b>		FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR
			DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEEIV
			DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVABFEGLT
			DFSDTFKLYRGKSDENEDPSVVGEFKGSFRIYPLPDDPSVPAPP
	i l		BORDEL DOCUMENTALINGUES OF COMPANY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
i	1		RQFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG
ł	1 1		KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD
	ļ		TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
	1 1		RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE
			FEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP
			NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE
	1		NKQKTDVHYRSLDGEGNFNWRFVFPFDYLPAEQLCIVAKKEHFW
			SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI
1			HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW
1	}		PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP
			KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL
			LFVAVLLYSLPNYLSMKIVKPNV
6021	4953	549	EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW
			AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI
1			QGKIPANQLAELWLKLIDBVIEDTRYTLPLTEGKANVTVLDTQI
l			DKI DCDGI COTIER FIDADCE FEBRUARY
			RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE
			EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
			GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE
Ì			GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF
			FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP
J i			GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR
			AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD
			LTQTASSTAGAMBELQDQEGWEYASLIGWKFHWKQRSSDTFRRR
			RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA
	]		TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP
[	[	[	VANICELUD COMPRET THE STANDARD COMPANDA TO THE STANDARD COMPRET THE STANDARD COMPANDA TO THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA THE STANDARD COMPANDA
]			YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ
]			NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW
	[	İ	HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP
] ]		ļ	QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGGERV
		1	BSVVIKNLKKTPNPPSSVLFMKVFLPKEBLYMPPLVIKVIDHRQ
	<u> </u>		FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR

	15-37-5	15-32-1	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Į.	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
[	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
<b>-</b>	1	<del> </del>	DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEEIV
İ	1		
	1		DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT
Į			DFSDTFKLYRGKSDENEDPSVVGEFKGSFRIYPLPDDPSVPAPP
l.			ROFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG
			KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD
		•	TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
1	i		RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE
			FEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP
	ļ		NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE
i			NKQKTDVHYRSLDGEGNFNWRFVFPFDYLPAEQLCIVAKKEHFW
			SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI
	1	1	HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW
I		1	PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP
			KLDLPNRPBTSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL
			LFVAVLLYSLPNYLSMKIVKPNV
6022	4953	549	1
0022	1,222	543	EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW
		1	AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI
ł	1		QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI
1			RKLRSRSLSQIHEAAVRMRSEATDVKSTLABIEDWLDKLMQLTE
1	}	1	EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
			GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE
			GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF
		1	FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP
		1	GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR
			AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD
		1	LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKORSSDTFRRR
		1	RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA
)			TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP
1			YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ
		1	
			NPFKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW
ľ		1	HPVMNGDKACGDVLVTABLILRGKDGSNLPILPPQRAPNLYMVP
1			QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGGERV
			ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ
		1	FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR
			DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEBEIV
		1	DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT
			DFSDTFKLYRGKSDENEDPSVVGEFKGSFRIYPLPDDPSVPAPP
		1	RQFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG
-			KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD
			TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
		1	RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE
		1	FEANKILHOHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP
1			NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE
			NKQKTDVHYRSLDGEGNFNWRFVFPFDYLPAEQLCIVAKKEHFW
		!	SIDQTEFRIPPR\LIQIW\DNDKFS\LDDYLGFPRTLTCRHTI
*			
			HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW
			PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP
			KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL
			LFVAVLLYSLPNYLSMKIVKPNV
6023	102	916	SQELGMFVELNNLLNTTPDRAEQGKLTLLCDAKTDGSFLVHHFL
			SFYLKANCKVCFVALIQSFSHYSIVGQKLGVSLTMARERGQLVF
		1	LEGL/IVCSGR\VFQAQKEPHPLQFLREANAGNLKPLFEFVREA
			LKPVDSGEARWTYPVLLVDDLSVLLSLGMGAVAVLDFIHYCRAT
		1	VCWELKGNMVVLVHDSGDAEDEENDILLNGLSHQSHLILRAEGL
		i	ATGFCRDVHGQLRILWRRPSQPAVHRDQSFTYQYKIQDKSVSFF
1		!	AKGMSPAVL
6024	3	3260	
3029	د	3200	FLSFLCYPRFRCLFCLQFAIPASRMEQLNELELLMEKSFWEEAR
ļ			LPAELFQKKVVASFPRTVLSTGMDNRYLVLAVNTVQNKEGNCEK
}			RLVITASQSLENKELCILRNDWCSVPVEPGDIIHLEGDCTSDTW
,			IIDKDFGYLILYPDMLISGTSIASSIRCMRRAVLSETFRSSDPA
	<u> </u>	L	TROMLIGTVLHEVFOKAINNSFAPEKLOELAFOTIOEIRHLKEM

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amino acid residue of amino acid sequence  ### A		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Residue of amino acid sequence   NeTryptophan, Y=Tyrosine, X=Unknown, *=stop Codon, (*possible nuclectide deletion)   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment   Veninsoperiment	1	amino acid	residue of	
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WIRSRLTEAVRLSNQGFQAYDFPAVTTAQYSFWLYELCDVYLEC LKPVLNGVDQVAAECARGTLYTCLDVGLRLLSPFMPFVTEELFQ RLPRRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP ARREIG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEAELRKVDRAIALPQKML  6026  2674  514  GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESIML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP				
LKPVLNGVDQVAAECARQTLYTCLDVGLRLLSPFMPFVTEELFQ RLPRRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEAELRKVDEAIALPQKML COERPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRRIEATNNPRLSYIHPNAFFRLPKLESIML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMMMKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP	1			KILGIRHFCNKLWNATKFALRGLGKGFVPSPTSQPGGHESLVDR
RLPRRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP ARELG\KLQ\AKKVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEAELRKVDEAIALPQKML 6026 2674 514 GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LURLHLNSRRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFDURRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESIML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMMMKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP	1	į į		
VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP ARELG\KLQ\\AKRVEAQ\RQAQ\RLIR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEAELRKVDEAIALPQKML  6026 2674 514 GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LURLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVVNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMMMKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP	}			
VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP ARELG\KLQ\\AKRVEAQ\RQAQ\RLIR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEAELRKVDEAIALPQKML  6026 2674 514 GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LURLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVVNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMMMKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP		]		
QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP ARELG\KLQ\AKRVEAQ\RQAQ\RLIR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEAELRKVDEAIALPQKML  6026 2674 514 GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVVNLEATANNPRLSYIHPNAFFRLPKLESIML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMMMKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP		}		VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVOGPG
ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEAELRKVDEAIALPQKML  6026  2674  514  GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVVNDLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMMMKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP				QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLOLOG\LLDP
VQEADEAKLQQTEAELRKVDEAIALPQKML  6026  2674  514  GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESIML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP	]			
G026  2674  514  GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNILISTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESIML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWNNMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP	1			
TCBIRPWFTPRSIYMEASTVDCNDLGLLTPFARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LURLHINSNRLQMINSKWFDALPNLBILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVVNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMMMKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP	6026	2674	514	
TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNILSTISPGAFIGLHN LURLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFDURLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRRIEATNNPPLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP	1		•	
YLEENKLTELPEKCLSELSNLQELYINHNILSTISPGAFIGLHN LURLHINSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPPLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMMMKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP	]			
LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP				
PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP				
VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP				
ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP				
ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP				VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL
NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP	1			
IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP	1			
	1			
CHARLES TO STRUCKMAN (EFGIETTALTI-SOGKLESMI (DID				
		<u> </u>		

SEQ	Predicted	T Book at the A Town	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
}			KFYVHSEGTLDINGVTPKEGGLYTCIATNLVGADLKSVMIKVDG
			SFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFVK
Ì			TENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNR
1			KKCVNVTTKGLHPDQKEYEKNNTTTLMACLGGLLGIIGVICLIS
			CLSPEMNCDGGHSYVRNYLQKPTFALGELYPPLINLWEAGKEKS
6027	5254	4148	TSLKVKATVIGLPTNMS
10027	3234	4140	GGRRAPGRPGRSIKDEEEBTVFREVVSFSPDPLPVRYYDKDTTK
ł	1	İ	PISFYLSSLEELLAWKPRLEDGFNVALEPLACROPPLSSQRPRT
1			LLCHDMMGGYLDDRFIQGSVVQTPYAFYHWQCIDVFVYFSHHTV TIPPVGWTNTAHRHGVCVLGTFITEWNEGGRLCEAFLAGDERSY
1		ĺ	QAVADRLVQIT\RFFFFDGWLINIENSLSLAAVGNMPPFLRYLT
•	ļ		TQLHRQVPGGLVLWYDSVVQSGQLKWQDELNQHNRVFFDSCDGF
			FTNYNWREEHLERMLGQAGERRADVYVGVDVFARGNVVGGRFDT
1			DKVGGGFRPRASGPVPPLGPHFLMDLPFPSAPQRNDSSCSSQSG
]		ļ	DPVALRNRCPAPAKLCPH
6028	120	3432	NCLLLQAKGFHGEIEDLQQWLTDTERHLLASKPLGGLPETAKEQ
		Í	LNVHMEVCAAFEAKEETYKSLMQKGQQMLARCPKSAETNIDQDI
			NNLKEKWESVETKLNER\KT\KLEEALNLA\MEFHNSL\ODFIN
			WLTQAEQTLNVASRPSLILDTVLFQIDEHKVFANEVNSHREOII
			ELDKTGTHLKYFSQKQDVVLIKNLLISVQSRWEKVVQRLVERGR
			SLDDARKRAKOFHEAWSKLMEWLEESEKSLDSELEIANDPDKIK
i			TQLAQHKEFQKSLGAKHSVYDTTNRTGRSLKEKTSLADDNLKLD
	'		DMLSELRDKWDTICGKSVERQNKLEEA\LLFSGQFTDALQALID
1			WLYRVEPQLAEDQPVHGDIDLVMNLIDNHKAFQKELGKRTSSVQ
1			ALKRSARELIEGSRDDSSWVKVQMQELSTRWETVCALSISKQTR
			LEAALRQAEEFHSVVHALLEWLAFAEQTLRFHGVLPDDEDALRT
İ			LIDQHKEFMKKLEEKRAELNKATTMGDTVLAICHPDSITTIKHW
}		t	ITIIRARFEEVLAWAKQHQQRLASALAGLIAKQELLEALLAWLQ
			WAETTLTDKDKEVIPQEIEEVKALIAEHQTFMEEMTRKQPDVDK VTKTYKRRAADPSSLQSHIPVLDKGRAGRKRFPASSLYPSGSQT
1			QIETKNPRVNLLVSKWQQVWLLALERRRKLNDALDRLEELREFA
			NFDFDIWRKKYMRWMNHKKSRVMDFFRRIDKDQDGKITRQEFID
,			GILSSKFPTSRLEMSAVADIFDRDGDGYIDYYEFVAALHPNKDA
			YKPITDADKIEDEVTRQVAKCKCAKRFQVEQIGDNKYRFFLGNQ
			FGDSQQLRLVRILRSTVMVRVGGGWMALDEFLVKNDPCRAKGRT
			NMELREKFILADGASQGMAAFRPRGRRSRPSSRGASPNRSTSVS
			SQAAQAASPQVPATTTPKILHPLTRNYGKPWLTNSKMSTPCKAA
			ECSDFPVPSARGTPIQGSKLRLPGYLSGKGFHSGEDSGLITTAA
			ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE
			IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK
6020		3500	LDKSSKR
6029	1	3533	IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM
			AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD
			PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA
			TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL
			VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS
			IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC
			IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP
			IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM
			TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK
į	1	ĺ	EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG
]	j		TFVDYQTTVVKYSKALAVTAQEMMTKSVTNPEELGGLASQMTSD
			YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\
			ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI
[	Ì		TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA
	1		KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA
			SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM
			YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ
	Ī		BLTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCROB
Ll			DVIATANLSRKAVSDMLTACKQASFHPDVSDEVRTRALRFGTEC

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	Amino acid segment containing signal peptide
1			(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W. Therefore V. Therefore V. There
1			W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
			TLGYLDLLEHVLVILQKPTPELKQQLAAFSKRVAGAVTELIQAA
			EAMKGTEWVDPEDPTVIAETBLLGAAASIEAAAKKLEQLKPRAK
		İ	PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAQGK
		1	VGSIPANAADDGQWSQGLISAARMVAAATSSLCEAANASVQGHA
		İ	SEEKLISSAKOVAASTAOLLVACKVKADODSEAMRRLQAAGNAV
1	1	1	KRASDNLVRAAQKAAFGKADDDDVVVKTKFVGGIAQIIAAQEEM
	1		LKKERELEEARKKLAQIRQQQYKFLPTELREDEG
6030	3	1777	FPGRGSPALQLEVLICLGLMGLERALNVLAPIFYRNIVNLLTEN
1			APWNSLAWTVTSYVFLKFLQGGGTGSTGFVSNLRTFLWIRVOOF
		i	
		Į.	TSRRVELLIFSHLHELSLRWHLGRRTGEVLRIADRGTSSVTGLL
		1	SYLVFNVIPTLADIIIGIIYFSMFFNAWFGLIVFLCMSLYLTLT
			IVVTEWRTKFRRAMNTQENATRARAVDSLLNFETVKYYNAESYE
		1	VERYREAIIKYQGLEWKSSASLVLLNQTQNLVIGLGLLAGSLLC
1		1	AYFVTEQKLQVGDYVLFGTYIIQLYMPLNWFGTYYRMIQTNFID
1		1	MENMFDLLKK\ETEVKDLPGAGPFRFQKGRIEFENVHFSYADGR
1			ETLQDVSFTVMPGQTLALVGPSGAGKSTILRLLFRFYDISSGCI
		1 .	
ì	1		RIDGQDISQVTQALFRFSHWELCPKDTVLFNDTIADNIRYGRVT
1	1	1	AGNDEVEAAAQAAGIHDAIMAFPEGYRTQVGERGLKLSGGEKQR
1			VAIARTILKAPGIILLDEATSALDTSNERAIQASLAKVCANRTT
1	1		IVVAHRLSTVVNADQILVIKDGCIVERGRHEALLSRGGVYADMW
			QLQQGQEETSEDTKPQTMER
6031	160	1694	LRMSENLDKSNVNEAGKSKSNDSEEGLEDAVEGADEALQKAIKS
			DSSSPQRVQRPHSSPPRFVTVEELLETARGVTNMALAHEIVVNG
1	1	!	
ł	•		DFQIKPVELPENSLKKRVKEIVHKAFWDCLSVQLSEDPPAYDHA
1		1	IKLVGEIKETLLSFLLPGHTRLRNQITEVLDLDLIKQEAENGAL
	ł	1	DISKLAEFIIGMMGTLCAPARDERVKKLKDIKEIVPLFREIFSV
	1 .		LDLMKVDMANFAISSIRPHLMQQSVEYERKKFQEILERQPNSLD
			FVTQWLEEASEDLMTQKYKHALPVGGMAAGSGDMPRLSPVAVON
	1		YAYLKLLKWDHLQRPFPETVLMDQSRFHELQLQ\REQLTILGAV
			LLVTFSMAAPGISSQADFAEKLKMIVKILLTDMHLPSFHLKDVL
1		į	
}		ľ	TTIGEKVCLEVSSCLSLCGSSPFTTDKETVLKGQIQAVASPDDP
1	1	ł.	IRRIMESRILTFLETYLASGHQKPLPTVPGGLSPVQRELEEVAI
			KFARLVNYNKMVFCPYYDAILSKILVRS
6032	39	2415	AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE
	1	ļ	SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS
1			YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK
1			
1			QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP
1.			PIGSSAGLLALSSALGGQSHLPIKDBKKHHDNDHQRDRDSIKSS
1	1		SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK
1	1		SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP
1		ļ	ASIASSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS
i			NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG
1			MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAAYGRSPVVGFD
1	1	1	PHHHMRVPAIPPNLTGIPGGKPAYSFHVSADGOMOPVPFPPDAL
1			
1	1	1	IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW
1			DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGRASTL
J	]		SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI
			AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS
1			W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V
1			EVLHVTKPDKYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLNA
1	1		W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\
1	1		
	<del> </del>		RATVYEVIY
6033	39	2415	AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE
1			SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS
1	1		YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHOOOVVQAVERAK
1			QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLOPPAIP
ł	İ		PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS
1	1		SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK
I			SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP
	1		ASIASSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS
1	1		NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG
	·	<del></del>	

070	T 8 37 - 5 - 3	1 5 37 4 3	
SEQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
ID NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
1		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
	amino acid		P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAAYGRSPVVGFD
1		Ì	PHHHMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL
			IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW
1			DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL
			SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI
			AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS
1			W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V
			EVLHVTKPDKYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLNA
]			W\RTPYG\ASIF\QSKES9S\VLSCDI\SVDDKYIVTGS\GDK\
6034	2683		RATVYEVIY
0034	2083	714	ESGRRRLKRRRSPCPGTAGGPGETNPGPGACPRGPREEAAAAM
1			EIAPQEAPPVPGADGDIEEAPAEAGSPSPASPPADGRLKAAAKR
1	1		VTFPSDEDIVSGAVEPKDPWRHAQNVTVDEVIGAYKQACQKLNC
			RQIPKLLRQLQEFTDLGHRLDCLDLKGEKLDYKTCEALEEVFKR
			LQFKVVDLEQTNLDEDGASALFDMIEYYESATHLNISFNKHIGT
	}		RGWQAAAHMMRKTSCLQYL\DARNTPLLDHSAPFVARALRIRSS
i			LAVLHLENASLSGRPLMLLATALKMNMNLRELYL\ADNKLNGLQ
			DSAQLGNLLKFNCSLQILDLRNNHVLDSGLAYICEGLKEQRKGL
1			VTL\VLWNNQLTHTGMAFLGMTLPHTQSLETLNLGHNPIGNEGV
1		1	RHLKNGLISNRSVLRLGLASTKLTCEGAVAVAEFIAESPRLLRL
1			DLRENEIKTGGLMALSLALKVNHSLLRLDLDREPKKEAVKSFIE TQKALLAEIQNGCKRNLVLAREREEKEQPPOLSASMPETTATEP
1			
1			QPDDEPAAGVQNGAPSPAPSPDSDSDSDSDGEEEEEEEGERDET PSGAIDTRDTGSSEPQPPPEPPRSGPPLPNGLKPEFALALPPEP
1		•	PPGPEVKGGSCGLEHELSCSKNEKELEELLLEASOESGOETL
6035	19	404	SVTYLGIILHKNTGALPADPVQLISQTPTPSTKQQLLSFLGMVG
0055	1	101	YFYLWIPGFAILTKPLCKLTKENLADAIDPKSFSHSSFRSLKTA
	1		LENASTLALPDSSQPF\SLHTAEVQGCVVEILTQGLGPLPV
6036	1745	356	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLORN
1	1		SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW
			VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD
ł			SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR
			EEGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRROD
		į	WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV
			DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS
			GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKOTLSSLK
1			LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK
			RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL
]	1		MEKGLINFMPKNRNLAVNIGEKK
6037	2936	1919	WTSWWMSSVLTILLFSLOGNKMLNYSAPSAGGYLLPRKPVGTPA
1	1		GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR
	1	1	SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG
	İ		DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI
1	1		HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL
	1	1	DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA
1			PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS
}	1		SSSSHSGSDSPTLDNSRRLPIFSRLSISDD
6038	1450	426	SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH
			YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS
1	1	J	SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG
			NSSCPSTETEEBKAKRLL\YCSLCKVAVNSASQLEAHNSGTKHK
			TMLEARNGSGTIKAFPRAGVKGKGPVNKGNTGLONKTFHCEICD
	!		VHVNSETQLKQHISSRRHKDRAAGKPPKPKYSPYNKLQKTAHPL
			GVKLVFSKEPSKPLAPRILPNPLAAAAAAAAVAVSSPFSLRTAP
			AATLFQTSALPPALLRPAPGPIRTAHTPVLFAPY
6039	4073	1000	LDEYEARLTLANLDDFEEDNEDDDENRVNQEEKAAKITELINKL
			NFLDEAEKDLATVNSNPFDDPDAAELNPFGDPDSEEPITETASP
		ľ	RKTEDSFYNNSYNPFKEVQTPQYLNPFDEPEAFVTIKDSPPOST
			KKKNIRPVDMSKYLYADSSKTEEEELDESNPFYEPKSTPPPNNL
			VNPVQBLETERRVKRKAPAPPVLSPKTGVLNENTVSAGKDLSTS

SEO	Predicted	Predicted end	Amino paid coment contri
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
		<del> </del>	PKPSPIPSPVLGRKPNASQSLLVWCKEVTKNYRGVKITNFTTSW
		Ì	RNGLSFCAILHHFRPDLIDYKSLNPQDIKENNKKAYDGFASIGI
1		1	SRLLEPSDMVLLAIPDKLTVMTYLYQIRAHFSGQELNVVQIEEN
			SSKSTYKVGNYETDTNSSVDQEKFYAELSDLKREPELQQPISGA
1			VDFLSQDDSVFVNDSGVGESESEHQTPDDHLSPSTASPYCRRTK
1			SDTEPQKSQQSSGRTSGSDDPGICSNTDSTQAQVLLGKKRLLKA
1		1	ETLELSDLYVSDKKKDMSPPFICEETDEQKLQTLDIGSNLEKEK
		1	LENSRSLECRSDPESPIKKTSLSPTSKLGYSYSRDLDLAKKKHA
	i	İ	SLRQTESDPDADRTTLNHADHSSKIVOHRLLSROEELKERARVL
			LEQARRDAALKAGNKHNTNTAAPFCNRQLSDQQDEERRROLRER
1	1	[	ARQLIAEARSGGKMSBLPSYGERAAEKLKERSKASGDENDNIEI
1			DTNEEIPEGFVVGGGDELTNLENDLDTPEQNSKLVDLKLKKLLB
			VQPQVANSPSSAAQKAVTESSEQDMKSGTEDLRTERLQKTTERF
			RNPVVFSKDSTVRKTQLQSFSQYIENRPEMKRQRSIQEDTKKGN
	1		EEKAAITETQRKPSEDEVLNKGFKDS\SQYVVGELAALENEQKQ
			IDTRAALVEKRLRYLMDTGRNTEEEEAMMQEWFMLVNKKNALIR
			RMNQLSLLEKEHDLERRYELLNRELRAMLAIEDWQKTEAQKRRE
	1		QLLLDELVALVNKRDALVRDLDAQEKQAEEEDEHLERTLEQNKG
6040	475	1052	KMAKKEEKCVLQ
0040	4/3	1052	PTALMTAPSCAFPVQFRQPSVSGLSQITKSLYISNGVAANNKLM
•			LSSNQITMVINVSVEVVNTLYEDIQYMQVPVADSPNSRLCDFFD
			PIADHIHSVEMKQGR\TLLHCAAGVSRSAALCLAYLMKYHAMSL
			LDAHTWTKSCRPIIRPNSGFWEQLIHYEFQLFGKNTVHMVSSPV GMIPDIYEKEVRLMIPL
6041	2	3886	TEXDEXTAHNLENVLIHFWERLSEICVAKISEPEADVESVLGVS
		3000	NLLQVLQKPKGSLKSSKKKNGKVRFADEILESNKENEKCVSSEG
			EKIECWELTTEPSLTHNSSGLLSPLRKKPLEDLVCKLADISINY
			VNERKSEQHLRFLSTLLDSFSSSRVFKMLLGDEKQSIVQAKPLE
			IAKLVQKNPAVQFLYQKLIGWLNEDQRKDFGFLVDILYSALRCC
			DNDMERKKVLDDLTKVDLKWNSLLKIIEKACPSSDKHALVTPWL
Į.			KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ
1	ļ		HVKNDYLIGDVYVERIIVRLHETLFKTKKLSEAESSDSSVSFIC
			DVAYNYFSSAKGCLLMPSSEDLLLTLFQLCAQSKEKTHLPDFLI
1			CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL
1			DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWEK
			MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIKTLPSHLCT
1			SALLSKMVLIALRKETVLENNELEKIIAELLYSLQWCEELDNPP
1			IFLIGFCEILQKMNITYDNLRVLGNMSGLLQLLFNRSREHGTLW
			SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP
{			FLSKEEKKEFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ
			TKSIDDGELLHGILKIIISWKKEHEDIFLFSCNLSEASPEVLGV
			NIEIIRFLSLFLKYCSSPLAESEWDFIMCSMLAWLETTSENQAL
			YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK
			EFFSQGIHSLLLPILVTVTGENKDVSETSFQNAMLKPMCETLTY
			ISKEQLLSHKLPARLVADQKTNLPEYLQTLLNTLAPLLLFRARP
			VQIAVYHMLYKLMPELPQYDQDNLKSYGDEEEEPALSPPAALMS
			LISIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI
	}		LTFFKAASSOLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAB
	1	-	TAVEVPNKDPKTFFTBELQLSIRETTMLPYHIPHLACSVYHMTL
			KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSFQEISSVQT STQLFNGMTVKARATTREVMATYTIEDIVIELIIQLPSNYPLGS
	İ		IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALWKNN
1			VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY
	ļ		KWFTSSNKSTCSLCRETFF
6042	1306	253	MAELAPASPSDIKASVSNGDTTLLCSRRQSCGMNEVRQVSLTYP
	Ì		GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY
	ļ		GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKE
	İ	İ	LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHQDWEV
			QYQQDTPVAPRFDVNAPDLYIPAMAFITYVLVAGLALGTQDRFS
			PDLLGLQASSALAWLTLEVLAILLSLYLVTVNTDLTTIDLVAFL
		ļ	GYKYVGMIGGVLMGLLFGKIGYYLVLGWCCVAIFVFMIRTLRLK

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
_		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	l .	A=Aranine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid		Codon, /=possible nucleotide deletion,
ļ	1	sequence	
	sequence		\-possible nucleotide insertion)
			ILADAAAEGVPVRGARNQLRMYLTMAVAAAQPMLMYWLTFHLVR
6043	403	599	LCLFFPFPCATPVLPLPSLISAL/CLSHLSVSSWFCPCQPPLPC
			PLPPLONKTAKGSLSTEOSERG
6044	793	412	KLEMWNFTLISKVKISREVTMIASKFGIGQOVRHSLLGYLGVVV
0044	,,,,	1 7	DIDPVYSLSEPSPDELAVNDELRAAPWYHVVMEDDNGLPVHTYL
1		1	1
			AEAQLSSELQDEHP\EQPSMDELAQTIRKQLQAPRLRN
6045	155	2299	SPLPQVAAMNYLRRRLSDSNFMANLPNGYMTDLQRPQPPPPPPG
		1	AHSPGATPGPGTATAERSSGVAPAASPAAPSPGSSGGGGFFSSL
			SNAVKOTTAAAAATFSEQVGGGSGGAGRGGAASRVLLVIDEPHT
		1	DWAKYFKGKKIHGBIDIKVEQAEFSDLNLVAHANGGFSVDMEVL
1			
			RNGVKVVRSLKPDFVLIRQHAFSMARNGDYRSLVIGLQYAGIPS
1		ł:	VNSLHSVYNFCDKPWVFAQMVRLHKKLGTEEFPLIDQTFYPNHK
			EMLSS\TTYPVVVKMGHGTLWGWGKVKVDNQHDFQDIASVVALT
			KTYATAEPFIDAKYDVRVQKIGQNYKAYMRTSVSGNWKTNTGSA
			MLEQIAMSDRYKLWVDTCSEIFGGLDICAVEALHGKDGRDHIIE
			VVGSSMPLIGDHQDBDKQLIVELVVNKMAQALPRQRQRDASPGR
1			GSHGQTPSPGALPLGRQTSQQPAGPPAQQRPPPQGGPPQPGPP
1			QRQGPPLQQRPPPQGQQHLSGLGPPAGSPLPQRLPSPTSAPQQP
!			
1	1		ASQAAPPTQGQGRQSRPVAGGPGAPPAARPPASPSPQRQAGPPQ
l	1		ATROTSVSGPAPPKASGAPPGGQQRQGPPQKPPGPAGPTRQASQ
}	1		AGPVPRTGPPTTQQPRPSGPGPAGRPKPQLAQKPSQDVPPPATA
1	1	į	AAGGPPHPQLNKSQSLTNAFNLPEPAPPRPSLSQDEVKAETIRS
ł	1	ł	LRKSFASLFSD
6046	212	1075	EGLTGPCERVPFLLGRGPPHGATRAGHRRAVRWAGPESLPPLPR
0040	212	1075	SLIMDSPRAGTHOGPLDAETEVGADRCTSTAYQEQRPQVEQVGK
	1	ļ	
		1	QAPLSPGLPAMGGPGPGPCEDPAGAGGAGAGGSEPLVTVTVQCA
ļ		ļ	FTVALRARRGADLSSLRALLGQALPHQ\AQLGQLSYLAPGEDGH
	1		WVPIPEEESLQRAWQDAAACPRGLQLQCRGAGGRPVLYQVVAQH
			SYSAQGPEDLGFRQGDTVDVLCEVDQAWLEGHCDGRIGIFPKCF
	1		VVPAGPRMSGAPGRLPRSQQGDQP
6047	49	1405	PVLVTSLRMREADTLRPPQLMEVSADIISTVEFNHTGELLATGD
1 0047	1	1403	KGGRVVIFQREPESKNAPHSQGEYDVYSTFQSHEPEFDYLKSLE
1		Į.	
		J	IEEKINKIKWLPQQNAAHSLLSTNDKTIKLWKITERDKRPEGYN
		İ	LKDEEGKLKDLSTVTSLQVPVLKPMDLMVEVSPRRIFANGHTYH
ļ	ł .		INSISVNSDCETYMSADDLRINLWHLAITDRSFTP\NIVDIKPA
		l .	NMEDLTEVITASEFHPHHCNLFVYSSSKGSLRLCDMRAAALCDK
			HSKLFEEPEDPSNRSFFSEIIS\SVSDVKFSHSDRYMLTR\DYL
			TVKVWDL\NMBARPIETYQVHDYLRSKLCSLYENDCIFDKFECA
		Į.	WNGSDSVIMTGA\YNNFFRMFDRNTKRDVTL\EASRESSKPRAV
1		1	LKPRRVCVGGKRRRDDISVDSLDFTKKILHTAWHPAENIIAIAA
1			
			TNNLYIFQDKVNSDMH
6048	1	3194	GIRTPKFCDSPTSDLEMRNGRGRGKRMRPNSNTPVNETATASDS
1			KGTSNSSKTRAGANSKGRRGSQNSSEHRPPASSTSEDVKASPSS
			ANKRKNKPLSDMELNSSSEDSKGSKRVRTNSMGSATGPLPGTKV
1			EPTVLDRNCPSPVLIDCPHPNCNKKYKHINGLKYHQAHAHTDDD
			SKPEADGDSEYGEEPILHADLGSCNG\ASVSOK\GSLSPARSAT
1			PKVRLVEPHSPSPSSKFSTKGLCKKKLSGEGDTDLGALSNDGSD
			DGPSVMDETSNDAFDSLERKCMEKEKCKKPSSLKPEKIPSKSLK
1			SARPI/APLAIPPQQIYTFQTATFTAASPGSSSGLTATVAQAMP
1			NSPQLKPIQPKPTVMGEPFTVNPALTPAKDKKKKKKKKKKESSKE
1			LESPLTPGKVCRAEEGKSPFRESSGNGMKMEGLLNGSSDPHQSR
	l		LASIKAEADKIYSFTDNAPSPSIGGSSRLENTTPTQPLTPLHVV
1			TONGAEASSVKTNSPAYSDISDAGEDGEGKVDSVKSKDAEQLVK
1	1	1	EGAKKTLFPPQPQSKDSPYYQGFESYYSPSYAQSSPGALNPSSQ
	ł	1	AGVESOALKTKRDEEPESIBGKVKNDICEEKKPELSSSSOOPSV
1		1	
i	1	1	IQQRPNMYMQSLYYNQYAYVPPYGYSDQSYHTHLLSTNTAYRQQ
1	1	1	YEEQQKRQSLEQQQRGVDKKAEMGLKEREAALKEEWKQKPSIPP
ļ			TLTKAPSLTDLVKSGPGKAKEPGADPAKSVI I PKLDDSSKLPGQ
		1	APEGLKVKLSDASHLSKEASEAKTGAECGRQAEMDPILWYRQEA
1			EPRMWTYVYPAKYSDIKSEDERWKEERDRKLKEERSRSKDSVPK
		L	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence		\=possible nucleotide insertion)
<u> </u>			EDGKESTSSDCKLPTSEESRLGSKEPRPSVHVPVSSPLTOHOSY
			IPYMHGYSYSQSYDPNHPSYRSMPAVMMONYPGSYLPSSYSFSP
1	Ì		YGSKVSGGEDADKARASPSVTCKSSSESKALDILQQHASHYKSK
İ			SPTISDKTSQERDRGGCGVVGGGGSCSSVGGASGGERSVDRPRT
'		ļ	SPSQRLMSTHHHHHHLGYSLLPAQYNLPYAAGLSSTAIVASQQG
		ļ	STPSLYPPPRR
6049	215	1089	AMTGVFDRRVPSIRSGDFQAPFQTSAAMHHPSQESPTLPESSAT
0015	1	1005	DSDYYSPTGGAPHGYCSPTSASYG\KALNPYQYQYHGVNGSAGS
Ĭ			YPAKAYADYSYASSYHQYGGAYNRVPSATNQPEKEVTEPEVRMV
			NGKPKKVRKPRTIYSSFQLAALQRRFQKTQYLALPERAELAASL
1			GLTQTQVKIWFQNKRSKIKKIMKNGEMPPEHSPSSSDPMACNSP
1	İ		QSPAVWEPQGSSRSLSHHPHAHPPTSNQSPASSYLENSASWYTS
1			AASSINSHLPPPGSLQHPLALASGTLY
6050		1710	· · · · · · · · · · · · · · · · · · ·
0050	566	1718	KGLERTCCAMEESDSEKTTEKENLGPRMDPPIGEPG\GSLGWVL
1			PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILD
	İ		RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLW
i		!	DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMHY
l			YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDLR
1			RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLRN
			FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ
			FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPSI
6053			PSAATLINIRNARKHFEKLERVDGPKQCLLMR
6051	566	1718	KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWVL
	Ì		PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILD
			RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLW
		j	DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMHY
		]	YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDLR
Ì	[	1	RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLRN
			FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ
		1	FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPSI
			PSAATLINIRNARKHFEKLERVDGPKQCLLMR
6052	566	1718	KGLERTCCAMEESDSEXTTEKENLGPRMDPPLGEPG\GSLGWVL
		1	PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILD
			RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLW
1	i		DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMHY
	ì		YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDLR
		1	RLSRPLECSCPRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLRN
	1	1	FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ
			FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPSI
			PSAATLINIRNARKHFEKLERVDGPKQCLLMR
6053	201	1704	KGTEMNKSRWQSRRRHGRRSHQQNPWFRLRDSEDRSDSRAAQPA
		J	HDSGHGDDESPSTSSGTAGTSSVPELPGFYFDPEKKRYFRLLPG
			HNNCNPLTKESIRQKEMESKRLRLLQEEDRRKKIARMGFNASSM
		1	LRKSQLGFLNVTNYCHLAHELRLSCMERKKVQIRSMDPSALASD
			RFNLILADTNSDRLFTVNDVTVGGSKYGIINLQSLKTPTLKVFM
			HENLYFTNRKV\NSVCWASLNHLDSHILLCLMGLAETPGCATLL
		1	PASLFVNSHPAGIDRPG\MLCSFRIPGAWSCAWSLNIQANNCFS
1	1	1	TGLSRRVLLTNVVTGHRQSFGTNSDVLAQQFALMAPLLFNGCRS
		1	GEIFAIDLRCGNQGKGWKATRLFHDSAVTSVRILQDEQYLMASD
1			MAGKIKLWDLRTTKCVRQYEGHVNEYAYLPLHVHEEEGILVAVG
		1	QDCYTRIWSLHDARLLRTIPSPYPASKADIPSVAFSSRLGGSRG
	<u></u>		APGLIMAVGQDLYCYSYS
6054	1	1054	PPIARLQEFGTSRRHMAAPSGVHLLVRRGSHRIFSSPLNHIYLH
			KQSSSQQRRNFFFRRQRDISHSIVLPAAVSSAHPVPKHIKKPDY
		1	VTTGIVPDWGDSIEVKNEDQIQGLHQACQLARHVLLLAGKSLKV
		1	DMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNNVLCH
		1	GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDECGKK
		1	LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF
1		1	VGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITEGSPE
			FKVLEDAWTVVSLD/TSKVSAQFEHTVLITSRGAQILTKLPHEA
	·	<del></del>	

SEQ   Predicted   Predicted end   Incleotide   Incleotide   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Inca	ing nucleotide (A=Alanine, C=Cysteine, Dide location Glutamic Acid, F=Phenylal Corresponding to first L=Leucine, M=Methionine,	D=Aspartic Acid, E=
NO: nucleotide location corresponding to first amino acid amino acid residue of amino acid sequence comments are sequence comments and acid sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence continued and sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comments are sequence comm	cide location Glutamic Acid, F=Phenylal H=Histidine, I=Isoleucine, conding to first L=Leucine, M=Methionine,	
location   corresponding   to first   amino acid   xmino acid   residue of   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmino acid   xmin	on corresponding H=Histidine, I=Isoleucine conding to first L=Leucine, M=Methionine,	anine, G=Glycine,
Corresponding to first amino acid amino acid residue of amino acid residue of amino acid sequence amino acid sequence   S-Serine, T-Threonine, V-Valine,	ponding to first L=Leucine, M=Methionine,	
to first amino acid residue of amino acid residue of amino acid sequence  6055  421  2364  PPPTOLINE, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Str. Codon, /=possible nuclectide deletion, _=possible nuclectide insertion)  PPYFLISFLAWMLYGGSDRTETDISGSAGPFGTLQCSALH GCANCSRFCRCSFPACQCHTHVPFGNALMGVQPFBLISRTLU SSREPPRKKKSQTETGKERERTSFLTQGGKRFELQHGLAG: TILLITGDSIVSAEAVWDHVTMANRELAFKAGDVIKVLDASN; WMGQIDDEEGWFPASFVRLWNNHEDZEVEGFSDVQNGHLDP; CLCLGFPLONRDQMRABVINE IMSTERHYIKHLZICGEGLI RKRRDMFSDEQLKVIFGNIEDIYRFQMGFVRDLEKQYNNDD; SEIGPCFLEHQDGFWIYSEYCNNHLDACMELSKIMKDSRYQ; BACRILQQMIDIA IDGFLLPYQKICKYPQLAELLKYTAM, SDYRYVAAALAVMRNVTQQINERKRRLENIDKIAQWQASVLI GEDILDRSSELIYTGSNAMIYQP\YGRNQQRVFFLEHDMVI KDLIRRDILYYKGRIDMDKVEGKGTEVYKGRYGVFFLEHDMVI KDLIRRDILYYKGRIDMDKVEGVICKYPQLAELLKYTAM, NKETEHLHFFAKKLEBKIRNLRAFREERKMVQEDEKIGFE: NQKRQAAMTVRKVPKQKGVNSARSVPPSYPPPQDPINHQQYI \DGIAQSQVFFTFPKKSQSPFWQNSSRITPFFKK  SGGGGPVRVRSEQLSFSAEQVSQISQISQISLGRRELSSLPFPF LAPTRAPDTALTIMEVAEVESPINPSCKIMTFRPSMEEFFEI YLAYMESKGARRAGLAKVIFPKBKFRQCYDDIDMLIPAP; MTGQSGLFTQYNIQKKAMTVKBFRGLANGKYCTFRYLDYI ERKYWKNLTFVAPIYGADIMSTYLBGAUFMTFYLBRALTNTULDI ECGISIEGVNTPYLYPGMMKTTFAWHTEDMDLYSINYLHPK KSWYAIPPEHGKRLERLAQGFFPSSSQCDAFLRHMTLISI LKKYGIPPDKITQBAGFMTTFPYGYHAGFMHGFNCAESTNI VRWIDYGKVAKLCTCRKDMVKISMDIFVRKPQPRYQLWKQC IYTIDHTKPTPASTPEVKANLQRARKVTRASRSFQCARSTSI KADBEEEVGSEVDAEVPUNDAGEVPNTPDLKVSEKSEAAVKLRNI SSEEBSSASRMQVSQNLSDHIKLSGNSCLSTSVTEDIKTEDI YAYRSVPSISSEADDSIPLSTGYEKKPEKSDPSELSWPKSPS SVABSNGVLTEGEESDVESRIGNGLEFGEIPAVPSGERNSFK IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELJEVI EEVEETESWAKPLIHLWQTKPPNFAAEQSYNATVARMKPHG CTLLMPYHKEPDSSNEENDAAWERTKLDEVVTSRGKTKPLIFE		
residue of amino acid sequence (Codon, /=possible nucleotide deletion, %=possible nucleotide insertion)  6055  421  2364  PPYFLLSFLAWWLYGQSDRTETDISQSAGPPPGTLQCSALHI GCANCSRPCRDCSPPACQCHTHYPFENALINGVQPPELSRTLI SREPPRKKKKSQSTETGERFENSLTQGGKRFELDHGLAG; TLLITGDSIVSAEAVWDHVTMANRELAFKAGDVIKVLDASNI WHGQIDDEEGWFPASFVRLWVMHEDEVERGPSDVQMGHLDPH CLCLGRPLQMRQMRANVINE IMSTERHYIKHLKDICEGYLI RKRRDMFSDEQLKVIFGNIEDIYRFQMFVRLEKQYNNDDJ SEIGPCFLEHQDGFRIYSSYCNHLDACMELSKLHKDSRYQI EACRLLQQMIDIA\IDFHLTPVQKICKYPLQLAELLKYTMG GEBILDRSSELIYTGEMAWIYQP\SGRNQQRYFFLEDHQMVI KDLIRDILYYKGRIDMDKYEVVDIEDGRDDDFNVSMKNAFI NKETEEIHLFFAKKLEEKIRWLRAFREEKKMVQBEKIGFE NGKRQAAMTVRVPKOKGVMSARSVPPSVPPPQDPDINHQQYI \DGIAQSQVFFTEPHKRQSPFWQNFSRLTFFKK  SGGRGFVRVRSEQLSPSAEQVSQISQISGISGRRPLSSLPPPF LAPTRAPDTALTIMEVAEVESPLNPSCKIMTFRSMEEFREI YLAYMESKGAHRAGLAKVIPPKEWKRQCYDDINLIPADI WTMOGSGLFTQYNIQKKAMVERFQCJADINLIPADI ERKYWKNLTFVAPIYGADINGSIYDEGVDEWNIARLNTVLDU EECGISIEGVNTPYLYFOMMKTTPAHTTEDMLYSINTHFK KSWYAIPPEHGKRLERLAGGFPSSSQCGDAFIRHMTLIL LKKYGIPFDKIRGREFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFRIEGRIFFFR		
amino acid sequence Codon, /=possible nucleotide deletion,	acid residue of S=Serine, T=Threonine, V=	-Valine,
Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence	e of amino acid W=Tryptophan, Y=Tyrosine,	X=Unknown, *=Stop
Sequence   Sepossible nucleotide insertion		
6055 421 2364 PPYFLLSFLAWMLYGQSDRTETDISQSAGPPFGTLQCSALHI GCANCSRFCRDCSFPACQCHTHVFPGNALNGVQPPELSRTLJ SSREPPRKKKSQTETGKERERTSFLTQGKRFELQHGLAG: TLLITGDSIVSAEAVWDHVTMANRELAFKAGDVIKVLDASNI WIGQIDDEEGWFPASFVRLWVMHEDEVEEGFSDVQNGHLDPI CLCLGRPLQNRDQMRANVINEIMSTERHYIKHLKDICEGYLI RKREMMFSDEQLKVIFGNIEDIYRFQMGFVRLEKGYNNDDI SEIGPCFLEHQDGFWIYSEYCNNHLDACMELSKLMKDSRYQI EACRLLQQMIDIA\IDGFLLTPVQKICKYPLQLAELLKYTAK SDYRYVAAALAVMRNVTQQINERKRRLENIDKIAQWQASVLI GEBILDRSSELIYTGBMAWIYQP\YGRNQQRVFFLFDHQMWI KDLIRRDILYYKGRIDMDKYEVVDIEDGRDDFNVSMKNAFI NKETEEIHLFFAKKLEEKIRWLRAFREERKMVQEDEKIGFE: NOKRQAAMTVRKVPKQKGVNSARSVPPSYPPPQDPLNHGQYI \DGIAQSQVFEFTEPKRSQSPFWQNFSRLTFFKK  6056 43 3358 SGGRGFVRVRSEQLSFSAEQVSQISGISLGRRFLSSLFPPPS LAPTRAPDTALTIMEVAEVESPLNPSCKIMTFRPSMEEFREI YLAYMESKGAHRAGLAKVIPPKEWKPRQCYDDINNLIPAPI MVTGQSGLFTQYNIQKKAMTVKEFRQLANSGKYCTPRYLDYI ERKYWKNLTFVAPIYGADINGSIYDEGVDEWNIARLNTVLDV EEKGISIEGVNTPYLYFGMWKTTFAWHTEDMDLYSINYLHFK KSWYAIPPEHGKRLERLAQGFFPSSSQGCDAFLRHKMTLISI LKKYGIPFDKITQEAGEFMITFYYGYHAGFNHGFNCAESTNI VRRIDYGKVAKLCTCREKDMVKISMDIFVRRPQPDRYQLWKQQ IYTIDHTKPTPASTPEVKAWLQRRRKVRKASRSFQCARSTSI KADBEEEVSDEVJGAEVPNPDSVTDDLKVSEKSERAVKLRNI SSEEESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDIKTEDI YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSSELSWPKSPES SVAESNGVLTEGEESDVESHGNGLEPGEIPAVPSGERNSFKY 1AEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSGEELIPEVI EEEVSETETSMAKPLIHLMQTKPPRFAAGGSYNATYANNKPRK CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEN		
SSREPPRKKKKSQTETGKERERTSFLTQGGKRFELQHGLAG: TILITGDSIVSAEAWUHUTMANRELAFKAGDVIKVLDASNI WHGQIDDBEGWFPASFVRLWVNHEDEVEEGPSDVQNGHLDPI CLCLGRPLQNRDQMRANVINEIMSTERHYIKHLKDICEGYLI RKRRDMFSDEQLKVIFGNIBDIYRFQMGFVRDLEKQYNNDDI SEIGPCFLEHQDGFWIYSEYCNNHLDACMELSKIMKDSRYQI EACRLLQMIDIA/1DGFLLTPVQNICKYPLQLAELLKYTAK SDYRYVAAALAVMRNVTQQINERKRRLENIDKIAQWQASVLI GBDILDRSSELIYTGGMANIYQP\YGRNQQRVFFLFDHQMVI KDLIRRDILYYKGRIDMDKYEVVDIEDGRDDDFNVSMKNAFI NKETEEIHLFFAKKLBEKIRWLRAFREERKMVQBDEKIGFE: NQKRQAAMTVRKVPKQKGVNSARSVPPSYPPPQDPLNHGQYI \DGIAQSQVFFFTEDKRSQSPFWQNFSRLTPFKK SGRGPVVRSEQLSFFSQUSQISQISLGRRPLSSLFPPPS LAPTRAPDTALTIMEVABEVESPLMPSCKIMTFRPSMEEFFREI YLAYMESKGAHRAGLAKVIPPKEWKPRQCYDDIDNLLIPAP: MVTGQSGLFTQYNIQKKANTVKEFRQLANSGKYCTPRYLDYY ERKYWKNLTFVAPIVADINGSIVDEGVDEWNIARLNTVLDD ECGISIEGVNTPYLYFGMWKTTFAWHTEDMDLYSINYLHFC KSWYAIPPEHGKRLERILQQFFPSSSQGCDAFLRHKWTLISI LKKYGIPFDKITQEAGFFMITFPYGYHAGFNCAESTNI VRWIDYSKVAKLCTCRKDMYKISMDIFVRKPQPDRYQLWKQC IYTIDHTKPTPASTPEVKAWLQRRRKVRKASRSFQCARSTSI KADEEEVSDEVDGAEVPRPDSVTDDLKVSEKSEAAVKLRMI SSEEESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDIKTEDI YAYRSYPSISSEADDSIPLSTGYEKPERSDPSELSWPKSPES SVAESNGVLTRGEESDVESHGNGLEPGEIPAVPSGERNSFKI IAEGENKTSKSWRHPLSRPPARSPMTLIKQQAPDGELPFWI IEEEVETESWAKPALIHLWQTKPPPARABGSYNATVARMKPHK CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEN	21 2364 PPYFLLSFLAWWLYGQSDRTETDIS	OSAGPPPGTLOCSALHHDP
SSREPPRKKKKSQTETGKERERTSFLTQGGKRFELQHGLAG: TILITGDSIVSAEAWUHUTMANRELAFKAGDVIKVLDASNI WHGQIDDBEGWFPASFVRLWVNHEDEVEEGPSDVQNGHLDPI CLCLGRPLQNRDQMRANVINEIMSTERHYIKHLKDICEGYLI RKRRDMFSDEQLKVIFGNIBDIYRFQMGFVRDLEKQYNNDDI SEIGPCFLEHQDGFWIYSEYCNNHLDACMELSKIMKDSRYQI EACRLLQMIDIA/1DGFLLTPVQNICKYPLQLAELLKYTAK SDYRYVAAALAVMRNVTQQINERKRRLENIDKIAQWQASVLI GBDILDRSSELIYTGGMANIYQP\YGRNQQRVFFLFDHQMVI KDLIRRDILYYKGRIDMDKYEVVDIEDGRDDDFNVSMKNAFI NKETEEIHLFFAKKLBEKIRWLRAFREERKMVQBDEKIGFE: NQKRQAAMTVRKVPKQKGVNSARSVPPSYPPPQDPLNHGQYI \DGIAQSQVFFFTEDKRSQSPFWQNFSRLTPFKK SGRGPVVRSEQLSFFSQUSQISQISLGRRPLSSLFPPPS LAPTRAPDTALTIMEVABEVESPLMPSCKIMTFRPSMEEFFREI YLAYMESKGAHRAGLAKVIPPKEWKPRQCYDDIDNLLIPAP: MVTGQSGLFTQYNIQKKANTVKEFRQLANSGKYCTPRYLDYY ERKYWKNLTFVAPIVADINGSIVDEGVDEWNIARLNTVLDD ECGISIEGVNTPYLYFGMWKTTFAWHTEDMDLYSINYLHFC KSWYAIPPEHGKRLERILQQFFPSSSQGCDAFLRHKWTLISI LKKYGIPFDKITQEAGFFMITFPYGYHAGFNCAESTNI VRWIDYSKVAKLCTCRKDMYKISMDIFVRKPQPDRYQLWKQC IYTIDHTKPTPASTPEVKAWLQRRRKVRKASRSFQCARSTSI KADEEEVSDEVDGAEVPRPDSVTDDLKVSEKSEAAVKLRMI SSEEESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDIKTEDI YAYRSYPSISSEADDSIPLSTGYEKPERSDPSELSWPKSPES SVAESNGVLTRGEESDVESHGNGLEPGEIPAVPSGERNSFKI IAEGENKTSKSWRHPLSRPPARSPMTLIKQQAPDGELPFWI IEEEVETESWAKPALIHLWQTKPPPARABGSYNATVARMKPHK CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEN	GCANCSRFCRDCSPPACQCHTHVFP	GNALNGVOPPELSRTLALI
TLLITGDSIVSAEAVWDHVTMANRELAFKAGDVIKVLDASNI WMGQIDDEEGWFPASFVRLWNHEDEVEBGPSDVQNGHLDPI CLCLGRPLQNRDQMRANVINEIMSTERHYIKHLKDICEGYLI RKRRDMFSDEQLKVIFGNIEDIYRFQMGFVRDLEKQYNNDDI SEIGPCFLEHQDGFWIYSEYCNNHLDACMELSKLMKDSRYQI EACRLLQQMIDIA\IDGFLLIPVQKICKYPLQLAELLKYTA SDYRYVAAALAWRNVTQQINERKRRLENIDKIAQWQASVLI GEBILDRSSELIYTGEMANIYQP\YGRNQQRVFFLFDHQMVI KDLIRRDILYYKGRIDMDKYEVVDIEDGRDDDFNVSMKNAFI NKETEEIHLFFAKKLBEKIRWLRAFREERKMVQEDEKIGFE: NQKKQAAMTVRKVPKQKGVNSARSVPPSYPPPQDPLNHGQYI \DGIAQSQVFEFTEPKRSQSPFWQNFSRLITPFKK  6056 43 3358 SGGRGPVRVRSEQLSFSAEQVSQISQISLGRRPLSSLPPPPS LAPTRAPDTALTIMEVAEVESPLMPSCKIMTFRPSMEEFREI YLAYMESKGAHRAGLAKVIPPKEWKKPQCYDDIDNLLIPAP; MYTGQSGLFTQYNIQKKAMTVKEFRQLANSGKYCTPRYLDYI ERKYWKNLTFVAPIYGADINGSIYDEGVDEWNIARLNTVLDV EECGISIEGVNTPYLYFGMWKTTFAWHTEDMDLYSINYLHPF KSWYAIPPEHGKRLERLAGFFPSSSQCCDAFLRHKWTLISI LKKYGIPFDKITQEAGEFMITFPYGYHAAGPHGFNCAESTNI VRWIDYGKVAKLCTCRKDMVKISMDIFVRKFQPDRYQLWKQC IYTIDHTKPTFASTPEVKAWLQRRRKVRKASRSFQCARSTSI KADEEEVSDEVDGAEVPDDSVTDDLKVSEKSEAAVKLRNT SSEEESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDIKTEDI YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSELSWPKSPES SVAESNOVLTEGEESDVESHGNGLEPGEIPAVPSGERNSFKI IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELFEVI IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELFEVI EEEVETESWAKPLLIHLWQTKPPPFAABGGYNATVARMKPHK CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEN	SSREPPRKKKKSQTETGKERERTSF	LTQGGKRFELQHGLAGICM
CLCLGRPLQNRDQMRANVINEIMSTERHYIKHLKDICEGYLL RKRRDMFSDEQLKVIFONIEDIYRFQMGFVRDLEKQYNNDDD SEIGPCFLEHQDGFWIYSEYCNNHLDACMELSKIMKDSRYQI EACRLLQQMIDIA\IDOFLLTPVQKICKYPLQLAELLKYTAK SDYRYVAAALAVMRNVTQQIRERKRRLENIDKIAQMQASVLI GBDILDRSSELIYTGEMAWIYQP\YGRNQQRVFFLFDHQMVI KDLIRDILYYKGRIDMDKYEVVDIEDGRDDDFNVSMKNAFI NKETEEIHLFFAKKLEEKIRWLRAFREERKMVQEDEKIGFE: NOKRQAAMTVRKVPKQKGVNSARSVPPSYPPPDQDPLNHQQVI \DGIAQSQVFEFTEPKRSQSPFWQNFSRLTPFKK  6056 43 3358 SGGRGPVRVRSEQLSFSAEQVSGISGISLGREPLSSLPPPPS LAPTRAPDTALTIMEVAEVESPLNPSCKIMTFRPSMEEFREI YLAYMESKGAHRAGLAKVIPPKEWKPRQCYDDIDNLLIPAP! MVTGQSGLFTQYNIQKKAMTVKEFRQLANSGKYCTPRYLDYI EERKYWKNLTFVAPIYGADINGSIYDEGVDENNIARLNTVLDV EECGISIEGVNTPYLYFGMWKTTFAWHTEDMDLYSINYLHFC KSWYAIPPEHGKRLERLAQGFFPSSSQGCDAFLRKMTLISI LKKYGIPFDKITQEAGEFMITFPYGHAAGFHAGFNCAESTNI VRWIDYGKVAKLCTCRKDMVKISMDIFVRKPQPDRYQLWKQC IYTTIDHTKRPTAASTPEVKAWLQRRRKVRKASRSFQCARSTSI KADBEEEVSDEVDGAEVVPNDSVTDDLKVSEKSEAAVKLRNT SSEEESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDIKTEDI YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSELSWPKSPES SVAESNGVITEGEESDVESHGNGLEFGEIPAVPSGERNSFK\ IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVI LAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVI EEEVEETTESWAKPLIHLWQTKPPNFAABGGYWATVARMKPHC CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEN		
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SEIGPCFLEHQDGFWIYSEYCNNHLDACMELSKLMKDSRYQI EACRLLQQMIDIA\IDGFLLTPVQKICKYPLQLAELLKYTAG SDYRYVAAALAVMRNVTQQINERKRRLENIDKIAQWQASVLI GBDILDRSSELIYTGEMAWIYQP\YGRNQQRVFFLFDHQMVI KDLIRRDILYYKGRIDMDKYEVVDIEDGRDDDFNVSMKNAFI NKETEEIHLFFAKKLBEKIRWLRAFREERKMVQEDEKIGFE: NQKRQAAMTVRKVPKQKGVNSARSVPPSYPPPQDPLNHGQYI \DGIAQQVFFFTEPKKSQSPFWQNFSRLTPFKK  GGS6 43 3358 SGGRGPVRVRSEQLSPSAEQVSQISQISLGRRPLSSLPPPPS LAPTRAPDTALTIMEVAEVESPLNPSCKIMTFRPSMEEFREI YLAYMESKGAHRAGLAKVIPPKEWKPRQCYDDIDNLLIPAPI MVTGQSGLFTQYNIQKKAMTVKEFRQLANSGKYCTPRYLDYS ERKYWKNLTFVAYGADINGSIYDEGVDEWNIARLNTVLDV EEGGISIEGVNTPYLYFGMWKTTFAWHTEDMDLYSINYLHFG KSWYAIPPEHGKRLERLAQGFFPSSSQGCDAFLRHKMTLISI LKKYGIPFDKITQEAGEFMITFPYGYHAGFNHGFNCAESTNI VRWIDYGKVAKLCTCRKDMVKISMDIFVKKPQPDRYQLWKQQ IYTIDHTKPTPASTPEVKAWLQRRKVVRKASRSFQCARSTSI KAADEEEVSDEVDGAEVPNPDSVTDDLKVSEKSEAAVKLRNT SSEEESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDIKTEDI YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSELSWPKSPES SVAESNGVLTEGEESDVESHGNGLEPGEIPAVPSGEERNSFKO IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVI IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVI EEEVEETESWAKPLIHLWQTKPPNFAARGGSYNATVARMKPRK CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEN	CLCLGRPLQNRDQMRANVINEIMST	TERHYIKHLKDICEGYLKQC
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G056  43  3358  SGGRGPVRVRSEQLSFSAEQVSQISQISLGRRPLSSLPPPPS LAPTRAPDTALTIMEVAEVESPLNPSCKIMTFRPSMEEFREI YLAYMESKGAHRAGLAKVIPPKEWKPRQCYDDIDNLLIPAP) MVTGQSGLFTQYNIQKKAMTVKEFRGLANSGKYCTPRYLDYS ERKYWKNLTFVAPIYGADINGSIYDEGVDEWNIARLNTVLDY EECGISIEGVNTPYLYFGMWKTTFAWHTEDMDLYSINYLHFG KSWYAIPPEHGKRLERLAQGFFPSSSQGCDAFLRHKMTLISI LKKYGIPFDKITQEAGEFMITFPYGYHAGFNHGFNCAESTNI VRWIDYGKVAKLCTCRKDMVKISMDIFVRKFQPDRYQLWKQG IYTIDHTKPTPASTPEVKAWLQRRRKVRKASRSFQCARSTSI KADEEEEVSDEVDGAEVPNPDSVTDDLKVSEKSEAAVKLRNT SSEEESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDIKTEDI YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSELSWPKSPES SVAESNGVLTEGEESDVESHGNGLEFGEIPAVPSGERNSFKV IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVI EEEVEETESWAKPLIHLWQTKPPNFAAEQEYNATVARMKPHG CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEN	NQKRQAAMTVRKVPKQKGVNSARSV	PPSYPPPQDPLNHGQYLVP
LAPTRAPDTALTIMEVAEVESPLNPSCKIMTFRPSMEEFREI YLAYMESKGAHRAGLAKVIPPKEWKPRQCYDDIDNLLIPAPI MVTGQSGLFTQYNIQKKAMTVKEFROLANSGKYCTPRYLDYI ERKYWKNLTFVAPIYGADINGSIYDEGVDEWNIARINTVLDV EEKSYWKNLTFVAPIYGAPGMKTTFAWHTEDMDLYSINYLHFO KSWYAIPPEHGKRLERLAQGFFPSSSQGCDAFLRHKMTLISI LKKYGIPFDKITQEAGERMITFPYGYHAGFNHGFNCAESTNI VRWIDYGKVAKLCTCRKDMVKISMDIFVRKFQPDRYQLWKQO IYTIDHTKPTPASTPEVKAWLQRRRKVRKASRSFQCARSTSI KADEBEEVSDEVDGAEVPNPDSVTDDLKVSEKSEAAVKLRNT SSEEESSASRMQVEQNLSDHIKLSGNSCLSTSTTEDIKTEDI YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSELSWPKSPES SVAESNGVLTEGEESDVESHGNGLEPGEIPAVPSGERNSFKV IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVI EEEVEETESWAKPLIHLWQTKPPNFAAEQEYNATVARMKPHO CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEN	\DGIAQSQVFEFTEPKRSQSPFWQN	<b>IFSRLTPFKK</b>
YLAYMESKGAHRAGLAKVIPPKEWKPRQCYDDIDNLLIPAPI MVTGQSGLFTQYNIQKKAMTVKEFRQLANSGKYCTPRYLDYI ERKYWKNLTFVAPIYGADINGSIYDEGVDEWNIARLNTVLDVI EECGISIEGVNTPYLYFGMWKTTFAWHTEDMDLYSINYLHFO KSWYAIPPEHGKRLERLAQGFFPSSSQGCDAFLRKMTLISI LKKYGIPFDKITQEAGEFMITFPYGYHAGFNHGFNCAESTNI VRWIDYGKVAKLCTCRKDMVKISMDIFVRKFQPDRYQLWKQC IYTIDHTKPTPASTPEVKAWLQRRRKVRKASRSFQCARSTSI KADBEEEVSDEVDGAEVPNPDSVTDDLKVSEKSEAAVKLRNT SSEEESSASRMQVEQNLSDHIKLSGNSCLSTSTTEDIKTEDI YAYRSVPSISSEADDSIPLSTGYEKPGKSDPSELSWPKSPES SVAESNGVLTEGEESDVESHGNGLEPGEIPAVPSGERNSFKV IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVI EEEVEETESWAKPLIHLWQTKPPNFAAEQEYNATVARMKPHO CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKFLIPEN	43 3358 SGGRGPVRVRSEQLSPSAEQVSQIS	QISLGRRPLSSLPPPPSRA
MVTGQSGLFTQYNIQKKAMTVKEFRQLANSGKYCTPRYLDYN ERKYWKNLTFVAPIYGADINGSIYDEGVDEWNIARLNTVLDV EECGISIEGVNTPYLYFGMWKTTFAWHTEDMDLYSINYLHFE KSWYAIPPEHGKRLERLAQGFFPSSSQGCDAFLRKMTLISI LKKYGIPFDKITQEAGEFMITFPYGYHAGFNHGFNCAESTNI VRWIDYGKVAKLCTCRKDMVKISMDIFVRKFQPDRYQLWKQC IYTIDHTKPTPASTPEVKAWLQRRRKVRKASRSFQCARSTSI KADEEEVSDEVDGAEVPNPDSVTDDLKVSEKSEAAVKLRNT SSEEESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDIKTEDI YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSELSWPKSPES SVAESNGVLTEGEESDVESHGNGLEPGEIPAVPSGERNSFKN IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVI EEEVEETESWAKPLIHLWQTKPPNFAAEQEYNATVARMKPHC CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKFLIPEN	LAPTRAPDTALTIMEVAEVESPLNP	SCKIMTFRPSMEEFREFNK
ERKYWKNLTFVAPIYGADINGSIYDEGVDEWNIARLNTVLDV EECGISIEGVNTPYLYFGMWKTTFAWHTEDMDLYSINYLHFO KSWYAIPPEHGKRLBRLAQGFFPSSSQCCDAFLRHKMTLISI LKKYGIPFDKITQEAGEFMITFPYGYHAGFNHGFNCAESTNI VRWIDYGKVAKLCTCRKDMVKISMDIFVRKFQPDRYQLWKQO IYTIDHTKPTPASTPEVKAWLQRRRKVRKASRSFQCARSTSI KADEEEVSDEVDGAEVPNPDSVTDDLKVSEKSEAAVKLRNT SSEEESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDIKTEDI YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSELSWPKSPES SVAESNGVLTEGEESDVESHGNGLEPGIPAVPSGERNSFKO IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVI EEEVEETESWAKPLIHLWQTKPPNFAAEQEYNATVARMKPHO CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKFLIPEN	YLAYMESKGAHRAGLAKVIPPKEWK	PRQCYDDIDNLLIPAPIQQ
EECGISIEGVNTPYLYFGMWKTTFAWHTEDMDLYSINYLHFC KSMYAIPPEHGKRLERLAQGFFPSSSQGCDAFLRHMTLISI LKKYGIPFDKITQEAGEFMITFPYGYHAGPNHGFNCAESTMI VRWIDYGKVAKLCTCRKDMVKISMDIFVRKFQPDRYQLWKQC IYTIDHTKPTPASTPEVKAWLQRRRVRKASRSFQCARSTSI KADEEEVSDEVDGAEVPNPDSVTDDLKVSEKSEAAVKLRNT SSEEESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDIKTEDI YAYRSVPSISSEADDSIPLSTGYEKFEKSDPSELSWPKSPES SVAESNGVLTEGEESDVESHGNGLEPGEIPAVVFSERNSFKN IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVI EEEVEETESWAKPLIHLWQTKPPNFAAEQEYNATVARMKPHC CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEN	MVTGQSGLFTQYNIQKKAMTVKEFR	QLANSGKYCTPRYLDYEDL
KSWYAIPPEHGKRLERLAQGFFPSSSQGCDAFLRHKMTLISI LKKYGIPFDKITQEAGEFMITFPYGYHAGFNHGFNCAESTNI VRWIDYGKVAKLCTCRKDMVKISMDIFVRKFQPDRYQLWKQC IYTIDHTKPTPASTPEVKAWLQRRRKVRKASRSFQCARSTSI KADEEEVSDEVDGAEVPNPDSVTDDLKVSEKSEAAVKLRNI SSEEESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDIKTEDI YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSELSWPKSPES SVAESNGVLTEGEESDVESHGNGLEFGEIPAVPSGERNSFKV IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVI EEEVEETESWAKPLIHLWQTKPPNFAAEQEYNATVARMKPHC CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEN	ERKYWKNLTFVAPIYGADINGSIYD	EGVDEWNIARLNTVLDVVE
LKKYGIPFDKITQEAGEFMITFPYGYHAGFNHGFNCAESTNI VRWIDYGKVAKLCTCRKDMVKISMDIFVRKFQPDRYQLWKQC IYTIDHTKPTPASTPEVKAWLQRRRKVRKASRSFQCARSTSI KADEEEEVSDEVDGAEVVPNPDSVTDDLKVSEKSEAAVKLRNI SSEEESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDIKTEDI YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSELSWPKSPES SVAESNGVLTEGEESDVESHGNGLEFGEIPAVPSGERNSFKV IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVI EEEVEETESWAKPLIHLWQTKPPNFAAEQEYNATVARMKPHC CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEN	. EECGISIEGVNTPYLYFGMWKTTFA	WHTEDMDLYSINYLHFGEP
VRWIDYGKVAKLCTCRKDMVKISMDIFVRKFQPDRYQLWKQC IYTIDHTKPTPASTPEVKAWLQRRRKVRKASRSFQCARSTSI KADBBEEVSDEVDGAEVPNPDSVTDDLKVSEKSEAAVKLRNT SSEEBSSASRMQVEQNLSDHIKLSGNSCLSTSVTEDIKTEDI YAYRSVPSISSEADDSIPLSTGYEKFPEKSDPSELSWPKSPES SVAESNGVLTEGEESDVESHGNGLEFGEIPAVPSGERNSFKV IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVI EEEVEETESWAKPLIHLWQTKPPNFAAEQEYNATVARMKPHC CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKFLIPEN	KSWYAIPPEHGKRLERLAQGFFPSS	SQGCDAFLRHKMTLISPSV
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KADEEEVSDEVDGAEVPNPDSVTDDLKVSEKSEAAVKLRNT SSEEESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDIKTEDI YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSELSWPKSPES SVAESNGVLTEGEESDVESHGNGLEPGEIPAVPSGERNSFKV IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVI EEEVEETESWAKPLIHLWQTKPPNFAAEQEYXATVARMKPHC CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEN	VRWIDYGKVAKLCTCRKDMVKISMD	)IFVRKFQPDRYQLWKQGKD
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SVAESNGVLTEGEESDVESHGNGLEPGEIPAVPSGERNSFKV IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVI EEEVEETESWAKPLIHLWQTKPPNFAAEQEYNATVARMKPHO CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEN		
IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVI EEEVEETESWAKPLIHLWQTKPPNFAAEQEYNATVARMKPHO CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEN	YAYRSVPSISSEADDSIPLSTGYEK	PEKSDPSELSWPKSPESCS
EEEVEETESWAKPLIHLWQTKPPNFAAEQEYNATVARMKPHO CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEN	1	
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EICDGWLCARCKRNAWTABCCLCNLRGGALKQTKNNKWAHVN		<del></del>
VAVPEVRFTNVPERTQIDVGRIPLQRLKLKCIFCRHRVKRVS		
CIQCSYGRCPASFHVTCAHAAGVL\MEPDDWPYVVNITCFRI	1	
NPNVKSKACEKVISVGQTVITKHRNTRYYSCRVMAVTSQTFY		-
MFDDGSFSRDTFPEDIVSRDCLKLGPPAEGEVVQVKWPDGKI	į į	<del>-</del>
AKYFGSNIAHMYQVEFEDGSQIAMKREDIYTLDEELPKRVKA	· · · · · · · · · · · · · · · · · · ·	
VSAGRCHLGTCQVNSLSSPHVSQAQQETYLGFWINSKKSQCN		<b>WETTLGFWINSKKSQCNIF</b>
LSGTY		
6057 1 853 FVARLKEQEGEGGLGPRKEKGRARGRERRRKMQLTRCCFVFI	i -	
GSLYLVICGODDGPPGSEDPERDDHEGQPRPRVPRKRGHISE		
RPMANSTLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKI		
WGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGN	1	
ISLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMEWEXVE\RG	1	·
TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTD		SQEERVACATIBLISIDAK
LVQKVCPDYNYHSDTPYYPSG		T BATAIDUI DUBBA BITA
6058 1 986 HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRARVG		
SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKO	1	
VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPAL	1	
ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYAC	<u> </u>	<del>-</del>
PTPLTHHNTGLSEALE ILAEAAGFEGSEGRLLTFCRAASVLK	PTPLTHHNTGLSEALEILAEAAGFE	
PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRS		•
RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAG	_	DDLKEQPQKLTQQQKAGEP
	RLFTQIFGVGVKTADRWYREGLRTL	
	RLFTQIFGVGVKTADRWYREGLRTL SREAGPWASLNCTLDPSASTP	
QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQ	RLFTQIFGVGVKTADRWYREGLRTL   SREAGPWASLNCTLDPSASTP   2   3650   QQDFESLADLTDHRAHRCPGDGDDDD	·
SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAA	RLFTQIFGVGVKTADRWYREGLRTL SREAGPWASLNCTLDPSASTP  QQDFESLADLTDHRAHRCPGDGDDD QMIGDGCDLGLGEEEGGTGLPYPCQ	FCDKSFIRLSYLKRHEQIH
RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKK	RLFTQIFGVGVKTADRWYREGLRTL SREAGPWASLNCTLDPSASTP  QODFESLADLTDHRAHRCPGDGDDD QMIGDGCDLGLGEEEGGTGLPYPCQ SDKLPFKCTYCSRLFKHKRSRDRHI	FCDKSFIRLSYLKRHEQIH KLHTGDKKYHCHECEAAFS
EHLAKSEKRAKKDDFMCDYCEDTFSQTEELEKHVLTRHPQLS	RLFTQIFGVGVKTADRWYREGLRTL SREAGPWASLNCTLDPSASTP  2 3650 QQDFESLADLTDHRAHRCPGDGDDD QMIGDGCDLGLGEEEGGTGLPYPCQ SDKLPFKCTYCSRLFKHKRSRDRHI RSDHLKIHLKTHSSSKPFKCTVCKR	FCDKSFIRLSYLKRHEQIH KLHTGDKKYHCHECEAAFS GFSSTSSLQSHMQAHKKNK

SEQ	Predicted	Predicted end	Amino and company contains
			Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
}	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1 1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid		delrypeophan, retyrosine, Asunknown, rescop
1		sequence	Codon, /=possible nucleotide deletion,
	sequence	0	\=possible nucleotide insertion)
			ADLQCIHCPEVFVDENTLLAHIHQAHANQKHKCPMCPE\QFSSV
1			\EGVYCHLDSHRQPDSSNHSVSPDPVLGSVASMSSATPDSSASV
1 1		l	BRGSTPDSTLKPLRGQKKMRDDGOGWTKVVYSCPYCSKRDFNSL
i l			AVLEIHLKTIHADKPQQSHTCQICLDSMPTLYNLNEHVRKLHKN
1			TA A DELIGATION TO THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF THE PROPERTY DELICATION OF TH
1			HAYPVMQFGNISAFHCNYCPEMFADINSLQEHIRVSHCGPNANP
1			SDGNNAFFCNQCSMGFLTESSLTEHIQ\Q\AHCSVGSAKLESPV
1			VQPTQSFMEVYSCPYCTNSPIFGSILKLTKHIKENHKNIPLAHS
1		}	KKSKAEQSPVSSDVEVSSPKRQRLSASANSISNGEYPCNQCDLK
ļ l			FSNFESFQTHLKLHLELLLRKQACPQCKEDFDSQESLLOHLTVH
i l			YMTTSTHYVCESCDKQPSSVDD\LQKH\LLDMPHPLCCTHCT\L
1 1			CQEVFDS\KVSI\QVHLAVKHSNEKKMYRCTACNWDFRKEADLQ
I i			VHVKHSHLGNPAKAHKCIFCGETFSTEVELQCHITTHSKKYNCK
		}	
)			FCSKAFHAIILLEKHLREKHCVFDAATENGTANGVPPMATKKAE
1 1			PADLOGMLLKNPEAPNSHEASEDDVDASEPMYGCDICGAAYTME
1			VLLQNHRLRDHNIRPGEDDGSRKKAEFIKGSHKCNVCSRTFFSE
1			NGLREHLQTHRGPAKHYMCPICGERFPSLLTLTEHKVTHSKSLD
{			TGTCRICKMPLQSEEEFIEHCQMHPDLRNSLTGFRCVVCMQTVT
			STLELKIHGTFHMQKLAGSSAASSPNGQGLQKLYKCALCLKEFR
}			SKQDLVKLDVNGLPYGLCAGCMARSANGQVGGLAPPEPADRPCA
1			GLRCPECSVKFESAEDLESHMQVDHRDLTPETSGPRKGTOTSPV
<b>!</b>			PRKKTYQCIKCQMTFENEREIQIHVANHMIBEGINHECKLCNQM
i I			FDSPAKLLCHLIEHSFEGMGGTFKCPVCFTVFVQANKLQQHIFA
			VHGQEDKIYDCSQCPQKFFFQTELQNHTMSQHAQ
6060	2145	202	SYEIVGKNKLEVNHSQLKALCKCSLPSRLLPLGENLPLLDRGFR
<b>,</b>			KEPRSRGSRERDNMLHLHHSCLCFRSWLPAMLAVLLSLAPSASS
1 1			DISASRPNILLLMADDLGIGDIGCYGNNTMRTPNIDRLAEDGVK
1			LTQHISAASLCTPSRAAFLTGRYPVRSGMVSSIGYRVLQWTGAS
			GGLPTNETTFAKILEEKGYATGLIGKWHLGLNCESASDHCHHPL
1			HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV
1			ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA
			DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV
			SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV
1 1			EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW
i			EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP
			QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR
]			GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD
1			LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ
[			LDRLGNIWRPWLQPCCGPFPLCWCLREDDPO
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1	110	1330	MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN
j l			VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK
1			ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSSRLASSPTVITS
			VSSASSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLQ
			SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG
1			HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA
1			RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRRQRTVLN
			PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY
			KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH
1-6000	74	3000	LALHRRRHMLV
6062	71	1079	ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT
			LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR
ļ			TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP
1			EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI
			LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE
			BEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP
1			1
			INDYTENGIEFDPMLDERGYCCIYCRGNRYCRRVCEPLLGYYP
1			YPYCYQGGRVICRVIMPCNWWVARMLGRV
6063	71	1079	ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT
1 I			LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR
;			max an agreement = ==================================
			TEIFRSGNGTDETLKVHDFKNGYTGIYFVGLQKCFIKTOIKVIP
			TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEOSVIWVPAEKPIENRDFLKNSKI
			TEIFRSGNGTDETLRVHDFKNGYTGLYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE

No: ucleotide location	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Decision   Corresponding to first amino acid residue of inst amino acid residue of anino acid anino acid sequence   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Sec	_			(A-Alapine C-Cysteine D A
Corresponding	1			Glutamic Acid Falbanilal de Carrier
COTTESPONDING to first amino acid residue of residue of amino acid sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence				W-Wichidian T Tables
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ESGELHFPANERKGIEGNEGOWINGVARUSTERLAGOSSEELL  DETERMINED BERONDERGYCCT VARRORMYCRAVCRYCLGUTY YPYCYCOGORYCCY IMPCHWYDAMAGAGW  NEPSISIDEPTSEIGFYSLEWTDLOWWVALDGOWINGVALDGOWING TISCKUVYVYOCKEETRERNDFALOGRIFY YGAAKTAATINID ALSCHYVYTOCKEETRERNDFALOGRIFY YGAAKTAATINID ALSCHYVYTOCKEETRERNDFALOGRIFY YGAAKTAATINID ALSCHYVYTOCKEETRERNDFALOGRIFY YGAAKTAATINID ALSCHYVYTOCKEETRERNDFALOGRIFY YGAAKTAATINID ALSCHYVYTALINGVALKATINDDSKTTRIVULINGGENFRIV  SSG VARKBGI INTI INDRE IPFIAS  6065  61153  641  MYVYARAVANVARGASTRAGASTRAGASSFPOPPPBGAGGVAELLEDDTG AEEEANMAATERRHEGOCSVLIPPOCOSGVVOWAGALLIN PRVR AEEEANMAATERRHEGOCSVLIPPOCOSGVVOWAGALLIN PRVR AEEEANMAATERRHEGOCSVLIPPOCOSGVVOWAGALLIN PRVR BLADAMBURGHEGHEVYONAAGSFVORERAALVFAGMMERAG  6066  68  3470  VIRBMOHATERRHEGOCSVLIPPOCOSGVVOWAGALLIN PRVR BLADAMBURGHAN TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA TORKHANDA T	}	1	sequence	Codon, /=possible nucleotide deletion,
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LEKDAMDWCNGKKLETAGEFYDDGTETHFSIGTI\ACYIKAV\ SGKKKKGI HILTUVNNKE IPEIAS  641 MSVRVARVANVGCIGASYRGASSFPVPP PEAGGVAELLEBAE  AEEEAWAATERMEGCSVLIFPGOGSGVUNGRIGLINY PEVR ELYAARARVLGYDLLEISLHGPGSTLDRTVHCOPAIFVASLAV RLIHHLGPSVLERCVAAAGRSVGSPALVFRAGMEEAG  6066 68 3470 VLEMMPATEKPMRYSHTGOTEVCFDDSGSFIVTGSDGDVRIW BLUDDDDERFINNGEKAYSCALKSGKLIVTAVSNNTIQVHTFPSK VPPGILITRFTTRANNVYRGODTIAAGSSID, IVAKITOVMPBS OOKTFRGIDAPVISIS PIPENDIFFLASASSODSVRWQISDGTGA LISWPLICKKRDVINAKSICRLAWPKSKKLLATPKAYSDVLYKTVOVMPBS OOKTFRGIDAPVISIS PROPKIF IFLASASCODSVRWQISDGTGA LISWPLICKKRDVINAKSICRLAWPKSKKLLATPKSVLYTRA ESMSHGFDLSDNTSQTLANIVMSPCGVLAAGSINGLIIVWRITTGKSVLYTRA ESMSHGFDLSDNTSQTLANIVMSPCGVLAAGSINGLIIVWRITTGKSVLYTRA ESMSHGFDLSDNTSQTLANIVMSPCGVLAAGSINGLIIVWRITTGKSVLYTRA ESMSHGFDLSDNTSQTLANIVMSSCRLAWPTGKSVLLYDRA COPESGKTESSKVSSRVEKDVSKDVDLDEDDDMSNAGPFLNDRAVEIF SPSKGIINDDEDDELDLAMSGGRFRGSSHILEDDENFSVLLSHEN COPESGKTESSKVSSRVEKDVSDLODDDMSNAGPFLNDRAVEIF SPSKGIINDDEDDELDLAMSGGRFRGSHILEDDENFSVLLSHEN GSSLLKEBEEDGGGESIHNLIVVTSGRFFYDGFMFTFRCKPDG GSTELHILHRPWNSISGIRCTWDSDONALDVEHTSHHAT HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSMDSSE ENIIDLPONBOILEACHAGOWAAAATSALLLELFTIGGVQKEVF SLAGPVVSMAGHSGLFIVVTHGTGFDCDCCCIGVOLLEIGKKKK OILHGPDFLTFRSVLLAWFGSAGATSTALLACESTDELASKLHCLHFSSMDSSE ENIIDLPONBOILEACHAGOWAAAATSALLALERTIGGVQKEVF SLAGPVVSMAGHSGLFIVVTHGTGFDCDCCCIGVOLLEIGKKKK OILHGPDFLTFRSVLLAWFGSAGATSTALLACESTDELAGKKHANINGLO NTWFFICTTEEHCKSKSDHWWVUHMALASKCKERRFSCVULLAD HANANILAIKVASKLARTAVATURELE EEEEDFRKKINAGYSTTATPKSQDRREPGCWFCHTSHIDVLA KNOYEYEESTKOQATKSQCLLAWRINGLANINGLAADTOVEEL EEEEDFRKKINAGYSTTATPKSQDRREPGCWFCHTSHIDVLA KNOYEYEESTKOQATKSQCLLAWRINGLANINGLABATOVUEBE EEEEDFRKKINAGYSTTATRKSQCRWPFKVNS. SKERAMSWAGARSTNILDMNCSSKKSTALSTTUTHKSKPFI IKP LIPKPKPKQASAASYFQKMSQTNATESVERENIKAVIJSEDETEN CPPQNTESMPLTFTCTFOWMLENSRSNILISDMPPDSEDADIIGEM HTONAANILAIKVASKKSTALSAVATIAKKULUSEBDTIN QERKARMILAIKKKKKKKKKKKKKKKKKKKKKKANILSBDETTSHID PROPKINGERTTSTATKKYTKKTSBCLURARTVASLAGAMGAGGEADTITEMA TAPA GERKARMINALSKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	1	ĺ	İ	AISGFAYEYTLEINGKSLKKYMEDDSKTTENTHULLIMDSENED TV
6065  1153 641 MSVEYARAVENGGASSYREASSEPUPPERACGYMARGLIRDATO ABERAPMANTERMINGGCSVILAPROCOSQUVAMORGLILIPPOTO BLYAAARRIVEYDLELSLINGPORTLORTHOPALIEVASLAV EKLIHLOPSVIENCVAAAGESVOEPRALVEAGAMEPAGG  6066 68 3470 VERMIPATEK WERKYGHTEGHTEVOEPDOSGSFIVTOCOPALIEVASLAV EKLIHLOPSVIENCVAAAGESVOEPRALVEAGAMEPAGG UVERMIPATEK WERKYGHTEGHTEVOEPDOSGSFIVTOCOPALIEVASLAV EKLIHLOPSVIENCVAAAGESVOEPRALVEAGAMEPAGG UVERMIPATEK WERKYGHTEGHTEVOEPDOSGSFIVTOCOPALIEVASLAVO EKLIHLOPSVIENCVAAAGESVOEPRALVEAGAMEPAGG UVERMIPATEK WERKYGHTEGHTEVOEPDOSGSFIVTOVATOMBOS OOKTFRGHDAPVISS PPOPUT ILABSACCOSVAVMOI SODOTO- ISWELLOKKONVINAKSI CELAMOP KSGKLLAIPVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSKULLIVVEKSITALIVITOODERKULVILIVITOODERKULVILIVITOODERKULVILIVUSSETTAL CPPONTEMORPKULDINGAMAAAASSASVEKSKULDSENGANTYSESDETEN OOKEMAAEVINKAKSKULDISTANOKALAIDOGERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILIJOODERKULVILI				I.EKDAMDVWCNGKKI.FTAGEEVDDCTETURG.ICTII\ A CV. T. T. C.
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ABERAWANTSRIMPOGOSULLPPOGOSOVOMGRGILINYPRVS BIYAAARRYLGYDLELSLHGPORTUPORTHOCPAITVASLAN RKLHHUGPSI LSCNCHAAGPSOVEPALLVBOKEPAGE BOLDDADPR TINVGEKAYSCLKSKULTVANGEPAGE  WEEMBATTKPMRYGHTSGHTEVCTPDOSGFIVTGSDGDYBIR BULDDDDPR TINVGEKAYSCLKSKULTVANGEPAGE VPDGILITRFTINANHVYNGDGTKIAAGSSD\FLVKIUDVMBS OOKTFRGHBAYULSLSPPDKU FLASASCSDAYWQISDQTCA ISWPLIGKKDVILNSLYDEVBLIASASCDSYWQISDQTCA ISWPLIGKKDVILNSLYDEVBLIASASCDSYWQISDQTCA ISWPLIGKKDVILNSLYDEVBLIASASCDSYDDAEGNIGLLERY ESWSHOPDLSDNFISQTINIVTWSQCYLAAGSINGLILIVMNY ETKUCHERVKHEKGVAI GULAWHPCGGTISTDAEGNIGLLERY CDPSGKTSSKVSSRVERDVINLFPGGNDYMSHAGSINDHAVEID SFSKGIINDDEDLMMASGRRPRGSHILEDSWIJSHLKT GSSLLKEEEDGGGSIHNLPUTVGROPPTORCHPDGS GSTFLHLHTRRWWNSIGIITGVINDEQDNAIDTGGDWSNAGDFINDNAVEID SFSKGIINDDEDLMMASGRRPRGSHILEDSWIJSHLKT GSSLLKEEEDGGGSIHNLPUTVGROPPTORCHPDGS GSTLLHINTTIADLSHEATLLACESTDELASKLHCLHFSSWDSK EWIILDPQNBID FAICLGGGWARAATSALLERTGGGVGEVF SLAGPVVSMAGHGBULFIVYHRGTOFFDOOCLGVOLLEGKKK OULHGDPLUTRSVLAM LGFSEOTPCVTDSBGIVMILNRGIG NTWTPICNTREHCKGKSDHWVGIHENDGCAIDCRICKSSRFPP TLERRAVALISKLEVPCIATEKGGMEEPGWSSVIFHMINGIG NTWTPICNTREHCKGKSDHWVGIHENDGCAIDCRICKSSRFPP TLERRAVALISKLEVPCIATEKGGMEEPGWSSVIFHMINGIG MTQNANNLAIKYASSSRKLLLAGKLERFRCVELADL MTQNANNLAIKYASSSRKLLLAGKLERFRCVELADL MTQNANNLAIKYASSSRKLLLAGKLERFRCVELADL MTQNANNLAIKYASSSRKLLLAGKLERFRCVELADL MTQNANNLAIKYASSSRKLLLAGKLERFRCVELADL LIPKPRFOOSSSKSKSTALERBEGGADDEE KPEIHFPGONSFSKSTNSDVSANSGAVTFSSQGRVNPPKVSAS SKEPAMSNISARSTRILDINGSSKSKSTALERBEGGADDEE KPEIHFPGONSFSKSTNSDVSANSGAVTFSSQGRVNPPKVSAS SKEPAMSNISARSTRILDINGSSKSKSTALERBEGGADDEE KPEIHFPGONSFSKSTNSDVSANSGAVTFSSQGRVDPFEVSAS SKEPAMSNISARSTRILDINGSPRFRONTERSPII THERESPII CPPQNTEMORPKTSGFWHATEKSPI IFF NA LIPKPKPSGSERSTRILDSHAGKRAVTVORSDOTTAN PTAP  DOKEMARENLAISKKORDIPSTNOKALADAGGNOLDEGDPAPAL GRARENLAISKKORDIPSTNOKALADAGGNOLDEGDPAPAL GRARENLAISKROKAPTGGERESRILLSDAPPTDAMA RSSBSADAGNASTFYPOTORTSKROPTGRAGAASTTPPPADAQL PPPRELAGRAGGSSSPEGGBISBREDONTCHNYCPPVKRETSSLTQ PPPRELAGRAGGSSPEGGBISBREDONTCHNYCPPVKRETSSLTQ FPPSUSBERSSGFILRPTLHGQAPSAGLPSKAPADAPDPTAMA RSSBSSADATHENSAAATYTKATARSPYPVFOONSSE	6065	1153	641	MCVPVARVAMIRGI CA GVCPCA GARRAGA
BLYAAARVICAYDLELSLHOPGETLORTHOOPAIFVASIAAV  RELHHLOPSUSENCVAAAGESVOEPRALLVEAGMEPAEG  OVERMIPATREMINGHTSCHTEVCPDDSGSFIVTGGSDGUVETM  EDDDDDPETNINGKAYSCLEKSKULTVATGSDGUVETM  EDDDDDDENTINGERSTELKSKEKULTVATGSDGUVETM  UNDELLGRENDVINARSICELAKSKULTVATGSDGUVETMUTUMDSS  OOKTFRGHDAPVILSSFUNGTIATUTMSPCGQYLAAGSINGLIJUMDV  ETKDCMERVIKHEKGVAIGGLAAMPENGKALTUTABECNGULLENV  ESMSHOPDLSDNFISGTIATUTMSPCGQYLAAGSINGLIJUMDV  ETKDCMERVIKHEKGVAIGGLAAMPTOGRISTUTDABCRUGLLENV  CDPSGKTSSSKVSSRVESDVENDLFPGGDSMANGDFINDNAVEIP  SPSKGIINDDEDDLMMASGRPRGRHILEDSVUISHLKT  GSSLLKEEEEDGGES INNIPUTUTSORPFYDDHPTROKEPPOS  GSTFLHLHTRAWNSIGIITUTUNDEDDAH JOSDFUNDTSIHLAT  HASHTINYTIADLSHEATLLACPSTDELASKLHCLHFSSUNGSK  EMIIDLPONDE BAILCLOGWARAATSALLRIPTIGSVOKEPP  SLAGPVUSMAGHGEQLPIVYHRGTOFPOGOCCHYGUETGKSSFPP  TLEPRAVAILSFKLEYCQIATEKGMBEGPWRSVIFHMUNGLG  NTWFFICNTERHCKKKSDHWWVGIHNNOLGCHYGUSUELGKKKK  OILHGDPLPLTRKSTLAAMFSSAGSTCVGVGUELGKKKK  MTONANNLAIKYASSSRTLILDNGSKSKKTALLSKEEPRCUELADL  KNOYEVESSTINAAYSONTATEMSORPFROVEDEGGSADDER  KPEIHKPGGNSFSKSTNSDVSAKSGAVTFSSQGRUNPPKVSAS  SKEPAMSNINSARSTNILDNGSSKSKKTALSBEGGGADDER  KPEIKFGGNSFSKSTNSSDVSAKSGAVTFSSQGRUNPFKVSAS  SKEPAMSNINSARSTNILDNGSSKSKTALSBEGGGADDER  KPEIKFGGNSFSKSTNSSDVSAKSGAVTFSSQGRUNPFKVSAS  SKEPAMSNINSARSTNILDNGSSKSKTALSBEGGGADDER  KPEIKFGGNSFSKSTNSDVSAKSGAVTFSSQGRUNPFKVSAS  SKEPAMSNINSARSTNILDNGSSKSKTALSBEGGGADDER  LIPKFKFROASAASYFOKRINGTNKTEEVKERNLKWIJESTPAI  CPPONTEMGRATGFGMHEENRINILSINDEDFSDEADIILTKEM  IRFVLSTEERKVMANAGAGETASEGTEAKKRKVUDESDETEN  GERAKSKNIALSKKOKEUPSTNOKLSAFAKKOV  GERAKSKNIALSKKOKEUPSTNOKLSAFAKKO  GERAKSKNIALSKKOKEUPSTNOKLSAFAKKO  GERAKSKNIALSKKOKEUPSTNOKLSAFAKKO  GERAKSKNIALSKKOKEUPSTNOKLSAFAKKO  FRANCUTSCHILTKENTYKKYYKKFSIPDLDRHQLPLDDALLSFA\T  FTAP  6068  13  1730  GSKMADLANEERPALAPPVEVGONGGSPAEGKNLSDSGEEP  RGBRASHVLOMOCKLFVFOKTSGSWERGGLEKKHDAFOTALBERDAG  PPPROBEERSSFILKPTLIHGQAPSAGLSSCKEGORSVLR  PAALGAPOFALKRENG  PAALGAPOFAKKHUTHEN GERBERDAGASTPPPFABGOL  PPPROBEERSSFILKPTHIHOQAPSAGLSPOKNEGORSVLR  PAALGAPOFAKKHUTHEN  GERBASHVLOMOCKLFVFOKTSGSWERGGLIKLENDMASTDDG  TLOSKLISABSBEDDSDDDDVARS		""	1 041	A SEE A DUA A MURGICAS Y RRGASS F PV PPPGAQGVAELLRDATG
6066 68 3470 VERMPATERE PMTROSTRE JOT COSTODURTY BULDDDD PKY INVOERAYS CALKS GKLVTAVS MIT TO LYNT PRE BULDDD PKY INVOERAYS CALKS GKLVTAVS MIT TO LYNT PRE BULDDD PKY INVOERAYS CALKS GKLVTAVS MIT TO LYNT PRE VERD COKT FROM THAS SICK STANK WO IS DOTTO.  LSPELLOK KENDY IN ARK SICK STANK WO IS DOTTO.  LSPELLOK KENDY IN ARK SICK STANK WO IS DOTTO.  LSPELLOK CHON YARK SICK STANK WO IS DOTTO.  LSPELLOK CHON YARK SICK STANK WO IS STANK WO IS DOTTO.  LSPELLOK CHON YARK SICK STANK WO IS STANK WO IS DOTTO.  COPS GKT SES KYS STRY ENVIOLED LAND KNOW SICK STANK WO IS STANK GSSLLKEE BEDOOGES IN HILP LUT SOR PY TO GMOT PTOR KNOW PRO GST PLIN LITH THAN THE LITH CALL STITLE LAND LITH AND THE PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY OF STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO IS STANK WO	1	1		ALEEAPWAATERRMPGQCSVLLFPGQGSQVVGMGRGLLNYPRVR
VKEMMATEKPMINGHTEGHTEVCPDDSGSFIVYGSDDDVERY  DEDLDDDDP FINVOEKASYSALKSGKUNTIOVITTPED  VPDGILTRFTTNANHVYFIGDGTKIAAGSSD\FLVKIVDVMDSS  OOKTFRGHDAPVLSLSFDPKDIFLASAGTGSSVEWINTIOVITTPED  VPDGILTRFTTNANHVYFIGDGTKIAAGSSD\FLVKIVDVMDSS  OOKTFRGHDAPVLSLSFDPKDIFLASAGTGSSVEWINTIOVITSDCTGA  LSWPLLGKCHDVINAKSICRLAMOPKSGKLLAIFVEKSVKLYRR  ESWSHGFDLSDNFISGTLANIVTMSPGCGYLAAGSINGLIIVMNY  ETKDCHERVKHEKGYAICLAMHTFGGTSTDAEGNIGLLENY  CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLINDNAVEIF  SPSKGIINDDEDDEDLMANGGRPRQNSHLDDENSVOISMLKT  GSSLLKEBEEDGOGESIHNLPLVTSQRPFYDGPMPTPRQKFPGS  GSTPLHLTHRFMVWNSIGIIRCTDBQDDNAIDVEFPTDSHLKT  HLSNTLNYTIADLSHEAILLACESTDELASKHICHFSSWDSSK  EMIIDLPQNBDIEAILLACESTDELASKHICHFSSWDSSK  EMIIDLPQNBDIEAILLACESTDELASKHICHFSSWDSSK  EMIIDLPQNBDIEAILLAGESTDELASKHICHFSSWDSSK  EMIIDLPQNBDIEAILLAGESTDELASKHICHFSSWDSSK  EMIIDLPQNBDIEAILLAGESTDELASKHICHFSSWDSSK  EMIIDLPQNBDIEAILLAGESTDELASKHICHFSSWDSSK  EMIIDLPGNBDIEAILLAGESTDELASKHICHFSSWDSSK  EMIIDLPGNBDIEAILLAGESTDELASKHICHFSSWDSSK  EMIIDLPGNBDIEAILLAGESTDELASKHICHFSSWDSSK  EMIIDLPGNBDIEAILLAGESTDELASKHICHFSSWDSSK  SLAGPWANSAGHGROJFT VYWRGTGFBGCJEVQLEUGLEGKKK  QILHGPDLPLTRKSYLAWIGFSAGTPCVUSBBITTRINGTERPI  LUPPAVALLSFKLDYCOLATEKGQMELAWIKANGETSAGTHENGERPP  TLPPAVALLSFKLDYCOLATEKGQMELGYBRSVIFFHNLDYLA  KNGYEYEBSTKNQATKEQGELLKHNALSCKLERPFRVELALL  MTONAVILLIKYSKRKARDVISKSKSTALSKITTNNEKSPI IKP  LIPPAVALLSFKLDYCOLATEKGQNECHTSSGGRWIPFKVSAS  SKEPANSNNSARSTNILDNMSKSSKSTALSKITTNNEKSPI IKP  LIPPAPKPLOSAASSYCKROSONTHEESUKTNINGSPORNIPFTVSAS  SKEPANSNNSARSTNILDNMSSSTFAKKRRVVDESDETEN  QEKKARENIKANGKORDJTNSKSTTAKKRRVVDESDETEN  QEKKARENIKANGKORDJTNSKSTTAKKRRVSLAGROGLEVUDPAL  GAGNILDPLIKESNNAPIFRKDTTOKSGFORNITHEEVERNYLKYL  GEABSHALDLSKKORDJDSTRAKAKORTSSGTAKKRRVDESDETEN  PDOKEMAERIKANSKYKYKYSKALGROGLEVGDDSPAL  GAGNILDPLIKESNNAPIFRKDTTOKSGFORNITHEEVERTSSITO  FPPSGSEERSGFRIXTPTITHOKAPSGROGLEVGDORSVLR  PAVLJAPOPKALSTRATUKTNKKYKYKKSLAGDGOLGVEGODAN  RSSEADOPKALSTRATUKTNKKYKYKKSLAGDGOLGVEGODAN  RABSGSSESSSEGGENDERGNATKORDSARSTNATARKCLLEKVEVIT  GEEABSNILDNOCKLIVTNIKKYNDREGGRILDFANTATNYFLOYTISS  SLENSTNNSADASSK	1			KLYAAARRVLGYDLLELSLHGPQETLDRTVHCQPAIFVASLAAV
BELDDDDPRFINVGERAYSCALKSGRUTYAVSNNTIQVITPERG VPDGILTRFTINAHVYNGGOTTIAAGSSD\FUNVUSVASS OOKTFSKHDAPVILLSEFDKDIFLAAGSSD\FUNVUSVASSOSOOKTFSKHDAPVILLSEFDKDIFLAAGSSD\FUNVUSVAGISDQTCA LSPFLUGKCNDVINAKSICCLAMQPKSGKILAIPVEKSYKLYRR ESMSHOPDLSDNFISOTIANIVTWSPCGYLAAGSINGLIVWNV ETKDCMERVKHEKGYAICGLAWHPTCGRISTIOABCHIGLENV CDFSGKISSSKYSSRVEKDYNDLIPDDDDDDLMSAGDFINDAVEILF SPSKGIINDEDDDEDLMANGGPRQNSHILBDDENSVISHLKT GSSLLKEBEEDGQGGSIHNLFLVTSGRFFYDGMPFPRGKPFQS GSTFLHLITHRFWWNSIGIRICRYNBKODNALDVEFHDTSIHHAT HLSNTLNYTIADLSHBATLLACRSTDELASKLHCLHFSSWDSK EMIIDLPQDBDIEAICGIRCYNBKONALDVEFHDTSIHHAT HLSNTLNYTIADLSHBATLLACRSTDELASKLHCLHFSSWDSK EMIIDLPQDBDIEAICGGWAAAATSALLLRFTISVOKEVF SLAGPVVSMAGHBGQLFIVYHRGTGFDGDCLGVULLELGKKKK QILHGDPLPLTRKSYLAWIGFSAEGTPCVVDSGRIVHANGGG NTWFJCCNTHERHCKGSSDHYWVOLHENPCQLRCIPCKGSRFP TLPRPAVAILSFKLBYCQIATEKGQMERQFWRSVIFHHADYLA KNOYEYEBSTRNOATERGGLLMMMLAISCKLRRFFRCVBLADL MTONAVNLAIKYSSRSKLLAKKLSELAVEKAABLTATQVEBE BEEBDFKKKLNAGYSNTATEWSGPRFRRQVEBDAEDSGADDEE KPEIHRPGGNSFSKSTNSSDVSAKSGAVTSSGGRVNDFKVSAS SKEPAMSHNSARSTNILDNMGKSSKKSTALSKTINNESPIIKP LIPKPKROSASASYFQKRKGTSNOTTREVEKERLIKNVLSSTPAI CPPONTENGRRKTGFOMHLEENSNILSDNPDFSDEADILKEGM IRRFVLSTBERKWANKKKGKTASGOTTAKREVYDESDETEN QEKARENLALSKKQKPLDPSTNQKLSAFAFKOB  6067 858 321 LPWGRIGVLISRGKWAVTGMLESLEKTACKTALLQOGGKKYHYLF PCOKEMBAETVEETSLIVKKNEVSSLAGMQUEVEGDPAPL GAGNLGPELKESHANDFFRKUTKHSFORKHYLDFENDYSV SVDQKBRCILTRYTNKKYYKKFSIPDLORHGLPLDDALLSFA\T PTAP  6068 13 1730 GSKMADLANEEKPAIAPPVFVFOKDKGCKSPAECKNLSDSGEEP RGEADAPHHATCHPSSAGERALEPPARAGASSTPPPABEAQL PFPFRELAGRSAGGSSPEGGEBDENDCHNCOPVARASPDTAM RSPSCAADEVALLEKERDJKNESSATSEEACKKDAPATQOAFV PGONLADRVKLINESVDEADMENAGHSPADTPTATNYFLQYTISS SLENSTNSADASSNKFVFGONNEEKMDSADLEFSSLTOR AAESGSESSSGEATPEKESLABSAAATKAARKCLLEKVEUTI GEEASSNVLOMCKLINESVDEADMENAGHSPADTPTATNYFLQYTISS SLENSTNSADASSNKFVFGONNEEKSAPATPAKABRADDRANA AAESGSESSSGEATPEKESLABSAAATKAARKCLLEKVEUTI GEEASSNVLOMCKLINTENDERGRGSLERLANATARGADBEDGOTTGS TOSKLISHAGDGRGSLEALLITTNYFLORYSIGS PTRPGGAGSSSAMAAGREGKRUSHSPGGAFAGAGGGGGGGGCORK MPAPFPGAAPSNEEDDSDDDDUTSKINGSPGAFAGFGGSPGGLORK M				EKLHHLQPSVIENCVAAAGFSVGEFAALVFAGAMEFAEG
BULDDDEPKTINNDEWATKGOTKIAASSSON PLUNIUTUWINES VPROILINFETTINAHVYTKGOTKIAASSSON PLUNIUTUWINES OOKTFRGHDAPVLSLEFDEKUI FILASASCOSGVRUMOISOOTCA ISWPLOKKONDVINANS I CERLAWOPKSCKLLAI PVEKSVKLYRY ESWSHOFDLSDNFISQTLNIVTWSPCGGVLAAGS INGLI IVMNV ETKOCMERVKHEKKYAI COLAMHFTGRISTTDAEMOILLENV CDPSGKTSSSKVSSRVENVYNDLFDCDDOMSNAGDFINDNAVEIF SPSKGI INDDEDDEDLMMASGRPRQNSHILEDDENSVISHLKT GSSILKEEBEDOGGGS INHLPLVINSORPTYDGWMPTPRQKEPOG GSTPLHLTHRFMVMNSIGIIRCYNDRODNAI DWEPHDTS INHAT HLSNTLNYTIADLSHBAI LLACESTELLSHLCHLFSSWDSK EMIIDLPQNEDIRAI CLGGGWAAAATSALLILIFTIGGVOKEVF SLAGPVVSMAGHGBQLFIVVHTGTFDGDDCLGVOLLGKKKK QILHGDPLETKRSYLAHIGFSAGTPCVVDSGIVRHANGIG NTWTPICNTERHCKGKSDHYMVVGILENPOQLKCIFCGGSFPP TLPRAVALLSFKLEPVGOJAREKGOMEPKRSVIFNHHLDYLA KNOYSFEBSTNOATKEQGELLMMMALSCKLEREFRCVELADL MTONAVNLAIKYASRSKILLAKUSELSKARELTATOVEE EEEEDPRKKLNAGYSNTATEMSOPRPROVVEEDAEDSGEADDEE KPEIHRFGONFSKSTNSSDVSAKSGAVTFSSOGRVDFFKVSAS SKEPAMSMNSARSTNILDNMASSSKKSTALSKTNNEKSPI IKP LIPKPAVALSTEERKVWANKAKGETASSGTEAKKRKVUDESDETEN CPPONTEMGRKTGFOMMLEBIRTAICKHDEPPSDEADIIKEGM IRRVLSTEERKVWANKAKGETASSGTEAKKRKVUDSDETEN CPRONTEMGRKTGFOMMLEBIRTAKKTALDOGRKKHTLFF PDOKEMAERINLSKKORDIDSTNOKLASPROSEDEDDIIKEGM IRRVLSTEERKVWANKAKGETASGGTEAKKRKVUDSDETEN GERKAERHINLSKKORDIDSTNOKLASPROSEDEDDIIKEGM IRRVLSTEERKVWANKAKGETASGGTEAKKRKVUDSDETEN CPRONTEMGRKTGFOMMLEBIRTAKKTALLDOGRKKHTLFF PDOKEMAERVDEKTSELLVYKRWIKKALGAMOQWOLEVGDPAPL GAGNLOPELIKESNANDIFMKOTTINGLSFTAKKRYVDS SVDKERCIIVRTTIKKYYKKFF I PDLDRIQUPLDDALLSFA\T PTAP  6068  13  1730  GSKMABLANEEKRAIAPPVFVOKOKGGKSPAEGKNLSDSGEEP PFPRELAGRSAGGSSPEGGEBDEDEDONYCPPVKRETTSSITO FPPSGSBERSSGFRLXPPTITHOAPSASATTATNYFLOYTISS SLENSTNSADASSNKFVFGONMSENLSPPKLNEWSSBARRENA AAESGSESSSGFRIFFEKSERSGFRLXPPTITHYFLOYTISS SLENSTNSADASSNKFVFGONMSENLSPPKLNEWSSBARRENA AAESGSESSSGFRIFFEKSERSGRAATTKAKARKCLLEKVEWIT GEEASSNULOMOCKLPVPDKTSGSWERGGGLLRINDMASTDOC TLOSKILGBAGFRSLIK, LIITRTHLAMOMOLSKEK\S ITITAM DNEDGWVRILINESVDEARBROANSASBERGACKKODPSAK MPAPPEGGAPSSIRALITATHALDAGARSASTPTATNYFLOYTISS SLENSTNSADASSNKFVFGONMSENLSPPKLNEWSSBARRENA AAESGSESSSGATPEKSESLABSAANTKAKARK	0000	68	3470	VKENMPATRKPMRYGHTEGHTEVCFDDSGSFIVTCGSDGDVRIW
VPDGILTRTTTMANHVVFNOEDTKLAAGSSED/LIKIVUTWINDSS OOKTFREHDAPVLSIS.PPRDH ILAAGSSED/SURWAGISDOTCA ISWPLIQKCNDVINAKSICELAAGPKSGKLLAIPVEKSVKLYRR ESWSHQFDLSDNFISOTLNIVTWSPCGGYLAAGSINGLIIVMRV ETKOCMERVKHEKGYAICGLAMPPCGGYLAAGSINGLIIVMRV ETKOCMERVKHEKGYAICGLAMPPCGGYLAAGSINGLIIVMRV CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLDNAVSIL SPSKGIINDEDDEDLEMMASGRPRGSITDABSMIGLENN CDSGKTELHIITRFWAVNASIGIIRCYNDEONAIDWFHDTSIHAT HISNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSWDSK EMIIDLPQNBDIEAICLGGGWAAAATSALLLELFFIGSVQKEVF SLAGPWVSNAGHGSQLFIVYHRGTGFOCLGVQLELGCKKK QILHGDPLEITRKSYLAWIGFSAECTFCYVDSEGTVMINRGLG NTWFICTONTREHCKGKSBUHWVVGIHENPQQLECIPCKGKSFPP TLPPAVAALLSKLPVOLATEKSQOELLMMLALSCKLERFERCVELADL MTQNAVALAIKYASRSRKLILAQKLSELAVERARELTATQVEEE EEEDFRKKLAAGTSNITATEMSQORIMMALSCKLERFERCVELADL MTQNAVALAIKYASRSRKLILAQKLSELAVERARELTATQVEEE EEEDFRKKLAAGTSNITATEMSQORFFRNQVEEDAADGGEADDEE KPEIHKPGGNSFSKINTSSDVASKSGKLEENENVISSGRVAN SKEPAMSNNSARSTNILDMNGKSSKKSTALSKTINDKSSFIKG LIPKPRYRQASAASYFQKRNSGTNTHFSGGGRWPFEVOSAS SKEPAMSNNSARSTNILDMNGKSSKKSTALSKTINDKSSFIKG IRRFULSTEERKVWANKAGGTASEGTAKKRKVVDESDETEN QEBKAKENLNLSKKQKPLDFSTNQKLSAPAFQG  6067 858 321 LPRQRIGVILSRGMAVTGHLESURTAQKTALLOGDERKVHYLF POCKEMAERVPEKTSELLVKKRVKSALGAMGOMGLEVGDPAPL GAGNLGPELIKESRANFIFMRGTKMSFOWRIRNLSPYEKDVSSV SVDQKBRCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T PTAP  6068 13 1730 GSKMADLANEEKPALAPFVFVFOKOKGKSPAEGKNLSDSGEEP RGEARAPHHGTGHFESAGGHALEPPARAGASASTPPPPAPEAQL PPFPRELAGRSAGGSSPEGGBISREDGRYCPVKRERTSSLTQ FPSGSBERSGFRLLPPTLHIGQAPSAGDATAGNAFCNA RSPSEAADEVCALEEKEPCKSESNASEEAACKHDPATQAFV PGQNLRDRVKLINESVDEADMENAGHSDGTTTATNYFLQYISS SLENSTNSADASSNKFVTGQNWSERVLSFPLINFSSDANRENA AAESGSESSSCATPTPERADCVALEEKEPLSPLAGFAGTTATNYFLQYISS SLENSTNSADASSNKFVTGQNWSERVLSFPLATRKVCLLEKVEVIT GEEASSNVLOMGCKLPVPNTTSGWVERGRGLISLADMSTDDG TLOSNLISDAGFRSIER, LILITKLMAQMGIDKASEK\STLTAM DNEDGGVKVFLISASSKDTGQVVALHHRILALRSRVEQEQEAK MPAPEPGAPSNEEDDSDDDVARPGGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1			EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHTFPEG
OOKTFRCHDAPVISISTPDRUTELASASCHGSVKULTAP PUEKSVLYTRR ISWPLICKCNDVINAKSI CICLAWQRKSKULAIP PUEKSVLYTRR ESWSHORDLSDMFISQTLATUTWSPCQQYLAAGSINGLIIVMIV ETKDCMERVKHEKGYAI COLAMHPTCGRISTTDASNIGLLENV CDPSGKTSSSKVSERVEKDYNDLFDGDMSNAGDFLINNAVEIP SPSKGIINDDEDDELMMASGRPRGRSHILEDDENSVDISMLKT GSSLLKEBEEDOGEGS THIN-PUTTSGPTDGMPTTPRGUPKPTG GSTPLHLTHERWINSIGIIRCYNDEQDNAIDVEPHDTSIHAT HLSNTLNYIADLSHEAILLACESTDELASATDGMPTPRGUPKPTG GSTPLHLTHERWINSIGIIRCYNDEQDNAIDVEPHDTSIHAT HLSNTLNYIADLSHEAILLACESTDELASATLLKHPTIGGVOKEVF SLAGPVVSNAGHGRQLFIVYHRGTGFDGDCLGVOKLEUGKKKK OILHGDPLDTHKSYLAWIGFSAGETCYVDESGIVMINRGLG NTWPICNTERECKGKSDHYWVGIHENPQOLGCIPCKGSRFPP TLDPRAVALLSFKLEVOLIATEKGMEGPHRSVIFHNHLDYLA KNGYEYEBSTKNQATLEGQMELMMALLSKLEREFRCVELADL MINNAVNLAIRYASRSKLILAQKLSLAVEKAABLTATQVEEE EEEDDFKKLANGYSTRATEWSQOPFENQVEEDABGSGEADDEE KPEIHRPGGNSFSKSTNSSDVSAKSGAVTFSSQGKVPFKVSAS SKSPAMSNMSARSTNILDINNGKSSKSKALSHTNINEKSPIIKP LIPKPKOASAASYPQKRNSQTNKTEEVKEENLKNVLSETPAI CPPQNTENQRPKTGFDMMLEENERSNILSDNFDSSEADLIKGGM IRRVLSTEERKWANKAKGGTASEGFEAKKRKVVDESETEN QEKKAENINLSKKOKPLDFSTNOKLSAPAFKQE  6067 858 321 LPMGRIGVLLSKGKMAVGUKLSELTAFALLDGGRRKVHYLF PDCKEMAEEYDEKTSLLUVRKWRVSALGAMGQWQLEVGDPAPL GAGNLGPELIKESNANPIFMRKDTKMSFOWRIRLPYPKDVYSV SVDCKERGLIVSTNIKKYYKKSIDLDRHQLPDDDLLSFA\T PTAP 6068 13 1730 GSKMADLANEEKPAIAPPVFVFQKDKSGKSPAEQKNLSDSGEEP RGEARAPHHGTGHPESAGRHALEPPAPAGASASTPPPPAPAGAL RSSSSRALEVPTLHGQABSACLPSCKYRERGSSUCH PPFPRELAGRSAGSSPBGGEDSDREEGRYCPPKKRERTSSLTO FPPSDSERRSSGRLKPPTLHGQABSACLPSCKYRERGSSUCH PPFPSCBERRSSGRRLKPPTLHGQABSACLPSCKYRERGSSLT GERMSDLVALLESCHARGHPSADTFATMYFLQYISS SLENSTNSADASSNKFVFGQNMSERVLSPPKRESSDATTAMY RSPSRAADEVCALEEEEPERPKNESSNASEACHEKDEATOOPAFV PGGNLRDRVKLINESVDEADMENNGHPSADTFATMYFLQYISS SLENSTNSADASSNKFVFGQNMSERVLSPPKRESSDATRENA AAESSISSSGCATPFKESLABSAANTKATARKCLLEKVEVUT GEEARSNVLOMQCKLFVFPKYSGSWVERGRGLIKLBINMASTDDG TLQSKLISDAGPGSUE, LILINTLINAQMGIDKASEK\STITMM DNEDGGVKVFLISASSKDTGQVVAALHHRILLALRSRVEOGOBAK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGGDGBGQQCTTGS T PTRPGQAGSSSAMAAGRLIGKKVLSKLUSSPERKGPGGSFGGLOK				VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDVMDSS
ISWPLICKENDVINAKSICHLAMOPKSGKLLAIPVEKSVKLYRR ESWSHOEDISJONFISOCIANITVENSPOLAAGSINGLIIVWNV ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAGGNIGLIENV CDPSGKTSSSKVSGRVEKDYNDLFDGDMSNAGDFLNDNAVEIP SPSKGIINDEDDEDLEMAGGRPRGKHIEDDENSVDISMLKT GSSLLKEBEDGGESIHNLPLVTSQRFFDGPMFTPRQKPPGS GSTPLHLTHERPWINASIGIIRCYNDEQNAIDVEPHDTSIHHAT HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSMDSSK EWIIDLPQNBDIEAICLGGGWAAAATSALLLRLFFTIGGVQKEVF SLAGPVVSNAGHGGGLEIPVHRGTGPGCLGVQLLEGKKKK QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDEGGIVMLHRGLG NTWPICONTREHCKGKSDHYWVUGIHADQLGVQLLEGKKKK QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDEGGIVMLHRGLG NTWPICONTREHCKGKSDHYWVUGIHAVKAABGLTATUVEE EEEDTRKKLNAGISNTATEWSQDFFRNQWEDABGGEADDEE KPEIHRPGONSFSKITHSSDVSAKSGAVTFSSGRVNPFKVSAS SKEPAMSMNSARSTNILDNMGKSSKKSTALSKITNNEKSFIIKP LIPKPRGOSSAASYPCKRNSGITNATEWSOPFFRNQWEDABGGEADDEE KPEIHRPGONSFSKITHSSDVSAKSGAVTFSSGRVNPFKVSAS SKEPAMSMNSARSTNILDNMGKSSKKSTALSKITNNEKSFIIKP LIPKPRFXQASSAASYPCKRNSGITNATEWSOPPFRNQWEDABGGEADDEE KPEIHRPGONSFSKITHSSDVSAKSGAVTFSSGRVNPFKVSAS SKEPAMSMNSARSTNILDNMGKSSKKSTALSKITNNEKSFIIKP LIPKPRFXQASSAASYPCKRNSGITNATEWSOPPFSDEADIIKGEM IRFRVLSTEERKWANKAKGETASGGTEAKKKRYVDESDETEN QEBKAREMINLSKKOKPUEDENTHERNTGNKGRKRINPYFKDVSVS SKEPAMSHNSARSTNILDNMGKSKKSTALSKTTNNEKSFIIKP POCKEMAEEYDEKTSELLVRKKRYKSALGAMOGMGLEVGPPAPL GAGNLOPSLIKESNABPIFMRDTINGRKRINPLYVSVVSV SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T PTAP  6066  13 1730 GSKMADLANEEKPAIAPPVFVFQKDKGGKSPAEQKNLSDSGEEP RGEAEAPHHGTGHPESAGGHALEPPAPAGASASTTPPPAPEAQL PPPRELAGRASGSSPESGBDSDREGRYPVPWERTSSLTQ PPPSGSEERSSGRLKPPTIHGQAPSAGLPSQKPKEQGRSVLR PAVLQAPQPKALSGTVPSSGTNGVSLPADCTGAVPAASPDTAAW RSPSEAADEVCALEEKEPCKNESNASEEACEKKDEATQOAFV PGGNLRDRVKLIHESVDEADMENNGHPSADTFTATNYFLQYTISS SLENSTNSDADASNKEYCGOMESEVLSPKINEVSSDAMRENA AASSGSESSSQEATPEKESLABSAAYYKATARKCLLEKVEVIT GEEASSNVLOMQCKLPVPDKTTGGWVERGRGLIKLBNMASTDDG TLOSNLISDAGPGSIEL, LILINTLMAQMGINKASEK\SITIAM DNEDGGVKVFLISASSKDTGGVVAALHHRILLARSKVEGGGBAK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGGGGGGGGGIOK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGGGGGGGGGIOK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGGGGGGGGIOK MPAPETVKYPORRELGRRLDVEKNIGGEFE	}			QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWOISDOTCA
ESWSHOPDLSDNFISOTINIUTWSPCGQVLAAGSINGLILIVNWY ETKDCMERVKHEKGVAI GCLAWHFTCGRISTYDABGNIGLILENV CDPSGKTSSSKVISTRVEKOVNDLFDGDDMSNAGDFINDNAVEIP SPSKGIINDDEDDEDLMMASGRFRQNSHILEBDENSVDISMIKT GSSLLKEBEEDGQCSS INN.PLVITSGRFFYDGPMFTGNFFTG GSSLLKEBEEDGQCSS INN.PLVITSGRFFYDGPMFTGNFFTG GSSLLKEBEEDGQCSS INN.PLVITSGRFFYDGPMFTGNFFTGNFFTG GSSLLKEBEEDGQCSS INN.PLVITSGRFFYDGPMFTGNFTGNFFTG HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINITAL HISTOTINI				ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVKLYRR
ETKDCMERVAHEKGYAIGGLAWHPTCGRISYTDAEGNIGILENY CDPSGKTSSKWSENSWENDYNDLODDMSNAGDFINDNAVEIP SPSKGIINDDEDDEDLMMASGRPRQRSHLIEDDENSVDISMLKT GSSLLKEBEEDGQEGS HINDLYTSGRPFYDGPMFTFRQRPFGG GSTELHLITHFRYWNSIGIIRCYNDAMAIOFHTSIHHAT HLSHTLNYTHADLSHEAILLACESTDELASKLHCLHFSSMDSK EWIIDDQNBDIBAICLGOWAAAATSALLLRLFTIGGVQKEVF SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELGKKKK QILHGDPLBLTEKSYLAWIGFSAEGTPCYVDSGGIVRMLNRGLG NTWFFICNTREEKCKKSCHYWVVGHIENPQDLCIPCKGSRFPP TLPRPAVALLSFKLPYCQIATEKGQMEEQFWKSVIFINHLDYLA KNGYEVESESTKOJGANEQQELLMKMLALSCKLERFRCVELADL MTQNAVNLAIKYAGRSRKLLLAQKASELAVEKAABLTATQVEEE EBEEDFRKKLNAGYSNTATEWSQPRFRNOVEEDAEDGGBADDEE KPEIHRPGGNSFSKSTNSDVSAKSOVTFSSQGRVWPFKVSAS SKEPAMSMNSARSTNILDNMGKSSKKSTALSGTTNNEKSPIIKP LIPPKPKQASASASYFQKRNSQTNKTEEVKEENLKNVLSETFAI CPPQNTENGRFKTGFQWHLEENESNILSDNDPFSDEADLIKEGM IRFRVLSTEERKVWANKAKGETASGCTEAKKRKVVDESDETEN QEKAKENLNIJSKKOKPLDFSTNGVERINLHYPFROYSYS SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T PDAP  6068 321 LPWGRIGVLLSRGKWAVTGWLESLRTAQKTALLQDGRRKVHYLF PDGKEMAEYDEKTSELLVRKWKVSALGANGOQUEVGDPAPL GAGNLOPELIKESNANIFINKDTKYGWKINLHYPROYSYS SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T PTAP  6068 13 1730 GSKMADLANEEKPAIAPPVFVFQKDKGGKSPAEQKNLSDSGEEP RGEARAPHHGTNHESSAGEHALEPPAPAGASASTPPPPAPEAQL PFPFRELAGRSAGGSSPEGGEDDSKONYCPPVKRERTSSLTO FPPSGSERSSSFLKSPTLLIHOQADSAGLPSQKPKEQORSVLR PAVLQAPQPKALSQTVPSSGTNGVSLPADCTGAVPAAGFDTAAM RSPSEAADEVCALEEKEPQNESSANSSEEACKKUPATAAM AASGSESSSGEATPEKESLARSAAAYTKATARKCLLEKVEVIT GEEAESNVLQMCCKLEVTFKTSQSTWERGRILLRINDAASTDDG TLQSKLSDAGPRGSLR\LILINTKAMASTUDG TLQSKLSDAGPRGSLR\LILINTKAMASTDDG TLQSKLSDAGPRGSLR\LILINTKAMASTDDG TLQSKLSDAGPRSSLR\LILINTKAMASTDDG TLQSKLSDAGPRSSLR\LILINTKAMASTDDG TLQSKLSDAGPRSSLR\LILINTKAMASTDDG TLQSKLSDAGPRSSLR\LILINTKAMASTDDG TLQSKLSDAGPRSSLR\LILINTKAMASTDDG TLQSKLSDAGPRSSLR\LILINTKAMASTDDG TLQSKLSDAGPRSSLR\LILINTKAMASTDDG TLQSKLSDAGPRSSLR\LILINTKAMASTDDG TLQSKLSDAGPRSSLR\LILINTAMASTDDG TLQSKLSDAGPRSSLR\LILINTKAMASTDDG TLQSKLSDAGPRSSLR\LILINTAMASTUDGG TLQSKLSDAGPRSSLR\LILINTAMASTDDG TLQSKLSDAGPRSSLR\LILINTAMASTDDG TLQSKLSDAGPRSSLR\LILINTAMASTDDG TLQ				ESWSHQFDLSDNFISQTLNIVTWSPCGOYLAAGSINGLTIVWNV
CDPSGKTSSSKVSSRVEIDNDEDGDMSNAGDFLENDNAVEIP SPSKGIINDDEDDGELMMASGRPRORALIEDDENSVDISMLKT GSSLLKEEEEDGQEGSIHNLPLVTSGRPFYDGPMFTRQKPFGS GSTPLHLTHIFPMYMSIGIIRCYNDEQDMAIDVEFHDTSIHHAT HLSHTLMYTIADLSHEAILLACESTDELASKLHCLHFSSMDSK EWIIDLPONBDIEAICLGQGWAAAATSALLLRLFTIGGVQKEVF SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLEIGKKK QILHGDPLETRKSYLAWIGFSAEGTPCYVDSBGIVKMINRGIG NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGSRFPP TLPRPAVALISKLPVQIATERGGPFWSVJFHNHLDYLA KNGYEYEESTKNQATKEQQELLMKMLALSCKLRREFRCVELADL MIQNAVNLAIKYASRSRKLILAGKLSELAVEKAAELTATQVEEE EEEEDFKKLNAGSVENTATEMSGPRAVVEGAEDGEADDDE KPEIHKPGONSFSKSTNSSDVSAKSGAVTFSSQGRVMPFKVSAS SKEPAMSMNSARSTNILDNMGKSSKKSTALSRTTNNEKSFIIKP LIPKPKGASAASYFCKRNSGTNKTEEVKEENLKWVLSSTPAI CPPQNTENGRPKTGFQMMLEENSNILSDNGDFBDEADIIKEGM IRRVLSTEERKVMANKAKGETASECTEAKKRKEVVDESDETEN QEEKAKENLNLSKKQKPLDFSTNQKLSAFAFKQE  6067 858 321 LPWGRIGVLLSRGKWAVTGHLESLETTAGKTALDGGGRKWHYLF POCKEMAEEYDEKTSELLVKKRWEVSALGAMGOMGLEVGDPAPL GAGNLGPELIKESNANDFIFRKDTWSSIGAMGOMGLEVGDPAPL GAGNLGPELIKESNANDFIFRKDTWSSIGAMGOMGLEVGDPAPL GAGNLGPELIKESNANDFIFRKDTWSSIGAMGOMGLEVGDPAPL GAGNLGPELIKESNANDFIFRKDTWSSIGSPAECKNLSDSGEEP RGEARSPHRGTOHFESAGEHALEPPAPAGASASTPPPPAPEAQL PPFPRELAGRSAGGSSPEGBIBSREDONYCPPVKRERTSSLTQ FPPSGSBERSSGFLKDPTLIHGQAPSAGJSSGKPKEQGRSVLR PAVLQAPQKALSTVPSSGTNUSTADCTGAVBAPDTATMYFLQYTSS SLENSTNSADASSNKFYFGQNNSESNASEEEACEKKDPATQAFV PGQNLRDRVKLINESVDEADMENAGHPSADTPTATTYFLQYTSS SLENSTNSADASSNKFYFGGNNSESVLSPPRILBEVSDANRNA AAESGSESSSGEAPPKESLABSAAAYTKATAKKCLLEKVBUTT GEEASSNULGMGCKLPVPDKTSGSWVERGGGLRLNDMASTDDG TLQSKLSDAGPRSSLR\LILMTKLMAGMQIDKASEK\SITTAM DMEDGGVKVFLISASSRDTGQVYAALHHRILALRSRVEGCGBAK MPAPEPGAAPSNEEDDSDDDDDVLAPSGATAAGAGGGGGGGGGGGEAG MPAPEPGAAPSNEEDDSDDDDDVLAPSGATAAGAGGGGGGGGGGEAG MPAPEPGAAPSNEEDDSDDDDDDVLAPSGATAAGAGGGGGGGGGGGGEAG MPAPEPGAAPSNEEDDSDDDDDVLAPSGATAAGAGGGGGGGGGGGGGGGAGGAGAGAAFATAGAGAGGGGGGGG				ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNIGLIENV
SFSKGIINDEDDEDLMMASGRPRQRSHILBDENSVDISMLKT GSSLLKEEEBDQGES INHLIVTSQRPFYDGPMPTPRQKPFQS GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSIHHAT HLSNTLNYTIADLSHEAILLACESTDELASKHCLHFSSWDSK EWIIDLDQNBBIE BEICLGGGWAAATSALLKLEFTIGGVQKEVF SLAGPVVSWAGHGEQLFIVYHRGTGFDGDQCLGVQLLELGKKKK QILMGDPLPLTRKSYLAWIGFSAEGTPCYVDBSGIVRMLNRGLG NTWTPICNTREHCKKKSDHYWVGHENPQQLKCIPCKGSRFPP TLPRPAVALLSFKLEVCQIATEKQGMEEQFWRSVIFHNHLDYLA KNGYEVESTSINQATEKQQELMKALSCKLEREFRCVELADL MTQNAVALAIKYASSRKLLAQKLSELAVEKAABLTATQVEEE EEEEDFRKKLNAGYSNTATEWSQRFRRDQVEBAABDGBADEE KPEIHKPGQNSFSKSTNSSDVSAKSGAVTFSSQGRVPFKVSAS SKEPAMSMNSARSTNILDNMGKSSKKSTALSKTTNNEKSBIIKP LIPRFPKQGNSFSKSTNSSDVSAKSGAVTFSSQGRVPFKVSAS SKEPAMSMNSARSTNILDNMGKSSKKSTALSKTTNNEKSBIIKP LIPRFPKQGNSFSKSTNSSDVSAKSGAVTFSSQGRVPFKVSAS SKEPAMSMNSARSTNILDNMGKSSKKSTALSKTTNNEKSBIIKP LIPRFPKQGNSFSKSTNSSDVSAKSGAVTFSSQGRVPFKVSAS SKEPAMSMNSARSTNILDNMGKSSKKSTALSKTTNNEKSBIIKP LIPRFPKQGNSFSKSTNSSDVSAKSGAVTFSSQGRVPFKVSAS SKEPAMSMNSARSTNILDNMGKSSKKSTALSKTTNNEKSBIIKP LIPRFPKGGNSFKSKTNSDVSAKSGAVTFSSQGRVPFKVSAS SKEPAMSMNSARSTNILDNMGKSSKKSTALSKTTNNEKSBIIKP LIPRFPKGGNSFKSKSTALSKTTNKEEVKEERLAKVILDEGTEPA CPPONTENQRPKTGPQMWLEENRSNILSDNPPSDEADLIKEGM IRRFULTSTERKVWANKAKGETASSGTEAKKRKVVDESBETPAI CPPONTENQRPKTGPQMWLEENRSNILSDNPPSDEADLIKEGM IRRFULTSTERKVWANKAKGETASSGTEAKKRKVVDESBETPAI CPPONTENQRPKTGPUMSLESKATAGKTALLQDGRRKVHYLF POCKEMAEEVLEKTSELLVRKHRVKSALGAMGQWQLEVGDPAPL GAGNLGPELIKESNANPITFMKNFGWRINNLEFFEDVYSV SVDQKERCIIVSTTTKKYYKKFSIPDLDRHQLPLDDALLSFA\T PTAP  6068  13 1730 GSKMADLANEEKPALAPPFFYFYFQKDKGGKSPAEQKNLSDSGEEP RGABAPHHGTGHPESAGEHALEPPAPAGASASTPPPPABEQL PFPFRELAGRSAGGSSPBGGBBSREDGNCCPVKREPTSSLTQ FPPSQSEERSSGFRLKPPTLHGQAPSAGLPSCKKEQORSVLR PAVLQAPQKALSQTVPSSGTNGSUSPADCTGAVPAASPDTAAW RSPSEAADEVCALEEKEPQNNESNASEERAGEKKDPATQQAFV PGQNLRDRKKLINESVDEADMENNGHPSADTTTATNYFLQYISS SLENSTNSADASSNFFYGGNMESVLSPALSPKLSSDANENA AABSGSESSGCATTPEKESLABSAAAYTKATARKCLLEKVEVIT GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLIRLNDMASTDDG TLQSKLSDAGPRGSLR\LLILINTKLWAQMGIDKASSK\SITTAM DNEDQGVKKYFLISASSKDTGQVVAALHHRILALRSRVEOEQEAK MPAPEPGGAPSNEEDDSDDDDDVLAPSGATAAGAG				CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNAVETD
GSSILKEBEEDGGGS INNLPLVTSORPTYDGNPTTGNPFTGS GSTPLHLTHRHYWMS IGIIRCYNDEQDNAIDVEFHDTS IHAT HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSMDSSK EWIIDLPQNBDIEAICLAGGWAAAATSALLLRLPTIGGVQKEVF SLAGPVVSNAGHSGULFIVYHKSTPLDGQCLGVQKEVF SLAGPVVSNAGHSGULFIVYHKSTPLDGQCLGVQKEVK QILHGDPLPLTRKSYLAWIGFSAGGTPCYVDSBGIVRMLNRGLG NTWTPICNTREHCKKKSDHYWVVGIHENPQLRCIPCKGSRFPP TLPRPAVALISFKLPYCQIATEKGQMEEQFWRSVJFENNHLDVLA KNGYEYEESTKNQATKEQQELLMKNHALSCKLEREFRCVELADL MTQNAVNLAIKYASRSKLILLAQKLSELAVEKABELTATQVEEE EEEEDFRKKLNAGYSNTATEWSQPFFRNQVEEDAEDSGEADDEE KPEIHRPGGNSFSKSTNSSDVSAKSGAVTFSGGGRVNPFKVSAS SKEPRAMSMNSARSTNILDNMGKSSKKSTALSGTTNMEKSPIIKP LIPPKPKOASAASYFQKRNSQTNKTEEVKEENLKNVLSETPAI CPPQNTENGRPKTGFQMMLEENRSNILSDNPPFSDEADLIKGGM IRFRVLSTEERKWANNKAKGTSAGSGETAKKRKVVDESDETEN QEEKAKENLNLSKKQKPLDFSTNOKLSAFAFKGE  6067 858 321 LPWGRLGVLLSRGKMAVTGWLESIRTAQKTALLQDGRRKVHYLF PDGKEMAEBYDEKTSELLVRKWRVKSALGAMGGWGLEVGDPAPL GAGNLGPELIKESNANPIFMRKDTKMSFOWRIKNLPYPKDVYSV SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T PTAD  6068 13 1730 GSKMADLANEEKFALAPPVFVFGXDKGGGSPAEGKNLSDSGEEP RGEAEAPHHGTGHPESAGGHALEPPAPAGASASTPPPPAPEAQL PPFPRELAGRSAGGSSPEGGEDSDREDGNYCPPVKRERTSSLTQ FPPSGSEERSSGFALXPPTLHGQAPSAGLPSQKKEQQRSVLR PAVLQAPOPKALSGTVPSSGTNGVSLPADCTGAVPAASPDTAAW RSPSEAADBVCALEEKEPQNESSNASEBEACEKKDPATQOAFV PGQNLRDRVKLINESVDEADMENAGHPATTATNYFLOYISS SLENSTNSADASSNKFVFGGNMSERVLSPPKLEVSSDANRENA AAESGSESSGEATPEKESLABSAAAYTKATARKCLLEKVBVIT GEEBASNVLOMGCKLFVPDKTSGSWVERGRGLLRLINDMASTDDG TLQSRLSDAGPRGSLR\LILNTKLMAQMGIDKASEK\SIRITAM DNEDGGVKKYFLISASSKDTGQVYAALHHHILALRSRVEQEGAK MPAPEBGAAPSNEEDDSDDDDDVLAPSGATAAAGDBEGGGQTTGS T PTRPGQAGSSSAMAAQRLIGKRVLSKLQSPERARPGGSPGGGGKA RHARTVTVKYDRRELGRRLDVEKWIDGRLEELKRGMEADMPDEIN RHARTVTVKYDRRELGRRLDVEKWIDGRLEELKRGMEADMPDEIN				SPSKGIINDDEDDEDLMMASGRPRORSHTLEDDENSVDIGMIVE
GSTPLHLTHRPMWNNSIGIRCYNDEODNAIDVEPHOTSIHHAT HLSNTIANTIADLSHBAILLACESTDELASKLHCLHFSSWDSSK EWIIDLPQNEDIEAICLGGGWAAAATSALLRIPTIGGVQKEVF SLAGPVVSWAGHGEQLFIVYHRGTGFDGDGCLGVQLLEJGKKKK QILMGDPLPLTRKSYLAWTGFAEACTPCYVDSBGIVRMLNRGLG NTWTPICNTREHCKGKSDHYWVGIHENPQQLRCIPCKGSRFPP TLPRPAVALLSFKLEYCQIATEKGMEEQPWRSVIFFINHLDYLA KNGYEVTESTKIN,QATEQOGLHMKHALISCKLEREFRCVELADL MTQNAVALAIKYASRSRKLILAQKLSELAVEKAAELTATQVEEE EEEEDFRKKLNAGYSNTATEWSQPRFRNQVEEDAEDSGEADDEE KPEIHKPGGNSFSKSTNSSDVSAKSGAVTFSSGGRVDFFKVSAS SKEPAMSMNSARSTNILDNMCKSSKKSTALSRTTNNEKSPIIKP LIPKPKPKQASASYFQKRNSQTNKTEVKEENLKNVLSETPAI CPPQNTENGRPKTGFQMMLEENRSNILSDNEPDEBADIIKEGM IRFRVLSTEERKVWANKAKGETASGCTEAKKRKVVDESDETEN QEEKAKENLNISKKOKPLDFSTNQKLSAFAFKQE GERAKENLNISKKOKPLDFSTNQKLSAFAFKQE FPOCKEMAEFYDEKTSELLVRKWRVKSALGAMGGWQLEVGDPAPL GAGNIGPELIKESNANPIFMRKDTKMSFQWRIRNLPYPKDVYSV SVDQKERCIIVRTTKKKYYKKFSIPDLDRIQLEDDALLSFA\T PTAP  6068 13 1730 GSKWADLANEEKPAIAPPVFVFQKDKGGKSPAEQKNLSDSGEEP RGEAEAPHHGTGHPESAGEHALEPPARAGASASTPPPRAPEAQL PFFPRELAGRSAGGSSPBGGBDSREEGINCPPVKRERTSSLTQ PFSPSELAGBEVCALEEKEPQKNESSNASEERACKKDPATQOFV PFSPSELAGBEVCALEEKEPQKNESSNASEERACKKDPATQOFV PAVLQAPQPKALSQTVPSSGTNGVSLPADCTGAVPAASPDTAAW RSPSEAADEVCALEEKEPQKNESSNASEERACKKDPATQOFV PGGNLINGBVKLIINESVDEAMENAGHPSADTPPTATWYLQVISS SLENSTNSADASSNKFVFGQNMSERVLSPPKLNEVSDANRENA AAESGSESSSQEATPEKESLASAAYTKATARKCLLEKVEVIT GEEAESNVLOMGCKIFVPDKTSGSWVERGGLLKILDMASTDDG TLOSKLSDAGPRGSLR\LIINTKLWAQMQIDKASEK\SIRITAM DNEDGGVKVFLISASSKDTGQVTVAALHHHILALRSRVEGGEAK MPAPPEGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGGDQTTGS T PTRPGQAGSSSAMAAORLIGKVLJSKLOSPSRARGPGGSPGGGLOK PTRPGQAGSSSAMAAORLIGKVLJSKLOSPSRARGPGSPGGGLOK PTRPGQAGSSSAMAAORLIGKVLJSKLOSPSRARGPGSPGGGGLOK PTRPGQAGSSSAMAAORLIGKVLJSKLOSPSRARGPGSPGGGLOK PARATVTVYNDRRELQRELDVEKWIDGRLEELLYRGMEADMPDEIN				GSSLLKEEEEDGOEGSTHNIDLVTSOPDEVDGDMDTDDOVDDOG
HLSNTINYTIADISHEAILLACESTELASKLHCLIFISBUDSSK EWIIDLEONBU EARICIGGOWAAAATSALLRIPTIGGVQKEVF SLAGPVVSMAGHGEQLFIVYHRCTGFDGDCLGVQLLEIGKKKK QILHGDPLPITRKSYLAWIGFSAEGTFP TVDESGIVRMINRGLG MTWTPICNTEHCKGKSCHWWVGIHENPQQLECIPCKGSRFPP TLPRPAVAILSFKLPYCQIATEKGQMEEQFWRSVIFHNHLDYLA KNGYSEYEESTKNQATKEQGELLMKMALSCKLERFEFRCVELADL MTQNAVNLAIKYASRSKILIAQKLSELAVEKABELTATOVEE EEEEDFKKLLNAGYSNTATEWSQPFRNQVEEDAEDSGEADDEE KPEIHKPGQNSFSKSTNSDVSAKSGAVTFSSQGRVPFKVSAS SKEPAMSMNSARSTNILDNMGKSSKKSTALSKITNNEKSPIIKP LIPKPKPKQASAASYFQKRNSQTNKTEEVKEENLKNVLSETPAI CPPONTENORPKTGPOMWLEENRSNILSDNPDFSDEADIIKEGM IRFVLSTEERKVWANKAKGETASEGTEAKKRKVVDESDETEN QEEKALENLINLSKKOKPLDFSTNQKLSAFAFKQE  6067 858 321 LPMGRIGVLLISKGMAVTGWLESLRTAQKTALLQGGRRKVHYLF PDGKEMAEEYDEKTSELLVRKWRVKSALGAMQQWGLEVGDPAPL GAGNLGPELIKESMANPIFMRNDTKMSFQWRTRNLPYPKDVYSV SVDQKERCIIVTRTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T PTAP  6068 13 1730 GSKMADLANEEKPAIAPPVFVFOKDKGOKSPAEQKNLSDSGEEP RGEAEAPHHGTCHPESAGEHALEPPAPAGASASTPPPPAPEAQL PPFPRELAGRSAGGSSPEGGBDSDREDGNYCPPVKRERTSSLTQ FPPSQSERRSGFRLXPPTLIHGQAPSAGLPSQKFRQGRSVLR PAVLQAPOFKALSQTVPSSGTMGVSLPADCTGAVPAASPDTAAM RSPSEAADEVCALEFKEPQKNESSNASEEACEKKDPATQQAFV FGGNLADRVLLINESVDEADMENAGHPSADTPTATNYFLQYISS SLENSTNSADASSNKFVFGGNKSENLSPPTANYFLQYISS SLENSTNSADASSNKFVFGGNKSENLSPPTANYKATARKCLLEKVEVIT GEEAESNVLJMQCKLIFVFNSGSWEERGGGLLKINDMASTDDG TLQSRLSDAGPRGSLR\LLINTKLWAQMQIDKASEK\SIRITAM DNEDGGVKVFLISASSKDTGQVYAALHHRILALRSRVEQEGEAK MPAPEGGAAPSNEEDDSDDDDDDVLAPSGALTAARAGDEGOTTGS T PTRPQAGSSSAMAAQRLGKRVLSKLQSPSRAKGPGGSEGGLKK PHARVTVYXYDRRELGORLGKRVLSKLQSPSRAKGPGGGDCICK RHARVTVYXYDRRELGORRIGKRVLSKLQSPSRAKGPGGSPGGLKK RHARVTVYXYDRRELGORRIGKRVLSKLGSPSRAKGPGGSPGGLKK RHARVTVYXYDRRELGORRIGKRVLSKLGSPSRAKGPGGSPGGLKK RHARVTVYXYDRRELGORRIGKRVLSKLGSPSRAKGPGGSPGGLKK RHARVTVYXYDRRELGORRIGKRVLSKLGSPSRAKGPGGSPGGLKK RHARVTVYXYDRRELGORRIGKRVLSKLGSPSRAKGPGGSPGGLKK RHARVTVYXYDRRELGORRIGKRVLSKLGSPSRAKGPGGSPGGLKK RHARVTVYXYDRRELGORRIGKRVLSKLGSPSRAKGPGGSDGLCK				GSTPLHITHREM/WNS IGTIPCVNDEODNAID/GERIDMCT*****
EWIIDLEONBDIRAICLIGGGWARAATSALLLELPTIGGUCKEVF SLAGPVUSMAGHGEOLFIVYHGTGFDGDQCLGVQLLELGKKK QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLNRGLG NTWTPICNTEHCKGKSDHYWVVGIHENPQQLRCIPCKGSRFPP TLPPAVALLSFKLPYCQIATEGGMEQFWRSVIFHNHLDYLA KNGYEYEESTKNQATKEQQELLMKMLALSCKLEREFRCVELADL MTQNAVALAIKYASRSRKLILAQKLSELAVEKARBLTATQUESE EEEBJFKKKLANGAYSNTATEGOPRENQVEEDAEDSGEADDEE KPEIHKPGQNSFSKSTNSSDVSAKSGAVTFSSQGRVNPFKVSAS SKEPAMSMASARSTNILDNMGKSSKKSTALSRITNNEKSPIIKP LIPPKPKQASAASYFÇKRNSGOTNKTEEVKEERLKNVLSETPAI CPPQNTENQRPKTGFQMWLEENRSNILSDNPDFSDEADIIKEGM IRFRVLSTEERKWANKAKGETASECTEAKKRKRVUDESDETEN GERKAKENLINSKKQKPLDFSTAKKKRVDFDBEDETEN GERKAKENLINSKKQKPLDFSTAKKGKAPATFKOE OEEKAKENLINSKKQKPLDFSTAKKGKAPATFKOE  6067 858 321 LPWGLGVLLSRGKMAVTGULESLRTAQKTALLQDGRRKVHYLF PDGKEMABEYDEKTSELLVRKWRVKSALGAMQWQLBVGDPAPL GAGNLGPELIKESANAPIFMRDTKMSFGMRTRNLPYFKDYSV SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T PTAP  6068 13 1730 GSKMADLANEEKPAIAPPVFVFOKDKGOKSPAEGKNLSDSGEEP RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPPAPEAQL PFPFRELAGRSAGGSSPEGGSDSREEDNYCPPVKRERTSSLTQ FPSSGSERSSGFRLXPPTILHIGQAPSAGLPSOKKEGORSVLR PAVLQAPQFKALSGTVPSSGTNSVLPADCTGAVPAASPDTAAW RSPSEAADEVCALEEKEPQKNESSNASEEACEKKDPATQQAFV FGGNLRDRVKLINESVDEADMENAGHPSADTPTANTYFLQYISS SLENSTINSADASSNKFVFGQNMSERVLSPPKLNEVSSDANRENA AAESGSESSSGEATPEKESLARSAAAYTKATARKCLLEKVEVIT GEEABSNVLQWCKLPFPTBKTTGSWVERGRGLIKLINDMASTDDG TLQSRLSDAGPRGSLR\LILNTKLWAQMQIDKASEK\SIRITAM DNEDQGVKVFLISASSKTGGUVYAALHRILALRSRVEQEORAK MPAPPEGGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGGTTGS T PTRPGQAGSSSAMAAQELGKRVUSKLOSPSRARGPGGSPGGLOK RHARVTVKYDRRELGRRLDVEKWIDGRLEELFRGMEADMPDE IN				HIGHTINYTIADI CHEATI I ACECEPERA SULVEY VIDENTA CONTROLLED
SLAGPVVSMAGHGEOLFIVHRCTGFDEDCCLGVOLLEIGKKKK QILHGDPLPLTRKSYLAWIGFSAGTPCYVDSEGIVRMLNRGLG NTWTPICNTEHCKGKSDHYWVGIHENPCQLRCIPCKGSRFPP TLPRPAVAILSFKLPYCOIATEKGQMEEQFWRSVIFHNHLDYLA KNGYEYEESTKNQATKEQQELLMKMLALSCKLEREFRCVELADL MTQNAVNLAIKYASRSKILIAQKLSELAVEKABELTATOVEE EEEEDFKKLINAGYSNTATEWSQPRFRNQVEEDAEDSGEADDEE KPEIHKPGQNSFSKSTNSDVSAKSGAVTFSSQGRVPFKVSAS SKEPAMSMNSARSTNILDMGKSSKKSTALSRITNNEKSPIIKP LIPPKPK KOASAASYFOKRNSQTNKTEEVEENLKNVLSETPAI CPPQNTENQRPKTGPQMWLEENSRILISNIPPSFSEADIIKEGM IRFRVLSTEERKWWANKAKGETASECTEAKKRKVVDESDETEN QEEKAKENLNLSKKQKPLDFSTNOKLSAFAFKQE  6067 858 321 LPWCRLGVLLSRGKMAVTUWLESLETAQKTALLQDGRRKVHYLF PDCKEMAEEVDEKTSELLVUKRVVKSALGAMOQMOLEVGDPAPL GAGNLGPELIKESNANPIFMRKDTKMSFQWRIRNLPYPKDVYSV SVDQKBRCIIVRTTNKKYYKKFSIPDLDRHQLPDDALLSFA\T PTAP  6068 13 1730 GSKMADLANEEKPAIAPPVFVFQKDKGGKSPAEQKNLSDSGEEP RGEAEAPHIGTCHPESAGEHALEPPAPAGASASTPPPAPEAQL PFFPRELAGRSAGGSSPEGEDSDREDGNYCPPVKRERTSSLIQ PFPFPELAGRSAGGSSPEGEDSDREDGNYCPPVKRERTSSLIQ FPPSQSEERSSGFRLXPPTLIHGQAPSAGLBSQKKECQRSVLR PAVLQAPQPKALSGTVPSSGTMGVSLPADCTGAVPAASPDTAAW RSPSEAADEVCALEKEPQKNESSNASEEBACEKIDPATQAFV FGQNLRDRVKLINESVDEADMENAGHPSADTTTATNYFLOYISS SLENSTNSADASSNKFVGQNNSERVLSPFKLNEVSSDANRENA AAESGSESSQEATPEKESLAESAAAYTKATARKCLLEKVEVUT GEEAESNYLQMQCKLFVFPKTSQSWVERGRGLLELINDMASTDDG TLQSRLSDAGPRGSLF, LILLNTKLMAQMOIDKASEK\SIRITAM DNEDQGVKVFLISASSKDTGQUVAALHRILLALRSTDDG TLQSRLSDAGPRGSLF, LILLNTKLMAQMOIDKASEK\SIRITAM DNEDQGVKVFLISASSKDTGQUVAALHRILLALRSTVOEGEEAK MPAPEFGAAPSNEEDDSDDDDDVLAPSGATAAGGADGEOGGTTGS T PTRFQQAGSSSAMAAQRILGKRVLSKLQSPSRARGPGGSPGGLOK RHARVTVYXYDRRELGRRLDVEKKILGSPSRARGPGGSPGGLOK RHARVTVYXYDRRELGRRLDVEKKILGSPSRARGPGGSPGGLOK RHARVTVYXYDRRELGRRLDVEKKILGSPSRARGPGGSPGGLOK RHARVTVYXYDRRELGRRLDVEKKILGSPSRARGPGGSPGGLOK RHARVTVYXYDRRELGRRLDVEKKILGSPSRARGPGGSPGGLOK RHARVTVYXYDRRELGRRLDVEKKILGSPSRARGPGGSPGLOK RHARVTVYXYDRRELGRRLDVEKKILGSPSRARGPGGSPGGLOK RHARVTVYXYDRRELGRRLDVEKKILGSPSRARGPGGSPGGLOK RHARVTVYXYDRRELGRRLDVEKKILGSPSRARGPGGSPGLOK				FWI IDLDONED TEXTOL COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOTT COCKER AS TO ALLE DE DOT
OILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMIMRGLG NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGSRFPP TLPRPAVAILSFKLPYCQIATEKGQMEEQFWRSVIFHHILDYLA KNGYEYEESTKNQATKEQQELLMKMIALSCKLEREFRCVELADL MTQNAVALAIKYASRSRKLILAQKLSELAVEKAAELTATQVEEE EEEEDFRKKLNAGYSNTATEWSQPFFRNQVEEDAEDSGEADDEE KPEIHRPGQNSFSKSTNSDVSAKSGAVTFSSQGRVNPFKVSAS SKEPAMSMNSARSTNILDNMGKSKKKTALSRTTNNEKSPIIKP LIPKPKPKQASAASYFGKRNSQTNKTEEVKEENLKNVLSETPAI CPPQNTENQRPKTGFQMMLEENRSNILSDNPDFSDEADIIKEGM IRFRVLSTEERKVWANKAKGETASEGTEAKKRKRVVDESDETEN QEEKAKENLNISKKQKPLDFSTNGKLSAFAFKQE UPPGRIGVILSRGGMAVTGHLESLRTAGKTAILADGGRKVHYLF PDGKEMAEEVDEKTSELLVRKWRVKSALGAMGQWQLEVGDPAPL GAGNLGPELIKESNANPIFHKBTKMSFQWRIRNLFYPKDVYSV SVDQKBECIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T PTAP  6068 13 1730 GSKMADLANEEKPAIAPPVFVFQKDKGQKSPAEQKNLSDSGEEP RGEAEAPHHGTGHPESAGGENDREDGNYCPPVKRETTSSLTQ PPFPRELAGRSAGGSSPEGGEDDREDGNYCPPVKRETTSSLTQ FPPSQSEERSSGFRLKPPTLIHGQAPSAGLPSQKPKEQQRSVLR PAVLQAPQPKALSGTVPSSGTNGVSLPADCTGAVPAASPDTAAW RSPSEAADEVCALEEKEPQKNESSNASEEEACEKKDPATQQAFV FGQNLRDRVKLINESVDEADMENAGHPSADTFTATNYFLQYISS SLENSTNSADASSNKFVFGQNMSERVLSPPKLNEVSSDANRENA AAESGSESSGEATPEKESLABSAAAYTKATAKKCLLEKVEVIT GEEAESNVLQMQCKLPVFDKTSGSWVERGRGLIRLENDRASTDDG TLQSKISDAGPRGSLR\LILITTKLMAQMQIDKASEK\SIRITAM DNEDQGVKVFLISASSKDTGQVVAALHHRILARSRVEGEGEAK MPAPEFGAAPSNEEDDSDDDDVLAPSGATAAGAGBGEGDQTTGS T PTRFQQAGSSSAMAAQRIJKRVLSKLQSPSRARGPGGSPGGLQK RHARVTVKYDRRELORRLDVEKWIDGSLEELYRGMEADMPDEIN RHARVTVKYDRRELORRLDVEKWIDGSLEELYRGMEADMPDEIN				CLACOUIGNACIGGO EXPRINGIBLE CONTROL OF THE
NTWTPICNTEHCKGKSDHYWVGILENPQQIRCIPCKGSRPPP TLPPRAVAILSFKLPYCQIATEKGQMEQFWRSVIFINHLDYLA KNGYEYESTKNQATKEQGELLMKMLALSCKLEREFRCYELADL MTONAVNLAIKYASRSRKLILAQKLSELAVEKAAELTATQUEEE EEEEDFRKKLNAGYSNTATEWSQPRFRNQUEEDAEDGGEADDEE KPEIHREGONSFSKSTNSDVSAKSGAVTFSSQGRUPPFKVSAS SKEPAMSMNSARSTNILDNMGKSSKKSTALSRTTNNEKSPIIKP LIPKPKPKQASAASYFQKRNSGTNKTEEVKEENLKNVLSETPAI CPPONTENQPRKTGFOMMLEENRSNILSDNDPFSDEADIIKEGM IRFRVLSTEERKVWANKAKGETASEGTEAKKRKVVDESDETEN QEBKAKENLALISKGKPLDFSTNQKLSAFAFKQE  1PPORGLGVLLSGGMAVTGLESLETATQKTALLQDGRRKVHYLF PDGKEMAEEYDEKTSELLVRKWRVKSALGAMGQWQLEVGDPAPL GAGNLGPELIKESNANPIFMKDTKMSFOMBIRNLPYPKDVYSV SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T PTAP  6068 13 1730 GSKMADLANEEKPALAPPVFVFOKDKGOKSPAEQKNLSDSGEEP RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPPADEAQL PPFPRELAGRSAGGSSPEGGEDSDREIGNYCPPVKRETKSSLTQ FPPSGSBERSSGFRLXPPTLHGQAPSAGLPSQKFKEQQRSVLR PAVLQAPQPKALSGTVPSSGTNGVSLPADCTGAVPAASPDTAAM RSPSEAADEVCALEEKEPOKNESNASEERCEKKDPATQAFV FGQNLRDRVKLINESVDEADMENAGHPSADTPTATNYFLQYISS SLENSTNSADASSNKYFGGNMSERVLSPPKLMEVSSDARRENA AAAESGESSSGEATPEKESLAESAAAYTKATARKCLLEKVEVIT GEEAESNVLQMQCKLFVFDKTSGSWVERGRGLLRLUDMASTDDC TLQSRLSDAGPRGSLR\LILINTKLWAQMQIDKASEK\SIRITAM DAEDQGVKVFLISASSRDTGGVYAALHHRILALRSRVEQEQEAK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEEGQGTTGS T PTRFGQAGSSSAMAAQRLGKRVLSKLQSPSRARGFGGSPGGLQK RHARVTVKYDRRELORRLDVEKWIDGRLEELYRGMEADMPDEIN				STAGE V SMAGHGEQLE I V YHRGTGFDGDQCLGVQLLELGKKKK
TLPRPAVAILSFKLPYCQLATERGQMEEQFWRSVIFHNHLDYLA KNGYEYEESTKNQATKEQQELLMKMALASKCHEREFRCVELADL MTCMAVNLAINYASRSKLILAQKLSELAVEKABELTATQUEEE EEEBDFRKKLNAGYSNTATEWSQPRFRNQVEEDAEDGEADDEE KPEIHKPGQNSFSKSTNSSDVSAKSGAVTFSSQGRWPFKVSAS SKEPAMSMNSARSTHILDNMGXSSKKSTALSRTTNNEKSPIIKP LIPKPKPKQASAASYFQKRNSQTNKTEEVKEENLKNVLSETPAI CPPCNTENQRPKTGFQMWLEENRSNILSDNPDFSDEADLIKEGM IRFRVLSTEERKVWANKAKGETASEGTEAKKRKVVDESDETEN QEEKAKENLALSKKQKPLDFSTNQKLSAFAFKQE GERALENLALSKKQKPLDFSTNQKLSAFAFKQE GERALENLALSKKQKPLDFSTNQKLSAFAFKQE GAGNLGPELIKESNANPIFMRKDTKMSFGWRIRNLPYPKDVYSV SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQDFLDDALLSFA\T PTAP  6068  13 1730 GSKMADLANEEKPAIAPPVFVFQKDKGQKSPAEQKNLSDSGEEP RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPPAPEAQL PPFPRELAGRSAGGSSPEGGBDSDREDGNYCPPVKRERTSSLTQ FPPSQSEERSSGFRLYPTLHGQAPSAGLPSQKPKEQQRSVLR PAVLQAPQPKALSGTVPSSGTNGVSLPADCTGAVPAASPDTAAW RSPSEAADEVCALEEKEPQKNESSNASEEEACEKKDPATQQFV PGGNLKBRVKLIHESVDEADMENAGHPSADTPTATHYFLQYISS SLENSTNSADASSNKFVFGQNMSERVLSPPKLNEVSDDANRENA AAESGSESSSGEATPEKESLABSAAAYTKATARKCLLEKVEVIT GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRLNDMASTDDG TLQSRLSDAGPRGSLR\LILNTKLMAQMQIDKASEK\SIRITAM DEMEDQGVKVFLISASSGTOGQVYAALHHRILALRSRVEQGEQEAK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGQTTGS T PTRPGQAGSSSAMAAQRIGKRVLSKLQSPSRARGPGSSPGGLQK RHARVIVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN	1			QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLNRGLG
KNGYEYEESTKNQATKEQQELLMKMLALSCKLEREFRCVELADL MTQNAVNLAIKYASRSKKILLAQKLSELAVEKAAELTATQUEEE EEEEDFRKKLMAGYSNTATEWSQPRFRNQVEEDAEDSGEADDEE KPEIHKPGONSFSKSTNSSDVSAKSGAVTFSSQGRVNPFKVSAS SKEPAMSMNSARSTNILDNMGKSKESTALSKTTNNEKSFJIKP LIPKPKPKQASAASYFQKRNSOTNKTEEVKEELLKNVLSETPAI CPPQNTENQRPKTGPQMWLEENRSNILSDNPDPSDEADLIKEGM IRFRVLSTEERKVWANKAKGETASECTEAKKRRVVDESDETEN QEEKAKENLNLSKKQKDJFSTNQKLSAFAFKQE  6067 858 321 LPWQRLGVLLSRGKMAVTGWLESLRTAQKTALLQDGRRKVHYLF PDCKEMAEEYDEKTSELLVRKWKVSALGAMGGWQLEVGDPAPL GAGNLGPELIKESNANPIFMRKDTKMSFQWRIRNLPYPKDVYSV SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPPLDDALLSFA\T PTAP  6068 13 1730 GSKMADLANEEKPALAPPVFVFQKDKGGKSPAEQKNLSDSGEEP RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPPAPEAQL PPFPRELAGRSAGGSSPEGGEDSDREDGNYCPPVKRERTSSLTQ FPPSQSEERSSGFRLKPPTLHGQAPSAGLPSQKFKEQQRSVLR PAVLQAPQPKALSQTVPSSGTNGVSLPADCTGAVPAASPDTAAW RSPSEAADEVCALEEKEPQKNESSNASEEEACEKKDPATQQAFV PGGNLKBRVKLIHESVDEADMENAGHPSADTPTATNYFLQYISS SLENSTNSADASSNKFVFGQNMSERVLSPPKINEVSSDAMRENA AAESGSESSSGEATPEKESLABSAAAYTKATARKCLLEKVEVIT GEEAESNVLQMQCKLPVFDKTSQSWVERGRGLLRLNDMASTDDG TLQSRLSDAGPRGSLR\LILTKLMAQMGIDKASEK\SIRITAM DMEDQGVKVFLISASSKDTQQVYAALHHRILALRSRVEQQEQEAK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAOAGDEGGQTTGS T PTRPGQAGSSSAMAAQRIGKRVLSKLQSPSRAKGPGGSPGGLOK RHARVIVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN				NIWIPICNIREHCKGKSDHYWVVGIHENPQQLRCIPCKGSRFPP
MTCMAVNILAIKYASRSRKLILAQKLSELAVEKAABLITATQUEEE EEEDFRKKLNAGYSNTATEWSQPRFRNQVEEDAEDSGEADDEE KPEIHKPGQNSFSKSTNSSDVSAKSGAVTFSSQGRVAPFKVSAS SKEPAMSMNSARSTNILDNMGKSSKKSTALSRTTNNEKSPIIKP LIPKPKPKQASAASYPQKRNSQTKKTEEVKEENLKNVLSETPAI CPPQNTENQRPKTGFQMWLEENRSNILSDNPDFSDEADIIKEGM IRFRVLSTEERKVWAMKAKGETASEGTEAKKRKRVVDESDETEN QEEKAKENINISKKQKPLDFSTNQKLSAFAFKQE  6067 858 321 LPWQRLGVLSRGKMAVTGWLESLRTAQKTALLQDGRRKVHYLF PDGKEMAEEYDEKTSELLVWKWRVKSALGAMGQWQLEVGDPAPL GAGNLGPELIKESNANPIFMRKDTKMSFQWRIRNLPYPKDVYSV SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T PTAP  6068 13 1730 GSKMADLANEEKPAIAPPVFVFQKDKGGKSPAEQKNLSDSGEEP RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPAPEAQL PFFPRELAGRSSAGGSSPEGGEBDREDGNYCPPVKRERTSSLTQ FPPSQSERSSGFRLKPPTLIHGQAPSAGLPSQKFKEQQRSVLR PAVLQAPQPKALSGTVPSSGTNGVSLPADCTGAVPAASPDTAAW RSPSEAADEVCALEEKEPQKNESSNASEEEACEKKDPATQQAFV FGQNLRDRVKLINESVDEADMEMAGHPSADTPTATNYFLQYISS SLENSTNSADASSNKFVFGGNMSERVLSPPKLNEVSSDANRENA AAESGSESSSQEATPEKESLABSAAAYTKATARKCLLEKVEVIT GEEAESNVLOMQCKLFVFDKTSQSWVERGRGLLRLNDMASTDDG TLQSRLSDAGPRGSLR\LILINTKLWAQMQIDKASEK,SIRITAM DNEDQGVKVFLISASSKDTGQVYAALHHRILALRSRVEQEGEAK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGQTTGS T PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRAKGPGGSPGGLQK RHARVIVKYDRRELQRRLDVEKKIDGRLEELYRGMEADMPDE IN				TLPRPAVAILSFKLPYCQIATEKGQMEEQFWRSVIFHNHLDYLA
MTCMAVNILAIKYASRSRKLILAQKLSELAVEKAABLITATQUEEE EEEDFRKKLNAGYSNTATEWSQPRFRNQVEEDAEDSGEADDEE KPEIHKPGQNSFSKSTNSSDVSAKSGAVTFSSQGRVAPFKVSAS SKEPAMSMNSARSTNILDNMGKSSKKSTALSRTTNNEKSPIIKP LIPKPKPKQASAASYPQKRNSQTKKTEEVKEENLKNVLSETPAI CPPQNTENQRPKTGFQMWLEENRSNILSDNPDFSDEADIIKEGM IRFRVLSTEERKVWAMKAKGETASEGTEAKKRKRVVDESDETEN QEEKAKENINISKKQKPLDFSTNQKLSAFAFKQE  6067 858 321 LPWQRLGVLSRGKMAVTGWLESLRTAQKTALLQDGRRKVHYLF PDGKEMAEEYDEKTSELLVWKWRVKSALGAMGQWQLEVGDPAPL GAGNLGPELIKESNANPIFMRKDTKMSFQWRIRNLPYPKDVYSV SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T PTAP  6068 13 1730 GSKMADLANEEKPAIAPPVFVFQKDKGGKSPAEQKNLSDSGEEP RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPAPEAQL PFFPRELAGRSSAGGSSPEGGEBDREDGNYCPPVKRERTSSLTQ FPPSQSERSSGFRLKPPTLIHGQAPSAGLPSQKFKEQQRSVLR PAVLQAPQPKALSGTVPSSGTNGVSLPADCTGAVPAASPDTAAW RSPSEAADEVCALEEKEPQKNESSNASEEEACEKKDPATQQAFV FGQNLRDRVKLINESVDEADMEMAGHPSADTPTATNYFLQYISS SLENSTNSADASSNKFVFGGNMSERVLSPPKLNEVSSDANRENA AAESGSESSSQEATPEKESLABSAAAYTKATARKCLLEKVEVIT GEEAESNVLOMQCKLFVFDKTSQSWVERGRGLLRLNDMASTDDG TLQSRLSDAGPRGSLR\LILINTKLWAQMQIDKASEK,SIRITAM DNEDQGVKVFLISASSKDTGQVYAALHHRILALRSRVEQEGEAK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGQTTGS T PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRAKGPGGSPGGLQK RHARVIVKYDRRELQRRLDVEKKIDGRLEELYRGMEADMPDE IN			İ	KNGYEYEESTKNQATKEQQELLMKMLALSCKLEREFRCVELADL
EEEEDFRIKKLNAGYSNTATEWSQPRIRAQVEDAEDSGEADDEE KPEIHKPGQNSFSKSTNSSDVSAKSGAVTFSSQGRVNPFFKVSAS SKEPAMSNNSARSTNILDNMGKSSKKSTALSRTTNNEKSPIIKP LIPKPKPKQASAASYFQKRNSQTNKTEEVKEENLKNVLSETPAI CPPQNTENQRPKTGFQMWLEENRSILLSDNPDFSDEADIIKEGM IRFRVLSTEERKVWANKAKGETASEGTEAKKRKRVVDESDETEN QEEKAKENLNISKKQKPLDFSTNQKLSAFAFKQE  6067 858 321 LPWQRLGVLLSRGKMAVTGWLESLRTAQKTALLQDGRRKVHYLF PDGKEMAEEYDEKTSELLVRKWRVKSALGAMGQWQLEVGDPAPL GAGNLGPELIKESNANPIHMKDTKNSFQWRIRNLPYRDVYSV SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T PTAP  6068 13 1730 GSKMADLANEEKPAIAPPVFVFQKDKGQKSPAEQKNLSDSGEEP RGEAEAPHHGTGHPESAGGSSPEGGBDSDREDGNYCPPVKRERTSSLTQ FPFPRELAGRSAGGSSPEGGBDSDREDGNYCPPVKRERTSSLTQ FPFPRELAGRSAGGSSPEGGBDSDREDGNYCPPVKRERTSSLTQ FPFPSQSEERSSGFRLKPPTLHGQAPSAGLPSQKPKEQQRSVLR PAVLQAPQPKALSQTVPSSGTNGVSLPADCTGAVPAASPDTAAW RSPSEAADEVCALEEKEPQKNESSNASEEEACEKKDPATQQAFV FGGNLRDRVKLINESVDEADMENAGHPSADTPTATNYFLQYISS SLENSTNSADASSNKFVFGQNMSERVLSPPKLNEVSSDANRENA AAESGSESSSQEATPEKESLABSAAAYTKATARKCLLEKVEVIT GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRILNDMASTDDG TLQSRLSDAGPRGSLR\LILNTKLWAQQMQIDKASEK\SIRITAM DNEDQGVKVFLISASSKDTQQVYAALHHRILALRSRVEQEQEAK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGQTTGS T OFTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK RHARVIVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN	1 1			MTQNAVNLAIKYASRSRKLILAQKLSELAVEKAAELTATQVEEE
KPEIHKPGGNSFSKSTNSSDVSAKSGAVTFSSQGRVNPFKVSAS SKEPAMSMNSARSTNILDNMGKSSKRTALSRITINEKSFI I KP LIPRPKPKQASAASYFQKRNSQTNKTEEVKEENLKNVLSETPAI CPPQNTENQRPKTGFQMWLEENRSNILSDNPDFSDEADIIKEGM IRFRVLSTEERKVWANKAKGFTASEGTEAKKRKVVDESDETEN QEEKAKENLNLSKKQKPLDFSTNQKLSAFAFKQE  6067 858 321 LPWQRLGVLLSRGKMAVTGWLESLRTAQKTALLQDGRRKVHYLF PDGKEMAEEYDEKTSELLVRKWRVKSALGAMGQWQLEVGDPAPL GAGNLGFELIKESNANFIFMRKDTKNSFQWRIRNLPYPKDVYSV SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T PTAP  6068 13 1730 GSKMADLANEEKPAIAPPVFVFQKDKGQKSPAEQKNLSDSGEEP RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPAPEAQL PPFPRELAGRSAGGSSPEGGBDSDREDGNYCPPVKRERTSSITQ FPPSQSEERSSGFRLKPPTLHGQAPSAGLPSQKPKEQQRSVLR RSPSEAADEVCALEEKEPQKNESSNASEEEACEKKDPATQQAFV PGQNLRDRVKLINESVDEADMENAGHPSADTPTATNYFLQYISS SLENSTNSADASSNKFVFGQNMSERVLSPPKLNEVSSDANRENA AAESGSESSQEATPEKESLABSAAAYTKATARKCLLEKVEVIT GEEAESNVLQMQCKLPVFDTTSQSWVERGRGLIRLNDMASTDDG TLQSRLSDAGPRGSLR\LILNTKLWAQQMQLDKASEK\SIRITAM DNEDQGVKVFLISASSKDTGQVYAALHHRILALRSRVEQEQEAK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDQQTTGS T PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK RHARVIVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN	1			EEEEDFRKKLNAGYSNTATEWSQPRFRNQVEEDAEDSGEADDEE
SKEPAMSMSARSTNILDNMGKSSKKSTALSRTTNNEKSPIIKP LIPKPKPKQASAASYFQKRNSQTMKTEEVKEENLKNVLSETPAI CPPQNTENQRPKTGFQMWLEENRSNILSDNPDFSDEADIIKEGM IRFRVLSTEERKVWANKAKGETASEGTEAKKRKRVVDESDETEN QEEKAKENLNLSKKQKPLDFSTNQKLSAFAFKQE  6067 858 321 LPMQRLGVLLSRGKMAVTGWLESLRTAQKTALLQDGRRKVHYLF PDGKEMAEEYDEKTSELLVRKWRVKSALGAMGQWLEVGDPAPL GAGNLGPBLIKESNANPIFMRKDTKMSFQWRIRNLPYPKDVYSV SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T PTAP  6068 13 1730 GSKMADLANEEKPAIAPPVFVFQKDKGQKSPAEQKNLSDSGEEP RGEABAPHHGTGHPESAGEHALEPPAPAGASASTPPPPAPEAQL PPFPRELAGRSAGGSSPEGGBDSDREDGNYCPPVKRERTSSLTQ FPPSQSEERSSGFRLXPPTLIHGQAPSAGLPSQKPKEQQRSVLR PAVLQAPQPKALSQTVPSSGTNGVSLPADCTGAVPAASPDTAAW RSPSEAADEVCALEEKEPQKNESSNASEEEACEKKDPATQQAFV FGQNLRDRVKLINESVDEADMENAGHPSADTFTATNYFLQYISS SLENSTNSADASSNKFVFGQNMSERVLSPPKLNEVSSDANRENA AAESGSESSQEATPEKESLABSAAAYTKATARKCLLEKVEVIT GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRINDMASTDDG TTQSRLSDAGPRGSLR\LILNTKLWAQMQIDKASEK\SIRITAM DNEDQGVKVFLISASSKDTGQVYAADHHRILALRSRVEQEGEAK MPAPEPGAAPSNEEDDSDDDDDVLAPSGATAAGAGDEGDGQTTGS T T PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK RHARVTVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN				KPEIHKPGQNSFSKSTNSSDVSAKSGAVTFSSQGRVNPFKVSAS
LIPKPKPKQASAASYFQKRNSQTNKTEEVKEENLKNVLSETPAI CPPQNTENQRPKTGFQMMLEENRSNILSDNPDFSDEADIIKEGM IRFRVLSTEERKVWANKAKGETASEGTEAKKRKRVDESDETEN QEEKAKENLNLSKKQKPLDFSTNQKLSAFAFKQE  6067 858 321 LPWQRLGVLLSRGKMAVTGWLESLRTAQKTALLQDGRRKVHYLF PDGKEMAEEYDEKTSELLVRKWRVKSALGAMGQWQLEVGDPAPL GAGNLGPELIKESNANPIFMRKDTKMSFQWRIRNLPYPKDVYSV SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T PTAP  6068 13 1730 GSKMADLANEEKPAIAPPVFVFQKDKGQKSPAEQKNLSDSGEEP RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPPAPEAQL PPFPRELAGRSAGGSSPEGGBDBREDGNYCPPVKRERTSSLTQ FPPSQSEERSSGFRLKPPTLIHGQAPSAGLPSQKPKSQQRSVLR PAVLQAPQPKALSQTVPSSGTNGVSLPADCTGAVPAASPDTAAW RSPSEAADEVCALEEKEPQKNESSNASEEEACEKKDPATQAFV PGQNLRDRVKLINESVDEADMENAGHPSADTPTATNYFLQYISS SLENSTNSADASSNKFVFGQNMSERVLSPPKLNEVSSDANRENA AAESGSSESSSQEATPEKESLABSAAAYTKATARKCLLEKVEVIT GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRLNDMASTDDG TLQSRLSDAGPRGSLR\LILITKLWAQMQIDKASEK\SIRITAM DNEDQGVKVFLISASSKDTGQVYAALHHRILALRSRVEQEQEAK MPAPEPGAAPSNEEDDSDDDDDVLAPSGATAAGAGDEGDGQTTGS T T PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK RHARVTVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN				SKEPAMSMNSARSTNILDNMGKSSKKSTALSRTTNNEKSPIIKP
CPPQNTENQRPKTGFQMWLEENRSNILSDNPDFSDEADIIKEGM IRFRVLSTEERKVWANKAKGETASECTEAKKRKKRVVDESDETEN QEEKAKENLNLSKKQKPLDFSTNQKLSAFAFKQE  6067 858 321 LPMQRLGVLLSRGKMAVTGWLESLRTAQKTALLQDGRRKVHYLF PDGKEMAEEYDEKTSELLVRKWRVKSALGAMGQWQLEVGDPAPL GAGNLGPELIKESNANPIFMRKDTKMSFQWRIRNLPYPKDVYSV SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T PTAP  6068 13 1730 GSKMADLANEEKPAIAPPVFVFQKDKGQKSPAEQKNLSDSGEEP RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPPAPEAQL PFFPRELAGRSAGGSPEGGEDSDREDGNYCPPVKRERTSSLTQ FPPSQSEERSSGFRLKPPTLIHGQAPSAGLPSQKFKEQQRSVLR PAVLQAPQPKALSQTVPSSGTNGVSLPADCTGAVPAASPDTAAW RSPSEAADEVCALEEKEPQKNESSNASEEEACEKKDPATQAFV FGQNLRDRVKLINESVDEADMENAGHPSADTPTATNYFLQVISS SLENSTNSADASSNKFVFGQNMSERVLSPPKLNEVSSDANRENA AAESGSESSQEATPEKESLABSAAAYTKATARKCLLEKVEVIT GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRLNDMASTDDG TLQSRLSDAGPRGSLR\LILINTKLWAQMQIDKASEK\SIRITAM DNEDQGVKVFLISASSKDTGQVYAALHHRILALRSRVEQEQEAK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGQTTGS T TTPPFGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK RHARVTVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN			ĺ	LIPKPKPKQASAASYFQKRNSQTNKTEEVKEENLKNVLSETPAT
IRFRVLSTEERKVWANKAKGETASEGTEAKKRKRVVDESDETEN QEEKAKENLNISKKQKPLDFSTTNQKLSAFAFKQE  LPWQRLGVLLSRGKMAVTGWLESLRTAQKTALLQDGRRKVHYLF PDGKEMAEEDEKTSELLVRKWRVKSALGAMGQWQLEVGDPAPL GAGNLGPELIKESNANPIFMRKDTKMSFQWRIRNLPYPKDVYSV SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T PTAP  GSKMADLANEEKPAIAPPVFVFQKDKGGKSPAEQKNLSDSGEEP RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPAPEAQL PFFPRELAGRSAGGSSPEGGEDSDREDGNYCPPVKRERTSSLTQ FPPSQSBERSSGFRLXPPTLIHGQAPSAGLPSQKPKEQQRSVLR PAVLQAPQPKALSQTVPSSGTMGVSLPADCTGAVPAASPDTAAW RSPSEAADEVCALEEKEPQKNESSNASEBEACEKKDPATQQAFV PGQNLRDRVKLINESVDEADMENAGHPSADTPTATNYFLQYISS SLENSTNSADASSNKFVFGQNMSERVLSPPKLNEVSSDANRENA AAESGSESSSQEATPEKESLABSAAAYTKATARKCLLEKVEVIT GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRLNDMASTDDG TLQSRLSDAGPRGSLR\LILNTKLWAQMQIDKASEK\SIRITAM DNEDQGVKVFLISASSKDTGQVYAALHHRILALRSRVEQEGEAK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGQTTGS T T T T T T T T T T T T T T T T T T				CPPQNTENQRPKTGFQMWLEENRSNILSDNPDFSDEADITKEGM
QEEKAKENLNLSKKQKPLDFSTNQKLSAFAFKQE  1	1		}	IRFRVLSTEERKVWANKAKGETASEGTEAKKRKRVVDESDETEN
LPWQRLGVLLSRGKMAVTGWLESLRTAQKTALLQDGRRKVHYLF PDGKEMAEEYDEKTSELLVRKWRVKSALGAMGQWQLEVGDPAPL GAGNLGPELIKESNANPIFMKDTKMSFQWRIRNLPYPKDYYSV SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T PTAP  6068  13  1730  GSKMADLANEEKPAIAPPVFVFQKDKGGQKSPAEQKNLSDSGEEP RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPPAPEAQL PPFPRELAGRSAGGSSPEGGEDSDREDGNYCPPVKRERTSSLTQ FPPSQSEERSSGFRLKPPTLIHGQAPSAGLPSQKPKEQQRSVLR PAVLQAPQPKALSQTVPSSGTMGVSLPADCTGAVPAASPDTAAW RSPSEAADEVCALEEKEPQKNESSNASEEEACEKKDPATQQAFV FGQNLRDRVKLINESVDEADMENAGHPSADTPTATNYFLQYISS SLENSTNSADASSNKFVFGONMSERVLSPPKLNEVSSDANRENA AAESGSESSSQEATPEKESLABSAAAYTKATARKCLLEKVEVIT GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRLNDMASTDDG TLQSRLSDAGPRGSLR\LILNTKLWAQMQIDKASEK\SIRITAM DNEDQGVKVFLISASSKDTGQVYAALHHRILALRSRVEQEQEAK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGQTTGS T T  PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK RHARVTVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN			İ	QEEKAKENLNLSKKOKPLDFSTNOKI.SAFAFKOF
PDCKEMAEEYDEKTSELLVRKWRVKSALGAMGQWQLEVGDPAPL GAGNLGPELIKESNANPIFMRKDTKMSFQWRIRNLPYPKDYYSV SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T PTAP  6068 13 1730 GSKMADLANEEKPAIAPPVFVFQKDKGQKSPAEQKNLSDSGEEP RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPPAPEAQL PFFPRELAGRSAGGSSPEGGEDSDREDGNYCPPVKRERTSSLTQ FPPSQSEERSSGFRLKPPTLIHGQAPSAGLPSQKPKEQORSVLR PAVLQAPQPKALSQTVPSSGTNGVSLPADCTGAVPAASPDTAAW RSPSEAADEVCALEEKEPQKNESSNASEEEACEKKDPATQQAFV PGQNLRDRVKLINESVDEADMENAGHPSADTTTATNYFLQYISS SLENSTNSADASSNKFVFGQNMSERVLSPPKLNEVSSDANRENA AAESGSESSSQEATPEKESLAESAAAYTKATARKCLLEKVEVIT GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRLNDMASTDDG TLQSRLSDAGPRGSLR\LILNTKLWAQMQIDKASEK\SIRITAM DNEDQGVKVFLISASSKDTGQVYAALHHRILALRSRVEQEQEAK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGQTTGS T T PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK RHARVTVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN	6067	858	321	LPWORLGVLLSRGKMAVTGWI,ESI,DTAOVTALI,ODGBDGTTT
GAGNLGPELIKESNANPIFMRKDTKMSFQWRIRNLPYPKDVYSV SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T PTAP  GSKMADLANEEKPAIAPPVFVFQKDKGQKSPAEQKNLSDSGEEP RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPPAPEAQL PPFPRELAGRSAGGSSPEGGEDSDREDGNYCPPVKRERTSSLTQ FPPSQSEERSSGFRLKPPTLIHGQAPSAGLPSQKPKEQQRSVLR PAVLQAPQPKALSQTVPSSGTNGVSLPADCTGAVPAASPDTAAW RSPSEAADEVCALEEKEPQKNESSNASEBEACEKKDPATQQAFV PGQNLRDRVKLINESVDEADMENAGHPSADTPTATNYFLQYISS SLENSTNSADASSNKFVFGQNMSERVLSPPKLNEVSSDANRENA AAESGSESSSQEATPEKESLABSAAAYTKATARKCLLEKVEVIT GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRLNDMASTDDG TLQSRLSDAGPRGSLR\LILNTKLWAQMQIDKASEK\SIRITAM DNEDQGVKVFLISASSRDTGQVYAALHHRILALRSRVEQEQEAK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGQTTGS T T PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK RHARVTVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN	1			PDGKEMAEEYDEKTSELLUPKWDUKCALCAMOONOLENGOS
SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T PTAP  6068  13  1730  GSKMADLANEEKPAIAPPVFVFQKDKGQKSPAEQKNLSDSGEEP RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPPAPEAQL PFFPRELAGRSAGGSSPEGGEDSDREDGNYCPPVKRERTSSLTQ FPPSQSEERSSGFRLKPPTLIHGQAPSAGLPSQKPKEQQRSVLR PAVLQAPQPKALSQTVPSSGTNGVSLPADCTGAVPAASPDTAAW RSPSEAADEVCALEEKEPQKNESSNASEEEACEKKDPATQQAFV PGQNLRDRVKLINESVDEADMENAGHPSADTTTATNYFLQYISS SLENSTNSADASSNKFVFGQNMSERVLSPPKLNEVSSDANRENA AAESGSESSSQEATPEKESLAESAAAYTKATARKCLLEKVEVIT GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRINDMASTDDG TLQSRLSDAGPRGSLR\LILNTKLWAQMQIDKASEK\SIRITAM DNEDQGVKVFLISASSKDTGQVYAALHHRILALRSRVEQEQEAK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGQTTGS T  PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK RHARVTVKYDRRELQRRIDVEKWIDGRLEELYRGMEADMPDEIN				GAGNI GPELIKE CNANDI EMDY PERMACEDOND TONT DURY
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PAVLQAPQPKALSQTVPSSGTNGVSLPADCTGAVPAASPDTAAW RSPSEAADEVCALEEKEPQKNESSNASEBEACEKKDPATQQAFV PGQNLRDRVKLINESVDEADMENAGHPSADTPTATNYFLQYISS SLENSTNSADASSNKFVFGQNMSERVLSPPKLNEVSSDANRENA AAESGSESSSQEATPEKESLABSAAAYTKATARKCLLEKVEVIT GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRLNDMASTDDG TLQSRLSDAGPRGSLR\LILNTKLWAQMQIDKASEK\SIRITAM DNEDQGVKVFLISASSKDTGQVYAALHHRILALRSRVEQEQEAK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGQTTGS T T  6069 583 27 PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK RHARVTVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN	, ,		1	FPPSQSEERSSGFRLXPPTLIHGQAPSAGLPSQKPKEQQRSVLR
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FGQNLRDRVKLINESVDEADMENAGHPSADTPTATNYFLQYISS SLENSTNSADASSNKFVFGQNMSERVLSPPKLNEVSSDANRENA AAESGSESSSQEATPEKESLABSAAAYTKATARKCLLEKVEVIT GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRLNDMASTDDG TLQSRLSDAGPRGSLR\LILNTKLWAQMQIDKASEK\SIRITAM DNEDQGVKVFLISASSKDTGQVYAALHHRILALRSRVEQEQEAK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGQTTGS T  6069 583 27 PTRPGQAGSSSAMAAQRIGKRVLSKLQSPSRARGPGGSPGGLQK RHARVTVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN	1 1	1		RSPSEAADEVCALEEKEPQKNESSNASEEEACEKKDPATOOAFV
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GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRLNDMASTDDG TLQSRLSDAGPRGSLR\LILNTKLWAQMQIDKASEK\SIRITAM DNEDQGVKVFLISASSKDTGQVYAALHHRILALRSRVEQEQEAK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGQTTGS T 6069 583 27 PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK RHARVTVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN	f 1			AAESGSESSSGEATPEKESLABSAAAYTKATARKCLLEKURUTT
TLQSRLSDAGPRGSLR\LILNTKLWAQMQIDKASEK\SIRITAM DNEDQGVKVFLISASSKDTGQVYAALHHRILALRSRVEQEQEAK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGQTTGS T  6069 583 27 PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK RHARVTVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN	] [		1	GEEAESNVLOMOCKI, FVFDKTSOSWVFDCDCI, I,DI,NDNA OMDOC
DNEDQGVKVFLISASSKDTGQVYAALHHRILALRSRVEQEQEAK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGQTTGS T  6069 583 27 PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK RHARVTVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN		ł		TLOSRISDAGPROSLP\T.TLUTKI WAGMOTOVA CEV\ CTS
MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGQTTGS T PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRAKGPGGSPGGLQK RHARVTVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN		I		DNEDOGVKVFLIGAGGYDTCOVVALIETTAN TERRITAN
6069 583 27 PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK RHARVTVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN			1	MDADEDGAADCHEEDDGDDDDHAADHHKILADKSKVEQEQEAK
6069 583 27 PTRPGQAGSSSAMAAQRIGKRVLSKLQSPSRARGPGGSPGGLQK RHARVTVKYDRRELQRRIDVEKWIDGRLEELYRGMEADMPDEIN				T T T T T T T T T T T T T T T T T T T
RHARVIVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN	6069	502.		_
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IDELLELESEEERSRKIOGLIKSCGKPVEDRIOGLIAKLOGLUB		İ		RHARVTVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN
				IDELLELESEEERSRKIQGLLKSCGKPVEDFIQELLAKLQGLHR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
!	amino acid	sequence	Codon, /=possible nucleotide deletion,
İ	sequence		\=possible nucleotide insertion)
			Q\PGLRQPSPSP\DGQPSAPFQGPGARTASPLTLLALFPGPPER
	1		RPALLCVLSCI
6070	478	858	IRVTVDGEFLHYIFPLQFLDSPEW/RFTETHRGRHF\QVTLTAE
1		""	TDCRYVSWRRKKLYLLFAQHRYISRLFSVLIGSDIADKLYALND
1		1	RVYIGKRYHYDIRLPNFYQMSTPEIRRSPLTQHFQNSRRYW
6071	2	1654	HEARTKGNMALARP\VRLFSLVTRLLLAPRRGLTVRSPDEPLPV
00/1	1	1034	VRIPVALQRQLEQRQSRRRNLPRPVLVRPGPLLVSARRPELNOP
1			ARLTLGRWERAPLASOGWKSRRARRDHFSIERAOOEAPAVRKLS
	ł		SKGSFADLGAWKPRVLHALQE\AAPEVVQ\PTTVQSSTIPSLLR
1			GRHVVCAAETGSGKTLSYLLPLLQRLLG\HPSLDSLPIPAPRGL
ł			
1			VLVPSRELAQQVRAVAQPLGRSLGLLVRDLEGGHGMRRIRLQLS RQPSADVLVATPGALWKALKSRLISLEQLSFLVLDEADTLLDES
]		į.	FLELVDYILEKSHIAEGPADLEDPFNPKAQLVLVGATFPEGVGQ
1			LINKVASPDAVTTITSSKLHCIMPHVKQTFLRLKGADKVAELVH
}			ILKHRDRAERTGPSGTVLVFCNSSSTVNWLGYILDDHKIQHLRL
i			QGQMPALMRVGIFQSFQKSSRDILLCTDIASRGLDSTGVELVVN
ì	•		YDFPPTLQDYIHRAGRVGRVGSEVPGTVISFVTHPWDVSLVQKI
			ELAARRRSLPGLASSVKEPLPQAT
6072	1	742	KMERTEMMPTINSQLEFKSKPFPLVSSSRWLVKRGELTAYVEDT
			VLFSRRTSKQQVYFFLFNDVLIITKKKŞEESYNVNDYSLRDQLL
i			VESCONEELNSSPGKNSSTMLYSRQSSASHLFTLTVLSNHANEK
			VEMLLGAETQSERARWITALGHSSGKPPADRTSLTQVEIVRSFT
			AKQPDELSLQVADVVLI\YQRVSDGWYEGER\LRDGERGWFPME
			CAKEITCQATIDKNVERMGRLLGLETNV
6073	620	860	PCRRGLARPLSRRPG/SILVHCAVGVSRSATLVLAYLMLYHHLT
			LVEAIKKVKDHRGIIPNRGFLRQLLALDRRLRQGLEA
6074	168	1110	PGARCMATELQCPDSMPCHNQQVNSASTPSPEQLRPGDLILDHA
		•	GGNRASRAKVILLTGYAHSSLPAELDSGACGGSSLNSEGNSGSG
			DSSSYDAPAGNSFLEDCELSRQIGAQLKLLPMNDQIRELQTIIR
		1	DKTASRGDFMFSADRLIRLVVEEGLNQLPYKECMVTTPTGYKYE
1			GVKFEKGNCGVSIMRSGEAMEQGLRDCCRSIRIGKILIQSDEET
1		İ	QRAKVYYAKFPPDIYRRKVLLMYPILQTG\NTVIEAVKVLIEHG
		1	VQPSVIILLSLFSTPHGAKSIIQEFPEITILTTEVHPVAPTHFG
			QKYFGTD
6075	320	1091	PPTCQPQEVEHH\YGYVPILGNKTLPSRCHQCVIVSSSSHLLGT
			KLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRV
1			LRRPQEFVNRTPBTVFIFWGPPSKMQKPQGSLVRVIQRAGLVFP
			NMEAYAVSPGRMRQFDDLFRGETGKDREKSHSWLSTGWFTMVIA
			VELCDHVHVYGMVPPNYCSQRPRLQRMPYHYYEPKGPDECVTYI
			QNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT
6076	1721	107	HPSPTEAPRVQHLTMDCTWRILFLVAAATGTHAQVQLVQSGAEV
1			KKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGAFDPED
[	1		GETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATD
1		1	HGDYAFDIWGQGTMVTVSSAPTKAPDVFPIISGCRHPKDNSPVV
1			LACLITGYHPTSV\TVTWYMGTQSQA\QRTFPEIQRRDSYYMTS
			SQLSTPLQQWRQGEYKCVVQHTASKSKKEIFRWPESPKAQASSV
			PTAOPQAEGSLAKATTAPATTRNTGRGGEEKKKEKEKEEQEERE
1		}	TKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFTCFVVGSDLKD
1			AHLTWEVAGKVPTGGVEEGLLERHSNGSQSQHSRLTLPRSLWNA
1			GTSVTCTLNHPSLPPQRLMALREPAAQAPVKLSLNLLASSDPPE
1		1	A\ASWLLCEVSGFSPPNILLMWLEDHGEVNTSGFAPARPLPKP\
1			RSTTFWA\WSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASRSL
			EVSYVTDHGPMK
6077	3687	1268	LLPDMNLQPIFWIGLISSVCCVFAQTDENRCLKANAKSCGECIQ
			AGPNCGWCTNSTFLQEGMPTSARCDDLEALKKKGCPPDDIENPR
1		1	GSKDIKKNKNVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGEP
1			QTFTLKFKRAEDYPIDLYYLM\DLSYSMKDDLENVKSLGTDLMN
	{	1	EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS
1			PFSYKNVLSLTNKGEVFNELVGKQRISGNLDSPEGGFDAIMQVA
1			VCGSLIGWRNVTRLLVFSTDAGFHFAGDGKLGGIVLPNDGQCHL
	<u> </u>	<del></del>	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
. (	amino acid	sequence	Codon, /=possible nucleotide deletion,
. 1	sequence	_	\=possible nucleotide insertion)
			ENNMYTMSHYYDYPSIAHLVQKLSENNIQTIFAVTEEFOPVYKE
. 1			LKNLIPKSAVGTLSANSSNVIQLIIDAYNSLSSEVILENGKLSE
			GVTISYQSY\CKNGVNGTGBNGRKCSNISIGDEVQFEISITSNK
			CPKKDSDSFKIRPLGFTEEVEVILQYICECECQSEGIPESPKCH
			EGNGTFECGACRCNEGRVGRHCECSTDEVNSEDIGCFTARKENO
			FQKSASNHGRVPSAGQCVCRKRDNTNEIYSGKFCECDNFNCDRS
: 1			NGLICGGNGVCKCRVCECNPNYTGSACDCSLDTSTCEASNGOIC
			NGRGICECGVCKCTDPKFQGQTCEMCQTCLGVCAEHKECVQCRA
			FNKGEKKDTCTQECSYFNITKVESRDKLPQPVQPDPVSHCKEKD
			VDDCWFYFTYSVNGNNEVMVHVVENPECPTGPDIIPIVAGVVAG
i l			IVLIGLALLLIWKLLMIIHDRREFAKFEKEKMNAKWDTGENPIY
;			KSAVTTVVNPKYEGK
6078	1426	180	ETEDVMELLEEDLTCPICCSLFDDPRVLPCSHNFCKKCLEGILE
			GSVRNSLWRPVPFKCPTCRKKTFSYWELIPLQVNYSLKGIVEKY
,			NKIKISPKMPVCKGH\LGQPLNIF\CL\TDMQLDL/CGIC\ATR
			GEHTKHVFCSIEDAYAQERDAFESLFQSFETWRRGDALSRLDTL
			ETSKRKSLQLLTKDSDKVKEFFEKLQHTLDQKKNEILSDFETMK
			LAVMQAYDPEINKLNTILQEQRMAFNIAEAFKDVSEPIVFLQQM
			QEFREKIKVIKETPLPPSNLPASPLMKNFDTSQWEDIKLVDVDK
			LSLPQDTGTFISKIPWSFYKLFLLILLLGLVIVFGPTMFLEWSL
. 1			FDDLATWKGCLSNFSSYLTKTADFIEQSVFYWEQVTDGFFIFNE
			RFKNFTLVVLNNVAEFVCKYKLL
6079	1586	141	ATARDLGCARRIDRVVMESTPSRGLNRVHLQCRNLQEFLGGLSP
- 1			GVLDRLYGHPATCLAVFRELPSLAKNWVMRMLFLEQPLPQAAVA
1			LWVKKEFSKAQEESTGLLSGLRIWHTQLLPGGLQGLILNPIFRQ
j			NLRIALLGGGKAWSDDTSQLGPDKHARDVPSLDKYAEERWEVVL
1			HFMVGSPSAAVSQDLAQLLSQAGLMKSTEPGEPPCITSAGFQFL
į			LLDTPAQLWYFMLQYLQTAQSRGMDLVEILSFLFQLSFSTLGKD
. 1			YSVEGMSDSLLNFLQHLREFGLVFQRKRKSRRYYPT/RALAINL
			SSGVSGAGGTVHQPGFIV\VETNYRLYAYTESELQIALIALFSE
. i			MLYPFP\NMVV\ARVTR\ESVQQAIASGITAQQIIHFLRTRAHP
i			VMLKQTPVLPPTITDQIRLWELERDRLRFTEGVLYNQFLSQVDF
			ELL\LAHAPKLGVLVFE/NTPAKRLMVVTPAGHSDVKRFWKRQK
			HSS
6080	1	1199	IETIDHVGEFAMAAQAAGVSRQRAATQGLGSNQNALKYLGQDFK
			TLRQQCLDSGVLFKDPEFPACPSALGYKDLGPGSPQTQGIIWKR
	•		PTELCPSPQFIVGGATRTDICQGGLGDCWLLAAIASLTLNEELL
			YRVVPRDQDFQENYAGIFHFQPLCPPSP\FWQYGEWVEVVIDDR
, 1			LPTKNGQLLFLHSEQGNEFWSALLEKAYAKLNGCYEALAGGSTV
		1	EGFEDFTGGISEFYDLKKPPANLYQIIRKALCAGSLLGCSIDVY
			SAAEAEAITSQKLVKSHAYSVTGVBEVNFQGHPEKLIRLRNPWG
, 1			EVEWSGAWSDDAPEWNHIDPRRKEELDKKVEDGEFWMSLSDFVR
. 1			QFSRLEICNLSPDSLSSEEVHKWNLVLFNGHWTRGSTAGGCQNY
	·		PGSS
6081	3	865	EMLPLLLPLPLLWA/GALAQDARFRLEMPESVTVQEGLCIFVHC
, 1			SVFYLEYGWKDSTPAYGHWFREGVSVDQETPVATNNSTQKVQKE
			TQGRFHLLGDPSRNNCSLSIRDARRRDNGSYFFWVARGRTKFSY
,			KYSPLSVYVTALTHRPDILIPEFLKSGHPSNLTCSVPWVCEQGT
,			PPIFSWMSAAPTSLGPRTLHSSVLTIIPRPQDHGTNLICQVTFP
,			GAGVTTERTIQLSVSWKSGTVEEVVVLAVGVVAVKILLLCLCLI
			ILSFHKKKAVRAVEVEENVYAVMG
6082	283	1288	EARSPGPTQTRTAPGLAAPGLAQPAALRLLLSRPPSAAMDGDGD
			PESVGQPEEASPEEQPEEASAEEERPEDQQEEEAAAAA\Y\LDE
,			LPEPLLA/LRVLAALPRHE\LVQACR\LVCLRWKELVDGAPLWL
	j		LKCQQEGLVPEGGVEEERDHWQQFYFLSKRRRNLLRNPCGEEDL
			LEGISCOURISCOCIONERI DODOGURERUDE GIRRAGES CORRIGO
1			EGWCDVEHGGDGWRVEELPGDSGVEFTHDESVKKYFASSFEWCR
			KAQVIDLQAEGYWEELLDTTQPAIVVKDWYSGRSDAGCLYELTV
			KAQVIDLQAEGYWEELLDTTQPAIVVKDWYSGRSDAGCLYELTV KLLSEHENVLAEFSSGQVAVPQDSDGGGWMEISHTFTDYGPGVR
6083	1865	309	KAQVIDLQAEGYWEELLDTTQPAIVVKDWYSGRSDAGCLYELTV

650	Predicted	Predicted end	Amino agid gogment containing
SEQ			Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ			
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	i	\=possible nucleotide insertion)
		1	DVQEETQLDLSGDSVKTIAKLWDSKMFAEIMMKIBEYISKQAKA
			SEVMGPVEAAPEYRVIVDANNLTVEIENELNIIHKFIRDKYSKR
1		ĺ	
l	{	1	FPELESLVPNALDYIRTVKELGNSLDKCKNNENLQQILTNATIM
1	1	1	VVSVTASTTQGQQLSEEELERLEEACDMALELNASKHRIYEYVE
1		1	SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG
1	ļ		AQRKTLSGFSSTSVLPHTGYIYHSDIVQSLPPIPPPFSVAP\DL
	ł		RRKAARLVAAKCTLAARVDSFHESTEGKVGYELKDEIERKFDKW
		Į.	QEPPPVKQVKPLPAPLDGQRKKRGGRRYRKMKERLGLTEIR\KO
.		İ	ANRMSFGEIEEDAYQEDLGFSLGHLGKSGSGRVRQTQVNEATKA
1	!	ł	
1		1	RISKTLQRTLQKQSVVYGGKSTIRDRSSGTASSVAFTPLQGLEI
			VNPQAAEKKVAEANQKYFSSMAEFLKVKGEKSGLMST
6084	1865	309	KQWCAERRGLGMSLADELLADLEEAAEEEEGGSYGEEEEEPAIE
1			DVQEETQLDLSGDSVKTIAKLWDSKMFAEIMMKIEEYISKQAKA
1			SEVMGPVEAAPEYRVIVDANNLTVEIENBLNIIHKFIRDKYSKR
		1	FPELESLVPNALDYIRTVKELGNSLDKCKNNENLQQILTNATIM
		1	
		1	VVSVTASTTQGQQLSEEELERLEEACDMALELNASKHRIYEYVE
	1		SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG
1			AQRKTLSGFSSTSVLPHTGYIYHSDIVQSLPPIPPPFSVAP\DL
		1	RRKAARLVAAKCTLAARVDSFHESTEGKVGYELKDEIERKFDKW
İ	1	1	QEPPPVKQVKPLPAPLDGQRKKRGGRRYRKMKERLGLTEIR\KO
1			ANRMSFGEIEEDAYQEDLGFSLGHLGKSGSGRVRQTQVNEATKA
1			RISKTLORTLOKOSVVYGGKSTIRDRSSGTASSVAFTPLOGLEI
1		1	
	ļ.,		VNPQAAEKKVAEANQKYFSSMAEFLKVKGEKSGLMST
6085	2	1456	SGPRSFQGNRAVGRISLGGKRNPEVTLLPGVSSERVRRWRRARV
ļ		1	GVARVKPGNPWKPSPATQVPR/VPAQVYLPGRGPPLREGEELVM
1	j	1	DEEAYVLYHRAQTGAPCLSFDIVRDHLGDNRTELPLTLYLCAGT
			QAESAQSNRLMMLRMHNLHGTKPPPSEGSDEBEEEEDEBDEEER
	1	1	KPQLELAMVPHYGGINRVRVSWLGEEPVAGVWSEKGQVEVFALR
		!	1
1		1	RLLQVVEEPQALAAFLRDEQAQMKPIFSFAGHMGEGFALDWSPR
	1		VTGRLLTGDCQKNIHLWTPTDGGSWHVDQRPFVGHTRSVEDLQW
1		1	SPTENTVFASCSADASIRIWDIRAAPSKACMLTTATAHDGDVNV
			ISWSRREPFLLSGGDDGALKIWDLRQFKSGSPVATFKQHVAPVT
ì			SVEWHPQDSGVFAASGADHQITQWDLG/IVERDPEAGDVEADPG
1	ļ		LADLPQQLLFVHQGETELKELHWHPQCPGLLVSTALSGFTIFRT
	İ		ISV
6006	2412	1050	
6086	2419	1357	GAATQHGGAMNLLPCNPHGNGLLYAGFNQDHGCFACGMENGFRV
			YNTDPLKEKEKQEFLEGGVGHVEMLFRCNYLALVGGGKKPKYPP
		<del> </del>	NKVMIWDDLKKKTVIEIEFSTEVKAVKLRR\DKIVVVLDSMIKV
			FTFTHNP\HQLHVFE\TCYNPKGLCVLCPNSNNSLLAFPGTHTG
I		1	HVOLVDLASTEKPPVDIPAHEGVLSCIALNLOGTRIATASEKGT
1	1		LIRIFDTSSGHLIQELRRGSQAANIYCINFNQDASLICVSSDHG
}		1	1
		1	TVHIFAAEDPKRNKQSSLASASFLPKYFSSKWSFSKFQVPSGSP
1			CICAFGTEPNAVIAICADGSYYKFLFNPKGECIRDVYAQFLEMT
	<del> </del>	<u> </u>	DDKL
6087	476	1877	QNSQRTGLPITIFSRSFPLLTGSDLCENMPCTCTWRNWRQWIRP
1		]	LVAVIYLVSIVVAVPLCVWBLQKLEVGIHTKAWFIAGIFLLLTI
1		i	PISLWVILQHLVHYTQPELQKPIIRILWMVPIYSLDSWIALKYP
1			GIAIYVDTCRECYEAYVIYNFMGFLTNYLTNRYPNLVLILEAKD
			1
l .			QQKHFPPLCCCPPWAMGEVLLFRCKLGVLQYTVVRPFTTIVALI
			CELLGIYDEGNFSFSNAWTYLVIINNMSQLFAMYCLLLFYKVLK
1	1		EELSPIQPVGKFLCVKLVVFVSFWQAVVIALLVKVGVISEKHTW
			EWQTVEAVATGLQDFIICIEMFLAAIA\HHYTFSYKPYVQEAEE
1	j	]	GSCFDSFLAMWDVSDIRDDISEQVRHVGRTVRGHPRKKLFPEDQ
1			DQNEHTSLLSSSSQDAISIASSMPPSPMGHYQGFGHTVTPOTTP
	ļ	<u> </u>	TTAKISDEILSDTIGEKKEPSDKSVDS
6088	1684	689	GASGLVRLLQQGHRCLLAPVAPKLVPPVRGVKKGFRAAFRFQKE
			LERGRLLRCPPPPVRRSEKPNWDYHAEIQAFGHRLGENFSLDLL
}		j .	KTAFVNSCYIKSEEAKRQQLGIEKEAVLLNLKSNQELSEQGTSF
ł			SQTCLTQFLEDEYPDMPTEGIKNLVDFLTGEEVVCHVARNLAVE
1		1	
			QLTLSEEFPVPPAVLQQTFFAVIGALLQSSGPERTALFIRDFLI
	L		TQMTGKELFEMWKIINPMGLLVBELKKRNVSAPESRLTRQSG\A

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	
,			(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	i	Bequence	
ļ	sequence		\=possible nucleotide insertion)
1		İ	PTALPLYFVGLYCDKKLIAEGPGETVLVAEEEAARVALRKLYGF
			TENRRPWNYSKPKETLRAEKSITAS
6089	3	3054	TRLGIPGSTISSRPRLCALAAEGHFLGHSWTGSRAGAHTGAPAW
1			PSRRLRDLPAGGMWRLRRAAVACEVCOSLVKHSSGIKGSLPLOK
l		1	LHLVSRSIYHSHHPTLKLQRPQLRTSFQQFSSLTNLPLRKLKFS
i		l	PIKYGYQPRRNFWPARLATRLLKLRYLILGSAVGGGYTAKKTFD
l	Ì	1	
1		1	QWKDMIPDLSEYKWIVPDIVWEIDEYIDFEKIRKALPSSEDLVK
}		1	LAPDFDKIVESLSLLKDFFTSGSPEETAFRATDRGSESDKHFRK
•		1	VSDKEKIDQLQEELLHTQLKYQRILERLEKENKELRKLVLQKDD
	{	1	KGIPFIESLRKSLIDMYSEVLDVLSDYDASYNTQDHLPRVVVVG
		1	DQSAGKTSVLEMIAQARIFPRGSGEMMTRSPVKVTLSEGPHHVA
			LFKDSSREFDLTKEBDLAALRHEIELRMRKNVKEGCTVSPETIS
			LNVKGPGLQRMVLVDLPGVINTVTSGMAPDTKETIFSISKAYMO
		1	DPNAILCIQDGSVDAERSIVTDLVSQMDPHGRRTIFVLTKVDL
			AEKNVASPSRIQQIIEGKLFPMKALGYFAVVTGKGNSSESIEAI
			REYEEEFFQNSKLLKTSMLKAHQVTTRNLSLAVSDCFWKMVRES
			VEQQADSFKATRFNLETEWKNNYPRLRELDRNELFEKAKNEILD
			EVISLSQVTPKHWEEILQQSLWERVSTHVIENIYLPAAQTMNSG
			TFNTTVDIKLKQWTDKQLPNKAVEVAWETLQEEFSRFMTEPKGK
	}		EHDDIFDKLKEAVKEBSIKRHKWNDFAEDSLRVIQHNALEDRSI
		1	SDKQQWDAAIYFMEEALQARLKDTENAIENMVGPD\WKKRWLYW
	1		KNRTQEQCVHNETKNELEKMLKCNEEHPAYLASDEITTVRKNLE
	1		
	1		SRGVEVDPSLIKDTWHQVYRRHFLKTALNHCNLCRRGFYYYQRH
			FVDSELECNDVVLFWRIQRMLAITANTLRQQLTNTEVRRLEKNV
İ			KEVLEDFAEDGEKKIKLLTGKRVQLAEDLKKVREIQEKLDAFIE
			ALHQEK
6090	194	1560	PVFVPAPGAVLEQAS/ASPPLATOTVVPLOHCKIPELPVOASIL
Ì	İ	i	FELQLFFCQLIALFVHYINIYKTVWWYPPSHPPSHTSLNFHLID
		1	FNLLMVTTIVLGRRFIGSIVKEASQRGKVSLFRSILLFLTRFTV
	ł		LTATGWSLCRSLIHLFRTYSFLNLL/FPLLSVWDVHSVPAAELR
		ĺ	
			P\RKTSLFNHMASMGPREAVSGLAKSRDYLLTLR\RRGSSTQDS
	ŀ		CMARTPCP/PHACCLSPSLIRSEVEFLKMDFNWRMKEVLVSSML
			SAYYVAFVPVWFVKNTHYYDKRWSCELFLLVSISTSVILMQHLL
		ì	PASYCDLLHKAAAHLGCWQKVDPALCSNVLQHPWTEECMWPQGV
Ĭ			LVKHSKNVYKAVGHYNVAIPSDVSHFRFHFFFSKPLRILNILLL
			LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL
		l	VLGKAYSYSASPORDLDHRFS
6091	3279	412	SSRTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG
	1		
	1		WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG
			PSDPPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK
			VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ
			LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE
	1		PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ
	1		LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR
			TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN
			KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS
			SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE
		1	TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLR
			RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA
	1		SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA
			RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY
			KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ
			RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV
	l .		AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN
	I		CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG
		I	ACPRGAQCQLLHRTOKRHSRRAATSPAPGPSDATARSRVSASHG
	ļ		
			PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS
			PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS
			PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL
6092	143	3190	PRKPSASQRPTRQTPSSAALITAAAVAAPPHCPGGSASPSSSKAS SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ
6092	143	3190	PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL

		Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	l ·	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
· .	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
. 1	corresponding	to first	Daneucine, Mamethionine, Namaparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			VIQLIKTNKKHIHSRSTLECAYRTHLVAGIGFYQHLLLYIQSHY
			QLELQCCIDWTHVTDPLIGCKKPVSASGKEMDWAQMACHRCLVY
l [		ł	LGDLSRYQNELAGVDTELLAERFYYQALSVAPQIGMPFNQLGTL
			AGSKYYNVEAMYCYLRCIQSEVSFEGAYGNLKRLYDKAAKMYHQ
		1	LKKCETRKLSPGKKRCKDIKRLLVNFMYLQSLLQPKSSSVDSEL
			TSLCQSVLEDFNLCLFYLPSSPNLSLASEDEEEYESGYAFLPDL
		i	LIFOMVIICLMCVHSLERAGSKQYSAAIAFTLALFSHLVNHVNI
		1	RLQAELEEGENPVPAFQSDGTDEPESKEPVEKEEEPDPEPPPVT
			POVGEGRKSRKFSRLSCLRRRRHPPKVGDDSDLSEGFESDSSHD
<b>i</b> !		1	SARASEGSDSGSDKSLEGGGTAFDAETDSEMNSQESRSDLEDME
}			
}			EEEGTRSPTLEPPRGRSEAPDSLNGPLGPSEASIASNLQAMSTQ
			MFQTKRCFRLAPTFSNLLLQPTTNPHTSASHRPCVNGDVDKPSE
Ì			PASEEGSESEGSESSGRSCRNERSIQEKLQVLMAEGLLPAVKVF
1		<b>S</b>	LDWLRTNPDLIIVCAQSSQSLWNRLSVLLNLLPAAGELQESGLA
1	į	}	LCPEVQDLLEGCELPDLPSSLLLPEDMALRNLPPLRAAHRRFNF
			DTDRPLLSTLEESVVRICCIRSFGHFIARLQGSILQFNPEVGIF
1	'		VSIAQSEQESLLQQAQAQFRMAQEEARRNRLMRDMAQLRLQLEV
		1	SQLEGSLQQPKAQSAMSPYLVPDTQALCHHLPVIRQLATSGRFI
ļ			VIIPRTVIDGLDLLKKEHPGARDGIRYLEAEFKKGNRYIRCQKE
ļ	1		VGKSFERHKLKRQDADAWTLYKILDSCKQLT\LAQGAGEEDPSG
ł	į	<u> </u>	MVTIITGLPLDNPSLLSGPMQAALQAAAHASVDIKNVLDFYKQW
ļ			KEIG
6093	76	1002	ACGRRAMLALRVART/SRWGAL\RGAVWAPGTRPSKRRACWALL
6093	10	1002	PPVPCCLGCLAERWRLRPAALGLRLPGIGQRNHCSGAGKAAPR\
1	}		PAAGAGAAAEAPGGQWGPASTPSLYENPWTIPNMLSMTRIGLAP
	1		VLGYLIIEEDFNIALGVFALAGLTDLLDGFIARNWANQRSALGS
1	Į.	<b>}</b>	ALDPLADKILISILYVSLTYADLIPVPLTYMIISRDVMLIAAVF
1			YVRYRTLPTPRTLAKYFNPCYATARLKPTFISKVNTAVQLILVA
Í			ASLAAPVFNYADSIYLQILWCFTAFTTAASAYSYYHYGRKTVQV
1	}	1	
		<u> </u>	IKD
6094	23	1010	PFLRCLRGDQKAKMSERKVLNKYYPPDFDPSKIPKLKLPKDRQY
{			VVRLMAPFNMRCKTCGEYIYKGKKFNARKETVQNEVYLGLPIFR
1		1	FYIKCTRCLAEITFKTDPENTDYTMEHGATRNFQAEKLLEEEEK
1	1	1	RVQKEREDEELNNPMKVLENRTKDSKLEMEVLENLQELKDLNQR
(	1		QAHVDFEAMLRQHRLSEEERRRQQQEEDEQETAALLEEARKRRL
	1		LEDSDSEDEAAPSPLQPALRPNPTAILDEAPKPKRKVEVWEQSV
1	1	*	GSLGSRPPLSRLVVVKKAKADPDCSNGQPQA/APHPRSPAEQEG
1	1		GQPYTPDAWRVLPEPTGCIPGQ
6095	1	1599	TRGRAAERSRGRGHGFLGGGFA\SVVDYFPSEDFYRCGYCKNES
0033	1	1	GSRSNGMWAHSMTVQDYQDLIDRGWRRSGKYVYKPVMNQTCCPQ
1			YTIRCRPLQFQPSKSHKKVLKKMLKFLAKGEVPKGSCE\DEPMD
1		]	STMDDAVAGDFALINKLDIQCDLKTLSDDIKESLESEGKNSKKE
<b>!</b>		}	EPQELLQSQDFVGEKLGSGEPSHS
(			

TRADOCS:1416257.1(%CSH011.DOC)

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	•	\=possible nucleotide insertion)
		<del> </del>	VKVHTVPKPGKGADLSKPPCRKAKEIRKERKRLKLMOONPAGEL
			EGFQAQGHPPSLFPPKAKSNQPKSLEDLIFESLPENASHKLEVR
			VVRSSPPSSQFKATLLESYQVYKRYQMVIHKNPPDTPTESQFTR
			FLCSSPLEAETPPNGPDCGYGSFHQQYWLDGKIIAVGVIDILPN
			CVSSVYLYYDPDYSFLSLGVYSALREIAFTRQLHEKTSQLSYYY
		1	MGFYIHSCPKMKYKGQYRPSDLLCPETYVWVPIEQCLPSLENSK
			YCRFNQDPEAVDEDRSTEPDRLQVFHKRAIMPYGVYKKQQKDPS
6096	2027		EEAAVLQYASLVGQKCSERMLLFRN
. 6036	2277	575	QRVRAALLSSAMEDSEALGFEHMGLDPRLLQAVTDLGWSRPTLI
	1	1	QEKAIPLALEGKOLLARARTGSGKTAAYAIPMLQLLLHRKATGP
İ	1	1	VVEQAVRGLVLVPTKELARQAQSMIQQLATYCARDVRVANVSAA
			EDSVSQRAVLMEKPDVVVGTPSRILSHLQQDSLKLRDSLELLVV
	· ·		DEADLLFSFGFEEELKSLLCHLPRIYQAFLMSATFNEDVQALKE
		1	LILHNPVTLKLQESQLPGPDQLQQFQVVCETEEDKFLLLYALLK
			LSLIRGKSLLFVNTLERSYRLRLFLEQFSIPTCVLNGELPLRSR
	ļ		CHI ISQFNQGFYDCVIATDAEVLGAPVKGKRRGRGPKGDKASDP
			EAGVARGIDFHHVSAVLNFDLPPTPEAYIHRAGRTARANNPGIV
			LTFVLPTEQFHLGKIEBLLSGENRGPILLPYQFRMEEIEGFRYR
			CRDAMRSVTKQAIREARLKEIKEELLHSEKLKTYFEDNPR\DLQ
			LLRHDLPLHPAVVKPHLGHVPDYLVPPALRGLVRPHKK\GRSCL
			PLVGRPREQSPRTHCAASSTKERNSDPQPSPPEVVGPLWS
6097	1673	192	APGTMSGGKKKSSFQITSVTTDYEGPGSPGASDPPTPQPPTGPP
			PRLPNGEPSPDPGGKGTPRNGSPPPGAPSSRFRVVKLPHGLGEP
			YRRGRWTCVDVYERDLEPHSFGGLLEGIRGASGGAGGRSLDSRL
			ELASLGLGAPTPPSGLSQGPTSWLRPPPTSPGPQARSFTGGLGQ
		1	LVVPSKAKAEKPPLSASSPQQRPPEPETGESAGTSRAATPLPSL
			RVEAEAGGSGARTPPLSRRKAVDMRLRMELGAPEEMGOVPPLDS
			RPSSPALYFTHDASLVHKSPDPFGAVAAOKFSLAHSMLAISGHL
			DSDDDSGSGSLVGIDNKIEQAMDLVKSHLMFAVREEVEVLKEQI
			RELAERNAALEQENGLLRALA\SPEQLGSAGPPRGVPR\LGPPA
			PNGPFVLSLPSLTIVPLGLPGLASAAWPPLPMPALIVPVFPGVG
	,		VQALSNGPWSPGPLPHLLIIPSLDGGGEGFRTGRQQGAPFGEET
			QPPPSLPGTPQQ
6098	168	1074	NYCLEHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKELD
0000	100	10/3	EGKIFKNWGTOTEKEDTSNINPROTETSVNASRSPEKCAOOROK
		1	RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE
		1	NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL
	İ		
		1	\QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR
		1	TAWEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D
6000	<del> </del>		ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD
6099	168	1074	NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKELD
	1		EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK
			RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE
	1		NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL
	1		\QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR
	1	1	TAWEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D
			ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD
6100	2	713	FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIIGDTGVGKSCLLL
	1		QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF
			RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM
			VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN
	1		VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP
		1	SASQRNSRDIGSNSGCC
6101	1	1399	FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR
			GKMVFPLSCAVQQYAWGKMGSNSEVARLLASSDPLAQIAEDKPY
			AELWMGTHPRGDAKILDNRISQKTLSQWIAENQDSLGSKVKDTF
	<del></del>	I	

SEQ	Predicted	Predicted end	Amino agid gogment control
ID		nucleotide	Amino acid segment containing signal peptide
	beginning		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Coden / Tarytosine, Asonknown, *stop
		seddelice	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			NGNLPFLFKVLSVETPLSIQAHPNKELAEKLHLQAPQHYPDANH
			KPEMAIALTPFQGLCGFRPVEEIVTFLKKVPEFQFLIGDEAATH
			LKQTMSHDSQAVASSLQSCFSHLMKSEKKVVVEQLNLLVKRISQ
			QAAAGNNMEDIFGELLLQLHQQYPGDIGCFAIYFLNLLTLKPGE
			AMFLEANVPHAYLKGDCVECMACSDNTVRAGLTPKFIDVPTLCE
			MI.SYTESSEVEDELEI DEDCOEDDYL CANDENDERTAINS / THE
İ			MLSYTPSSSKDRLFLPTRSQEDPYLSIYDPPVPDFTIMKA\EVP
1			G\SVTEYKDLALDSASILLMVQGTVIASTPTTQTPIPLQRGGVL
			FIGANESVSLKLTEPKDLLIFRACCLL
6102	70	2415	QTPQATLAANGAEDSRGGEMLPAGEIGASPAAPCCSESGDERKN
			LEEKSDINVTVLIGSKQVSEGTDNGDLPSYVSAFIEKEVGNDLK
			SLKKLDKLIEQRTVSKMQLEEQVLTISSEIPKRIRSALKNAEES
			KQFLNQFLEQETHLFSAINSHLLTAQPWMDDLGTMISQIEEIER
			HLAYLKWISQIEELSDNIQQYLMTNNVPEAASTLVSMAELDIKL
	1		QESSCTHLLGFMRATVKFWHKILKDKLTSDFEEILAQLHWPFIA
			PPQSQTVGLSRPASAPEIYSYLETLFCQLLKLQTSHELLTEPK\
1			HSQKNTLFLPPLLSS/WPIQVMLTPLQKRFRYHFRGNRQTNVLS
			KPEWYLAQVLMWIGNHTEFLDEKIQPILDKVGSLVNARLEFSRG
			LMMLVLEKLATDIPCLLYDDNLFCHLVDEVLLFERELHSVHGYP
			GTFASCMHILSEETCFQRWLTVERKFALQKMDSMLSSEAAWVSQ
			YKDITDVDBMKVPDCAETFMTLLLVITDRYKNLPTASRKLQFLE
1			LQKDLVDDFRIRLTQVMKEETRASLGFRYCAILNAVNYISTVLA
1			DWADNVFFLQLQQAALEVFAENNTLSKLQLGQLASMESSVFDDM
1			INLLERLKHDMLTRQVDHVFREVKDAAKLYKKERWLSLPSQSEQ
			AVMSLSSSACPLLLTLRDHLLQLEQQLCFSLFKIFWQMLVEKLD
}	•		VYIYQEIILANHFNEGGAAQLQFDMTRNLFPLFSHYCKRPENYF
			KHIKEACIVLNLNVGSALTAGKDVLPVQLQGSFPAT
6103	207	2523	ESNSTMTTYLEFIQQNEERDGVRFSWNVWPSSRLEATRMVVPVA
ŀ			ALFTPLKERPDLPPIQYEPVLCSRTTCRAVLNPLCQVDYRAKLW
1	1		ACNFCYQRNQFPPSYAGISELNQPAELLPQFSSIEYVVLRGPQM
i .			PLIFLYVVDTCMEDEDLQALKESMQMSLSLLPPTALVGLITFGR
			MVQVHELGCEGISKSYVFRGTKDLSAKQLQEMLGLSKVPVTQAT
	1		RGPQVQQPPPSNRFLQPVQKIDMNLTDLLGELQRDPWPVPQGKR
1			DIDECULATED ANGLE ECHEDING A TAMETOON TO THE
į			PLRSSGVALSIAVGLLECTFPNTGARIMMFIGGPATQGPGMVVG
}	}		DELKTPIRSWHDIDKDNAKYVKKGTKHFEALANRAATTGHVIDI
			YACALDQTGLLEMKCCPNLTGGYMVMGDSFNTSLFKQTFQRVFT
			KDMHGQFKMGFGGTLEIKTPR\EIKISGAIGPCVSLNSKGPCVS
	1		ENEIGTGGTCQWKICGLSPTTTLAIYFEVVNQHNAPIPQGG\RG
	İ		A\IQFVTQY\QHSSGQRRIRVTTIARN\WADAQTQIQNIAASFD
	ļ		QEAAAILMARLAIYRAETEEGPDVLRWLDRQLIRLCQKFGEYHK
			DDPSSFRFSETFSLYPQFMFHLRRSSFLQVFNNSPDESSYYRHH
			FMRQDLTQSLIMIQPILYAYSFSGPPEPVLLDSSSILADRILLM
	į		
			DTFFQILIYHGETIAQWRKSGYQDMPEYENFRHLLQAPVDDAQE
J I			ILHSRFPMPRYIDTEHGGSQARFLLSKVNPSQTHNNMYAWGQES
-			GAPILTDDVSLQVFMDHLKKLAVSSAA
6104	124	732	KVSEYIILSKDKILFHALAMLVLVVSPWSAARGVLRNYWERLLR
			KLPQSRPGFPSPPWGPALAVQ\AQPCLQSQQMIPVEVKRI/RSL
			LDSIFWMAAPKNRRTIEVNRCRRRNPQKLIKVKNNIDVCPECGH
			LKQKHVLCAYCYEKVCKETAEIRRQIGKQEGGPFKAPTIETVVL
			YTGETPSEQDQGKRIIERDRKRPSWFTQN
6105	3	989	DI MCV CLGI AI OD ECABBBBB CY DA BURE
5205	·	707	PLHGACTSLVLQRFCHRRPRPCAPARPEDMRRPAAVPLLLLLCF
1			GSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHF
į l			CGGSLIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAM
; I			YARVRQVESNPLYQGTASSADVALVELEAPVPFTNYILPVCLPD
[ ]	ļ		PSVIPETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDT\PR
			CNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSAGPLV
			CLVGQSWLQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPK
. 1			

Deginning nuclectide location corresponding to first amino acid amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence seque	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:   nucleotide   corresponding to first   saino acid residue of amino acid residue of amino acid residue of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of amino acid sequence   section of acid sequence   section of acid sequence   section of acid sequence   section of acid sequence   section of acid sequence   section of acid sequence   section of acid sequence   section of acid sequence   section of acid sequence   section of acid sequence   section of acid sequence   section of acid sequence   sectio				
corresponding to first Laucine, Metchionine, N-Asparagine, Perioline, O-Glutamine, R-Arginine, Perioline, O-Glutamine, R-Arginine, Perioline, O-Glutamine, R-Arginine, Perioline, O-Glutamine, R-Arginine, Perioline, O-Glutamine, R-Arginine, Perioline, O-Glutamine, R-Arginine, Perioline, O-Glutamine, R-Arginine, Perioline, O-Glutamine, R-Arginine, Perioline, O-Glutamine, R-Arginine, Perioline, O-Glutamine, R-Arginine, Perioline, O-Glutamine, R-Arginine, Perioline, O-Glutamine, R-Arginine, Perioline, O-Glutamine, R-Arginine, Perioline, O-Glutamine, R-Arginine, Perioline, O-Glutamine, R-Arginine, Perioline, O-Glutamine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Responsibility, R-Arginine, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R-Responsibility, R	1 1	, ,		
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence se	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence se		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
to first and nacid residue of anino acid eletion, *possible nucleotide deletion, *possible nucleotide deletion, *possible nucleotide deletion, *possible nucleotide insertion)  LOVOPSEVERSEYPTPHORDS  6106 3 1302 GEPFTAPHTGREPTANEGOPELDLKRGCARLITSIESSGEPANS AGENCHARACHER PERAPERAPERAPERAPERAPERAPERAPERAPERAPERA		corresponding	to first	
amino acid residue of amino acid sequence    WTTYPTOPHAN, YTTYPOSHAN, X-WUNKNOWN, **Stop   Codon, /*possible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,   Vpossible nucleotide deletion,	1		1	
residue of amino acid sequence con, "possible nucleotide deletion (Con, "possible nucleotide deletion) (Con, "possible nucleotide disertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con, "possible nucleotide insertion) (Con,				
amino acid sequence   Codon, /-possible nuclectide insertion				
Sequence   LovoPseUgsPsyProPageAp		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence   LovoPseUgsPsyProPageAp		amino acid	sequence	Codon, /=possible nucleotide deletion.
1302   GEPETAPHTERS PETANGSPELDLKSGCARLLTSTESEGEPAS			•	
1302   GRPPTAPHTGRPPTANGGDPRLDLKSGCARLLTSLESGGPAB   AGLERGRCALLINGHERBALARARRAGSSPRACHGON     AGLERGRCALLINGHERBALARARRAGSSPRACHGON     AGLERGRCALLINGHERBALARARRAGSSPRACHGON     LYXTELSKEEGCSTGLISTSWTBEDDVONDTLYSWIN PROGRADN     IPCKETCENVDCGPGKKCRMKRNKERCVCAPDCSNITWKGPVC     GLOGKTYRRCALLKARCKEQPELEVY(ORCKKTCADVFCSS     STCV_VODTNAN_FAUCTIONICTB PBASSQD/LGGNGVTYS\SAC     HLKKATCLLGRSIGLAYEGKCIKAKSCEDIQCTGGKKCLMPKKV     GRGGSLCDBLCPDSKSDBPVCASDNATYASECAHACSSGV     HLKKATCLLGRSIGLAYEGKCIKAKSCEDIQCTGGKKCLMPKV     GRGGSLCDBLCPDSKSDBPVCASDNATYASECAHACSSGV     LLEVYHSGSCNSISEDTEBEEDDDDDVSFPISSILBW     SGCSSSPRPBORGGKK/LSPSERKWVEVFKACDDHKGYLSRE     DFYTAVWLBGYKSPSKIEVDSWSSINPNTSGILLEGFLNIVTK     KKEAQRYNNEVRIFTAFDTYTYGFTLTEDKKARACSSGV     LLEVYHSGSCNSISEDTDSEEDEDDDVSFPISSILBW     GSLEFSSPREVSGRK/LSPSERKWVEVFKACDDHKGYLSRE     DFYTAVWLBGYKSPSKIEVDSWSSINPNTSGILLEGFLNIVTK     KKEAQRYNNEVRIFTAFDTYTYGFTLTEDKARACSSGV     LLAPTIPUNSLOPPEGGCOLPSWASSGNDSSTPPM     CLPRRYMMHRRDDGBERQBDBAUDVTPWMTCVFVWACCSNLLLY     YYFYDLLVYVVIG IFFCLASATGLVSCLAGVCRUPL   SASAGSSA     LLAPTIPUNSLOPPEKKPQARNLLLLALFCVAVSVVWAGVPRNED     MAWULQDALGIAFCLYNLKTIR.PFFKACTLLLLVLFLIVISCAMBWREL     GVWTGSGFAKVLPPSFWAPAGARAFREKDFWLSVRANSSPL     ALCDRFFSLLGGBDLTVFSLAVACTHARACSTRATARRAGER     ACHTARAGAVAGAAALARAGVARALARARCHARARCAGAAALARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA ARACTARA AR		Bequence		
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1433   222   VGVPSPAPPCSWEVGPGGGWTPGILKEGQGGRRTPLLLLATRTR   GLLSLFPPAAMHPAAFPLPVVVAAVLWGAAPTRGLIRATSDHNA   SMDFADLPALFGATLSQEGLQGFLVEAHPDNACSPIAPPPPAPV   NGSVFIALLRRFDCNFDLKVLNAQKAGYGAAVVHNVNSNELLINM   VWNSEBIQQQIWIPSVFIGERSSEYLRALFVYEKGARVLLVPDN   TFPLGYYLIPFTGIVGLLVLAMGAVMIARCIQHRKRLQRNRLTK   \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \				· · · · · · · · · · · · · · · · · · ·
GLLSLFPPAAMHPAAFPLPVVVAAVLWGAAPTRGLIRATSDHNA SMDFADLPALFGATLSQEGLQGFLVEAHPDNACSPIAPPPPAPV NGSVFIALLRRFDCNFDLKVLNAQKAGYGAAVVHNVNSNELLNM VWNSEBIQQQIWIPSVFIGERSSEYLRALFYYEKGARVLLVPDN TFPLGYYLIPFTGIVGLLVLAMGAVMIARCIQHRKRLQRNRLTK \EQLKQI\PTHDYQKGDQYDVCAICLDEYEDGDKLRVLPCAHAY HSRCVDPWLTQTRKTCPICKQPVHRGPGDEDQEEETQQQEEGDE GEPRDHPASERTPLLGSSPTLPTSFGSLAPAPLVFPGPSTDPPL SPPSSPVLLV  6118 1044 247 STISCRACTSGATPGAQSHRSARGHAAGGKETAALGMERGKVKK KEKEKETQKEKIGEKGREEKVKRKEVEQKIKQEKQEKQERRKGK EKEEKRTKQKETNKEKEQFKGQEEKGENKDSTLTRTPLEPLEK NKQILVIGLDCAGKTSVLHSLASNRVOHSVAPTQGFHAVCINTE DSQMEFLBIGGSKPFRSYWEMYLSN/ADSLARSFSVGFKQDSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA II 6119 1217 462 DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR QELLAKALETLLLNGVLTLVLEEDGTAVDSSDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ				
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RONGLRAYTE DERGELLERS DPLAYTUCKGS RGVUCDRCLIGKE KLMRCSQCRVAKYCSAKCQKKAMPDHKRECKCLKSCKPRYPPDS VRLIGRUVFKLMGAPSSSEKLYSFYDLESNINKLTEDKKEGLR QLVMTFQHFMRESIQDASQLPAFDLERAFAVICNSFTICNAE MCGVGVGLYPS ISLLMHSCDPNCS IVFNGHLLLRAVRDIEVGE ELTICYLDMLMTSEERKQLRDQYCFECD\CFRCQTODKDADML TGDEQVWKEVQESLKKIEELKAHWKWEQVLAMCQAIISSNSERL PDINIYQLKVLDCAMDACINLGLEEALPYGTRTMKPYRISFDE SHPVRGVQVWKVCKLQLHQGMFPQAMKNLRLAFDIMRVTHGREH SLIEDLILLLE/MRRONGS ILBERSQREIRRVSLINALLRSHT LCFVSCVNLSYWKFCSVFV  6122 2 2324 RFRKMADGGAASQDESSAAAAAADSRMNNPSETSKPSMESGDC NTGTOTROLPFOKQDYPVGGAISTAQAQAFLGHLHQVQLAGTSL QGAITGLITLPAQOQDLLQQAQAQLLAAAVQOHASQOHSAA GGGITGLITLPAQOQDLLQQAQAQLLAAAVQOHASQOHSAA GGGITGLITLPAQOQDLLQQAQAQLAAAAVQAACLAAAVQOHSAGQHSA LLGSQPRI/TLTSPQDCQDLLQQAQAQLAAAVQALYGND FSPTITFFFRAINLSFKMCKLKAPLFUGDAGLAMVKLYGND FSPTITFFFFRAINLSFKMCKLKAPLFUGDAGLAMVKLYGND FSPTITFFFFRAINLSFKMCKLKAPLEKKINDPSSGGATSSSP LEBP\SDLEBLEGFAKTFKQRRIKLGFT\CGDAGLAMVKLYGND FSPTITFFFFFAINLSFKMCKLKAPLEKKINDPSSGGATSSSP LAIFFSFFSTLVATTFSLVTSSAATTIVSPVLPLTSAAVTNLS VTGTSDTTSNTATVISTAPPASSAVTSSELSPSBASASTSEA SSASETSTTOTTSTPISSPLGTSAATTIVSPVLPLTSAAVTNLS VTGTSDTTSNTATVISTAPPASSAVTSSELSPSBASASTSEA SSASETSTTOTTSTPISSPLGTSAAASAGRAAPVASLHA TSTSAESIQNSLFTVASSAGGASTTTTASKQA  6123 3 2944 HLLHRWFGTDMQMINFTTGEFFQLTEACYFIGTHSEESRFGILHL HQCJEMKRWGVYTPADYGKVTSLLIURNLTVIDMICVEGFG ARELLKVGGRIPGAGGSLFKVPESTLMDCRQLKDSKQILSIT VRIFKVENIGPLETIVSSLKINGVOGGFGEVLDCHOFSLDNTI SRDISIVFTPDFTSSWIRDLSLUGYGFGVLDCHOFSLDNTI SRDISIVFTPDFTSSWIRDLSLUGYGFFFTLMVTLPHHLL PLCADVVPGPSWEESFWRLTVFFVSLSLGVILIAFQQAQYILM EFMKTRGRQNAMSSSSQQNNGFMVJSFSXKSKKRKCSVYYSK HKSTAAASSTSTTTEEKGTSFLASSLASSLPAKEDICTDAMRNWII SLRYASGINVNLQKNLTLPKNLLAKEERTLKNTIVSPSSESCS MKEGIQTTMFFKETDILKTSENTAEFKEELCPLKTSKKLEPNLL PRISSPYHQDPLEFISRKNKGNGVVYKEVLDEKNLKKUDTKYSH SLRYASGINVNLQKNLTLPKNLLAKEERTLKNTIVSPSSESCS MKEGIQTTCMFFKETDILKTSENTAEFKEELCPLKTSKKLEPNLL	6202	1612	107	
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TSTSAESIQNSLFTVASASGAASTTTTASKAQ  6123  3  2944  HLLHRWFGTDMQMINFTTGEFQLTEACPYLGTHSEESRFGILHL  HLQPLEMKRVGVVFTPADYGKVTSLILIRNNLTVIDMIGVEGFG  ARELLKVGGRLPGAGGSLRFKVPESTLMDCRQLKDSKQILSIT  KNFKVENIGPLPITVSSLKINGYNCQGYGFEVLDCHQFSLDPNT  SRDISIVFTPDFTSSWVIRDLSLVTAADLEFRFTLNVTLPHHLL  PLCADVVPGPSWEESFWRLTVFFVSLSLLGVILIAFQQAQYILM  EFMKTRQRQNASSSSQQNNGPMDVISPHSYKSNCKNFLDTYGPS  DKGRGKNCLPVNTPQSRIQNAAKRSPATYGHSQKKHKCSVYYSK  HKTSTAAASSTTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI  SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVFSNPSSECS  MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL  PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK	Į.			
6123 3 2944 HILHRWFGTDMQMINFTTGEFQLTEACPYLGTHSEESRFGILHL HLQPLEMKRVGVVFTPADYGKVTSLILIRNNLTVIDMIGVEGFG ARELLKVGGRLPGAGGSLRFKVPESTLMDCRRQLKDSKQILSIT KNFKVENIGPLPITVSSLKINGYNCQGYGFEVLDCHQFSLDPNT SRDISIVFTPDFTSSWVIRDLSLVTAADLEFRFTLNVTLPHHLL PLCADVVPGPSWEESFWRLTVFFVSLSLLGVILIAFQQAQYILM EFMKTRQRQNASSSSQQNNGPMDVISPHSYKSNCKNFLDTYGPS DKGRGKNCLPVNTPQSRIQNAAKRSPATYGHSQKKHKCSVYYSK HKKTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVFSNPSSECS MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK				-
HLQPLEMKRVGVVFTPADYGKVTSLILIRNNLTVIDMIGVEGFG ARELLKVGGRLPGAGGSLRFKVPESTLMDCRRQLKDSKQILSIT KNFKVENIGPLPITVSSLKINGYNCQGYGFEVLDCHQFSLDPNT SRDISIVFTPDFTSSWVIRDLSLVTAADLEFRFTLNVTLPHHLL PLCADVVPGPSWEESFWRLTVFFVSLSLLGVILIAFQQAQYILM EFMKTRQRQNASSSSQQNNGPMDVISPHSYKSNCKNFLDTYGPS DKGRGKNCLPVNTPQSRIQNAAKRSPATYGHSQKKHKCSVYYSK HKTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVFSNPSSECS MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK		<u> </u>		
ARELLKVGGRLPGAGGSLRFKVPESTLMDCRRQLKDSKQILSIT KNFKVENIGPLPITVSSLKINGYNCQGYGFEVLDCHQFSLDPNT SRDISIVFTPDFTSSWVIRDLSLVTAADLEFRPTLNVTLPHHLL PLCADVVPGPSWESFWRLTVFFVSLSLLGVILLTAFQQAQYILM EFMKTRQRQNASSSSQQNNGPMDVISPHSYKSNCKNFLDTYGPS DKGRGKNCLPVNTPQSRIQNAAKRSPATYGHSQKKHKCSVYYSK HKTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVFSNPSSECS MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK	6123	3	2944	
KNFKVENIGPLPITVSSLKINGYNCQGYGFEVLDCHQFSLDPNT SRDISIVFTPDFTSSWVIRDLSLVTAADLEFRPTLNVTLPHHLL PLCADVVPGPSWEESFWRLTVFFVSLSLLGVILIAFQQAQYILM EFMKTRQRQNASSSSQQNIGPMDVISPHSYKSNCKNFLDTYGPS DKGRGKNCLPVNTPQSRIQNAAKRSPATYGHSQKKHKCSVYYSK HKTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVFSNPSSECS MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK				· ·
SRDISIVFTPDFTSSWVIRDLSLVTAADLEFRFTLNVTLPHHLL PLCADVVPGPSWEESFWRLTVFFVSLSLLGVILIAFQQAQYILM EFMKTRQRQNASSSSQQNNGPMDVISPHSYKSNCKNFLDTYGPS DKGRGKNCLPVNTPQSSIQNAKRSPATYGHSQKKHKCSVYYSK HKTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVFSNPSSECS MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK	]			
PLCADVVPGPSWEESFWRLTVFFVSLSLLGVILIAFQQAQYILM EFMKTRQRQNASSSSQQNNGPMDVISPHSYKSNCKNFLDTYGPS DKGRGKNCLPVNTPQSRIQNAAKRSPATYGHSQKKHKCSVYYSK HKTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVFSNPSSECS MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK				
EFMKTRQRQNASSSQQNNGPMDVISPHSYKSNCKNFLDTYGPS DKGRGKNCLPVNTPQSRIQNAAKRSPATYGHSQKKHKCSVYYSK HKTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVFSNPSSECS MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK				
DKGRGKNCLPVNTPQGRIQNAAKRSPATYGHSQKKHKCSVYYSK HKTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVFSNPSSECS MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK				PLCADVVPGPSWEESFWRLTVFFVSLSLLGVILIAFQQAQYILM
HKTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVFSNPSSECS MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK	1			
HKTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVFSNPSSECS MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK				DKGRGKNCLPVNTPQSRIQNAAKRSPATYGHSQKKHKCSVYYSK
MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK	1			
MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK		1		SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVFSNPSSECS
PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK	1			
	1	1		
ONLNWSKSRTCRKNKKRGVAPVSRPPBOSDLKLVCSDFERSELS				
SDINVRSWCIQESTREVCKADAEIASSLPAAQREABGYYQKPEK		1		
KCVDKFCSDSSSDCGSSSGSVRASRGSWGSWSSTSSSDGDKKPM	1	1		
VDAQHFLPAGDSVSQNDFPSEAPISLNLSHNICNPMTGNSLPQY				
AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE				
NGVPCVIQESAPVHNSFIDWSATCEGQPSSAYCPLBLNDYNAFP				
EENMNYANGFPCPADVQTDFIDHNSQSTWNTPP\NMPAS\WGNA	1	1	1	EENMNYANGFPCPADVQTDFIDHNSQSTWNTPP\NMPAS\WGNA
QFPSSSRPYLKSTPKACLPMSGLFGPI\WAP\QSDVYENCCPIN		1		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	İ	\=possible nucleotide insertion)
			PTTEHSD/THMENQA\VVCKEYYPGF\NPFRAYMNLDIWTTT\A
			NRNANFPLSRDSSYCGNV
6124	1573	236	SDEALRLAGERGMGRVQLFEISLSHGRVVYSPGEPLAGTVRVRL
			GAPLPFRAIRVTCIGSCGVSNKANDTAWVVEEGYFNSSLSLADK
			GSLPAGEHSFPFQFLLPATAPTSFEGPFGKIVHQVRAAIHTPRF
			SKDHKCSLVFYILSPLNLNSIPDIEQPNVASATKKFSYKLVKTG
			SVVLTASTDLRGYVVGQALQLHADVENQSGKDTSPVVASLLQKV
			SYKAKRWIHDVRTIAEVEGAGVKAWRRAQWHEQILVPALPQSAL
			PGCSLIHIDYYLQVSLKAPEATVTLPVFIGNIAV/NPCPSEPPA
			RPGAASWGPTPGG\PSAPPQEEAEARAAAGGPHFLDPVFLSTKS
	!		HSQRQPLLATLSSVPGAPEPCPQDGSPASHPLHPPLCISTGATV
			PYFAEGSGGPVPTTSTLILPPEYSSWGYPYEAPPSYEQSCGGVE
			PSLTPES
6125	1	904	KTCPKLTCAFTVSVPDSCCRVCRGDGELSWEHSDGDIFRQPANR
			EARHSYHRSHYDPPPSRQAGGLSRFPGARSHRGALMDSQQASGT
i			IVQIVINNKHKHGQVCVSNGKTYSHGESWHPNLRAFGIVECVLC
			TCNVTKQECKKIHCPNRYPCKYPQKIDGKCCKVCPG/KKAKEEL
1			PGQSFDNKGYFCGEETMPVYESVFMEDGETTRKIALETERPPQV
			EVHVWTIRKGILQHFHIEKISKRMFEELPHFKLVTRTTLSQWKI
			FTEGEAQISQMCSSRVCRTELEDLVKVLYLERSEKGHC
6126	1224	389	RLLSEAPCPRSRRRFQMNPEWGQAFVHVAVAGGLCAVAVFTGIF
			DSVSVQVGYEHYARAPVAGLPAFLAMPFNSLVNMAYTLLGLSWL
]			HRGGAMGLGPRYLKDVFAAMALLYGPVQWLRLWTQWRRAAVLDQ
1			WLTLPIFAWPVAWCLYLDRGWRP\WLFLSLECVSLASYGLALLH
			PQGFEVALGAHVVPAVGQALRT\HRHYG/SATPSATYLALGVLS
			CLGFVVLKLCDHQLARWRLFQCLTGHFWSKVCDVLQFHFAFLFL
			THFNTHPRFHPSGGKTR
6127	1335	463	VLPRRCLVFVVNTMDSSREPTLGRLDAAGFWQVWQRFDADEKGY
			IEEKELDAFFLHMLMKLGTDDTVMKANLHKVKQQFMTTQDASKD
1			GRIRMKELAGMFLSEDENFLLLFRRENPLDSSVEFMQIWRKYDA
1			DSSGFISAAELRNFLRDLFLHHKKAISEAKLEEYTGTMMKIFDR
			NKDGRLDLNDLARILALQENFLLQFKMDACSTEKRKGDFEKIFA
1			YYDVSKTGALEGP\EVDGFVKDMMELVQPSISGVDLDKFREILL
6128	2511	042	RHCDVNKDGKIQKSELALCLGLKINP
6125	2511	843	TCRMSRRQLERWVWSSQQVQARGRNVRAPRLGKIAMGLEMSSKD
			SPGSLDGRAWEDAQKPQSAWCGGRKTRVYATSSRRAPPSEGTRR
			GGAARPEKTAEEGPPAAPGSLRHSGPLGPHACPTALPEPQVTSA
			MSSQVVGIEPLYIKAEPASPDSPKGSSETETEPPVALAPG\PAP
			TRCLPGHKEEEDGEGAGPGEQGGKLVLSSLPKRLCLVCGDVAS
			GYHYGVASCEACKAFFKRTIQGSIEYSCPASNECEITKRRRKAC
1			QACRFTKCLRVGMLKEGVRLDRVRGGRQKYKRRPEVDPLPFPGP
1			FPAGPLAVAGGPRKTAAPVNALVSHLLVVEPEKLYAMPDPAGPD
			GHLPAVATLCDLFDREIVVTISWAKSIPGFSSLSLSDQMSVLQS VWMEVLVLGVAQRSLTLQDELAFAEYLVLDEEGARPAGLGELG\
1			AALLQLVRRLQALRLEREEYVLLKALALANSDSVHIEDEPRLWS
			SCEKLLHEALLEYEAGRAGPGGGAERRRAGRLLLTLPLLRQTAG
	-		KVLAHFYGVKLEGKVPMHKLFLEMLRAMMD
6129	1764	771	ARFARSAHEGKMPKKKTGARKKAENRREREKQLRASRSTIDLAK
		, , <u>.</u>	
		!	HPCNASMECDKCQRRQKNRAFCYFCNSVQKLPICAQCGKTKCMM
			KSSDCVIKHAGVYSTGLAMVGAICDFCEAWVCHGRKCLSTHACA CPLTDAEC\VECERGVWDHGGRIFSCSFCHNFLCEDDQFEHQAS
	i	'	CQVLEAETFKCVSCNRLGQHSCLRCKACFCDDHTRSKVFKQEKG
			KQPPCPKCGHETQETKDLSMSTRSLKFGRQTGGEEGDGASGYDA YWKNLSSDKYGDTSYHDEEEDEYEAEDDEEEEDEGRKDSDTESS
			DLFTNLNLGRTYASGYAHYEEQEN
6130	3	577	GRGGTMREYKVVVLGSG\GVGKSALTV\QFVTCTFIEKYDPTIE
	<del>ا                                      </del>		THE THE TAXABOOG (GARWOTTA (GLAICILITY (DLII)

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
		nucleotide	Amino acid segment containing signal peptide
ID	beginning		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of		Section, Tempeonine, Vevaline,
	1	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	i	\=possible nucleotide insertion)
			DFYRKEIEV\DSSPSVAGISWTQQGTEQF\ASMRDLYIKKGQGC
ł	1	ł	ILVYSLVNQQSFQ\DIKPMRDQIIRVKVSEKVPVI\LVGN\SVD
1		1	LESEREVSSSEGRALAEEWGCPFMETSAKSKTMVDELFAEIVRO
1	Į.		
(2.2.2.			MNYAAQPDKDDPCCSACNIQ
6131	3	1811	SSPREKTSDSSHRPSRHGFLFLRLVGLSPFSYLCVPPSRPVPGS
		Í	PRSLSAMRLLPLAPGRLRRGSPRHLPSCSPALLLLVLGGCLGVF
1		l	GVAAGTRRPNVVLLLTDDQDEVLGGMTPLKKTKALIGEMGMTFS
		1	SAYVPSALCCPSRASILTGKYPHNHHVVNNTLEGNCSSKSWQKI
			QEPNTFPAILRSMCGYQTFF\AGKYLNEYGAPDAGGLEHVPLGW
	1		QEFNITFAIDRSWCGIQIFF (AGRIENEIGAPDACGLEHVPLGW
1	1		SYWYALEKNSKYYNYTLSINGKARKHGENYSVDYLTDVLANVSL
1	]		DFLDYKSNFEPFFMMTATP\APHSPWTAAPQYQKAFQNVFAPRN
1			KNFNIHGTNKHWLIRQAKTPMTNSSIQFLDNAFRKRWQTLLSVD
			DLVEKLVKRLEFTGELNNTYIFYTSDNGYHTGQFSLPIDKRQLY
			EFDIKVPLLVRGPGIKPNQTSKMLVANIDLGPTILDIAGYDLNK
1			TQMDGMSLLPILRGASNLTWRSDVLVEYQGEGRNVTDPTCPSLS
1			DGUSOCEDDGUCEDA YARITTA CUMTUGA TURI CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA CUCTURA C
1		<b>]</b>	PGVSQCFPDCVCEDAYNNTYACVRTMSALWNLQYCEFDDQEVFV
ì	ſ	(	EVYNLTADPDQITNIAKTIDPELLGKMNYRLMMLQSCSGPTCRT
			PGVFDPGYRFDPRLMFSNRGSVRTRRFSKHLL
6132	96	1241	AAGLLPPGLVPEDPRRTRNLLPFGIQGPPFALSRPLFSCVESGW
1			AWEAMEPEFLYDLLQLPKGVEPPAEEELSKGGKKKYLPPTSRKD
İ			PKFEELQKPA\VLMEWINATLLPEHIVVRSLEEDMFDGLILHHL
			FQRLAALKLEAEDIALTATSQKHKLTVVLEAVNRS\CSWRSGRP
	1		CON (WESTERWELL OF W. 1911 AND BORDE OF BENEVISCHED
}			SGA/WESIFNKDLLSTLHLLVALAKRFQPDLSLPTNVQVEVITI
	1		ESTKSGLKSEKLVEQLTEYSTDKDEPPKDVFDELFKLAPEKVNA
			VKEAIVNFVNQKLDRLGLSVQNLDTQFADGVILLLLIGQLEGFF
1	i		LHLKEFYLTPNSPAEMLHNVTLALELL/IGRGPAQLPC/LALK/
1			TIVNKDAKSTLRVLYGLFCKHTQKAHRDRTPHGAPN
6133	2	4256	FVHGSMADTDLFMECEBEELEPWQKISDVIEDSVVEDYNSVDKT
1	}		TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
			KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
			PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
1			IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
1			STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
1			TATOPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSLASFVT
			VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
			GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
1			RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
			/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
	j j		CDDCCAANOL MEDALINGEBRODS CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONT
1			GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
1			LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
			KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
			VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
1			CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
1			SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS
1			IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST
1		i	
			CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
1	1		SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
1			NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA
			STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE
1		ļ	LASGGGGGGGGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPO
1			RRIRRWLRRFQASQGENLEGKYLSFEAEBKLAEWVLTOREOOLP
		1	VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
			VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
			DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLPTLVFY
1			RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ
1	1		RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL
[		· · · · · · · · · · · · · · · · · · ·	RSKGPLVPDCHRIHLSEEVLAMLSASSTIDAVVDAGCSEVTODT I

_	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
1	ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	- {	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł			residue of	S=Serine, T=Threonine, V=Valine,
		amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1		residue of	amino acid	
		amino acid	sequence	Codon, /=possible nucleotide deletion,
<u></u>		sedneuce		\=possible nucleotide insertion)
1				DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
ì				LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
'				LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
L.				FYGFEEADLDLMEI
	6134	2	4256	FVHGSMADTDLFMECEEEELEPWQKISDVIBDSVVEDYNSVDKT
1		· ·		TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
1				KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
				PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
				IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
				STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
				TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT
				VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
1				GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
1		}		RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
				/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
				GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
1				LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
1				KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
				VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
1				CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
ļ				SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS
				IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST
1				CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
1				SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
		2		NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA
				STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE
				LASGGGGGGGGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ
1				RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP
				VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
				VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
1				DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY
		·		RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ
			)	RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL
				DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
				LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
				LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
				FYGFEEADLDLMEI
	6135	2	4256	FVHGSMADTDLFMECEEEBLEPWQKISDVIEDSVVEDYNSVDKT
		[	[	TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
			1	KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
1		1		PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
-		1		IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
1				STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
				TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT
				VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
1		1		GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
			1	RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
		1		/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
1				GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
		[		LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
			1	KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
			i	VHFRMIHEDTRHLLCPYCLKVFKNGNAFOOHYMRHOKR\NVYH\
			i	
1				CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
				CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS
		•		CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA

beginning coation corresponding continued to first amino acid residue of simino acid residue of simino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence seq	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO: location corresponding to first anino acid reidue of anino acid reidue of anino acid reidue of anino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence s				
corresponding to first samino acid serious to first samino acid serious of serious of samino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequ	l			
to first anino acid residue of amino acid residue of amino acid sequence  Perciaire, Jedilamaine, N-Asparagine, amino acid sequence  Sescrine, T-Threonine, V-Valine, amino acid sequence  Sescrine, T-Threonine, V-Valine, amino acid sequence  Sequence  Sescrine, T-Threonine, V-Valine, W-Ty-Yposhan, Y-Tyroshan, Y-Unknown, *-Stop Codon, /=possible nucleotide deletion, V-possible nucleotide insertion)  SVGDANAKHIVENPSHRSSSILERGITHIAMSHRGOTRDRVIDR NVCNMYPPSPFTHEMAATVKSAGAT-PAEPELLITPLANALDSPA STATPPPTPHHOALALPHATEGAECLAVUDQDEGSPVTQSPE LASGGGGGGVUKKEGLGVKKERVVLACCCYTEQAALHSPA RETHRUBERGOSGGGVUKKEGLGVKKERVVLACCCYTEQAALHSPA RETHRUBERGOSGGGVUKKEGLGVKKERVVLACCCYTEQAALHSPA RETHRUBERGOSGGGVUKKEGLGVKKERVVLACCCYTEQAALHSPA RETHRUBERGOSGGGVUKKEGLGVKKERVVLACCCYTEQAALHSPA RETHRUBERGOSGGGVKKEGLGVKKERVVLACCCYTEQAALHSPA RETHRUBERGOSGGGVKKAGUTAALCCCYTEQAALHSPALDEGSCG RETHRUBERGOSGGGVKKAGUTAALCCCYTEQAALHSPALDEGSCG RETHRUBERGOSGGVKAGUTAALCCCTTCAALCCCTTCAALCCCTTCAALCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCCTTCAACCCTTCAACCCCTTCAACCCCTTCAACCCTTCAACCCCTTCAACCCTTCAACCCTTCAACCCCTTCAACCCTTCAACCCTTCAACCCTTCAACCCTTCAACCCTTCAACCCTTCAACCCTTCAACCCTTC	NO.			
to first amino acid residue of amino acid sequence  sequence  #TYPTOSHAR, Y=TYTOSHAR, X=UNKNOWN, *=Stop coden, /=possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide		1		
amino acid residue of amino acid sequence whypophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=ytycophan, y=yt				
main acid sequence  amino acid sequence  w=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, *possible nucleotide deletion) _possible nucleotide deletion; _possible nucleotide deletion; _possible nucleotide insertion)  ### VCMMYPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	ļ	1		
amino acid sequence SvGDAMAKHLVENPSHRSSSILERGITWIAISHRGOTEDRVIDE SVGDAMAKHLVENPSHRSSSILERGITWIAISHRGOTEDRVIDE SVGDAMAKHLVENPSHRSSSILERGITWIAISHRGOTEDRVIDE NVCMPY PPSPTFINAATVKSAGAT PABERLITIPAALISPA STATPPPTPHHOALALPRIATEGRECLAVUDQDEGSPVTQSPE LASGGGGSGGVGKREQLAVKLRVILVALCANTEQAABHRWHQ RRIRRHIRRFQAKGGNILECKTLSFRAMKHLAFWVLTQREQQLP VHSETLFQAKATKIGRSLEGOFKSISTERAVRFMIARHHITPHARRA VANTIDERVAKRHGLISPFVAKRHUADDELISHTVALDSTILEPILAVE RGMODPANNPSILLEAKESGYSDEIHEMSTRWAMKHTACA RSKGHLVMICHTHILESEVLAMIGASSTIDPAVVPAGCSSKIQPIL DVCIKRTVKHFLHKKKRGARRMADTACDSVLLGALVUMLGEV LGVIGGCPELVQRSFLVASVLROPDGNINSPTRADHQEELLAS LEPQLKISGGRHSSFSTPRPRSSPETTETPSBLLQFRESSETES FYGFEEADLLHEI FORWALLEGNSKRKKRSVQBGENPDDGVRGSPPEDVRLGQVAS SIPRGHHSRGOTERLASLFSSLEPGIQPVYVPYRKLSSLASA LEPGLKISGGRHSSRGOTERLASLFSSLEPGIQPVYVPYRKLSSLASA SLFRGHHSRGOTERLASLFSSLEPGIQPVYVPYRKLSSLASA BLEEBHINKGOGKNSKOPGWKADATNINDVYKRESSETES FYGFEEADLLHEI NOBERLKVERTYPVGNLPVTCNKKLKSFFKKYQGKKID INGEBERLKVERTYPVGNLPVTCNKKLKSFFKKYQGKKID INGEBERLKVERTYPVGNLPVTCNKKKLKSFFKKYQGKKID SLFRGGHLSKALALKKHAPDOKNINAVVYKRESALFKK RGAQIADGFIRVDLASSTSSDKRSVVVGNLPYKVRESALFKK RGAGGIAGGFIRVDLASSTSSDKRSVVVGNLPYKVRESALFKK RGAGGIAGGFIRVDLASSTSSDKRSVVVGNLPYKVRESALFKK RGAGGIAGGFIRVDLASSTSSDKRSVVVGNLPYKVRESALFKK RGAGGIAGGAFTFYDLASSTSSDKRSVVVGNLPYKVRESALFKK RGAGGIAGGAFTFYDLASSTSSDKRSVVVGNLPYKVRESALFKK RGAGGIAGGAFTFYDLASSTSSDKRSVVVGNLPYKVRESALFKK RGAGGIAGGAFTFYDLASSTSSDKRSVVVGNLPYKVRESALFKK RGAGGIAGAGAFTFYSTANTAVRTAMFTARGGGENAVALTARGGGAGAATACAL RGAGGRAGAVARGVARGFRAMFTARGGGAATATRAGGGAATACAL RGAGGRAGAVARGVARGFRAMFTARGGGAATATRAGGGAATACALFS LICKTNAMSSTALTARGGAATATRAGGGAATATRAGGAATATRAGGGAATACALFS LICKTNAMSSTALTARGGAATATRAGGGAATATRAGGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAATATRAGGAA				
Sequence    V=possible nucleotide insertion	}			
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RNGAQIADGFRIRVDLASSTSSRDKRSVPVONLPYKVEBSAIEK HFLDCGSIMAVRIVRDKMTGIGKGFGYVLFENTDSVHLALKLAN SELMGRKLRVMRSVNKEKFKQQNSMFRLKNYSKPKQGLNFTSKT AEGHPKSLPIGEKAVLLKYKKKQQKKSGRPKKQKKOK 6137 141 2656 RALRKRCGPGRRGALGSGPGPQRPKRERPAPPRERKHPG MWNNLIVAMCLA\LLGLPGKAGELGGHVS\IILAGEGLGDLAKK YLMGG\LFQLYLDEAGRGISPSFHGALTAPKQQGELMAKALES LSCPKDMAPSHCAEHKDQFIQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYSVPFFAYAPDIARNINSSCRPGPGAMLRVV LEKPFGIDHPSAQQLATELGTFFQBEEMFRUHTYLGKQAVAQIL PFRDQNRKALDGLMNRHHVERVEIIMKETVDAEGRTSFYBEYGY RDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHLQVFQALRGL QRGSAVVGQVQSYSEQVRELQKPDSFHSLTFTFAGVLVHIDNI. RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFFILGBGDLGSPAVLVSRNLFRPSLPSSWKEMBGPPG LRLPGSPLSDYYAYSPVBRDAHSVLLSHIFHGKNNFFITTENL LASWNFWTPILESLAHKAPPLYPGAENGRLDFFSSGRLFFS QQQPEQLVPGFGFGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGGFHLALSGGSSPVALFQQLATHAYGFPW AHTHLWLVDERCVPLSDPBSNFQGLAGHLQHVLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYARBISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGGLVVITTSPSQPHRRMSLSLPLINRAKKV AVLVMRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWMMDY APLG BFSKLTDRWQNAVQGVQRKGDDGLVRQQDFTTSVENLFFFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLABMIKQ FQSTVETWQCEKKIKELKSRLQVUKAGSEPDLPELHEDLHNEK ELIKELGSLASWTQNLKELGTMKADLTRHVLVEDUVMVLKEQIE HLHRQMBDLCLRVAIRKQEIBDRLMTWVTPEKNKELCAMLVQM ENKVLCTADISIEBMIFKLQKDCMEBINLFSENKLQLKQMDQDI IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETAFI QQLDKNNSNLRTWLARIESELSKPVVYDVCDDQEIQKRLEQQD LQRDIEGHSAGVESVFNICDVLLHDSDACAMETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETHVRLWQKFLDDYSFFEDWLKSAB RTAACPNSSEVLITSAKBELBRAFAPQRQIBERLITGLELLINKQY				
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AEGHPKSLPIGEKAVLLKTKKKGQKKSGRPKKQRKQK 6137  141  2656  RALKKRRGPGRRGALGSGFGFGRFBGRVPEERPAPPRERKHEG MWNMLIVAMCLA\LIGLFGKAQELQGHV9\ERPAPPRERKHEG MWNMLIVAMCLA\LIGLFGKAQELQGHV9\IILAGGLGDLAKK YLMGG\LFQLYLDEAGRGHSFSFHGAALTAPKQQGELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTABDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAMLRVV LEKFFGHDHFSAQQLATELGTFFGBEEMYRVDHYLGKQAVAQIL PFRDONRKALDGLWRHHVERVEIIMKETVDABGRTSFYBEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTTFFAQVLVHIDNI. RWEGVPFILMSGKALDERWGYARILFKNQACCVQSKKHMAAQGS QCLFRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLEGSPLSDYYAYSPVEREDAHSVLLSHIFHGRKKFFTTTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEPSSGRLFFS QQQFEQLVPGRGPGPMPSDFQVLARKYRBSSLVSAWSEELISKL ANDIEATAVRAVRRGGPHALSGGSSPVALFQQLATHAYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHYYARSISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEGLVVLTTSPSQPHRRMSLSJPLINRAKKY AVLWMGRKKRITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFIG  6138  4587  934  EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQEFFSLYQTRSLHELKNKEIHFQRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPOLABMIKQ FQSTVETWDQCEKKI KELKSRLQVLKAGSEDPLPELHEDLHNEK ELIKELGSLSLASWTONLKELOTMKADLTHHVLVEDUWVLKEQIE HLHRQWEDLCLRVAIRKQEIBDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEBMIEKLQKDCMESINLFSBNKLQLKQMGDL IKASNKSRAABIDDKINKINDRWQHLFPUIGGRVKKILKTFFAFI QQLDKNMSNLRTWLAR IESELSKPVVYDVCDDQEIQKRLAEQQD LQRDIEGHSAGYESVFNICDVLIHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKPLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFQRGIHBRLTQLELINKQX	1		1	HFLDCGSIMAVRIVRDKMTGIGKGFGYVLFENTDSVHLALKLNN
6137  141  2656  RALRKRRCGPGRRGALGSGPGPQRRFGRVPEERPAPPRERKHPG MWNNHLIVAMCLA\LIGLBGKAQELGOHYS\IIIAGEQLGDLAKK YLWGG\LFGUYLNDEAGRGHSFSFHGAALTAPKQGGLMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPFFAYEDIARNINSSCRPGPGAMLRVV LEKKPFGHDHPSAQQLATELGTFFGREEMYRVPNHYLGKQAVAQTL PFRDQNRKALDGLWNRHHVERVEIIMKETVDABGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHINVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYGSYSSQVRRELQKPDSFHSLTPFFAGVLVHIDNI. RWEGVPFILMSGKALDERVGYRRILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGBLGSPAVLVSRNLFRPSLPSSKKEMEGPPG LRLFGSPLSDYYAYSPVRREDAHSVLLSHIFHGRNKFFTTENL LASMNFWTPLLESILAHKAPRLYPGGAENGRLLDFEPSSGRLFFS QQQPBQLVPGFGPGPMSDFQVLARKYRSSSLVSAWSEELISKL ANDIEATAVRAVRRFGQFHLALSGGSSPVALPQQLATAHYGFPW AHTHLMLVDERCVPLSDPESMFQGLQAHLLQHVRIPYYNTH\AM PVHLQQRLCAEEDQGAHTYAREISALGAMSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLWMGRMKREITTLVSRVGHEPKKWPISGVLPHSQLVWYMDY DAFLG  6138  4587  934  EFSKLTDRWQNAVGGVRQRKGDVDGLVRQWQFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLHELKNKEIHFQRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ PQSTVETWDQCEKK KELKSRLQVLKAGSEPPLPELHEDLHBEK ELIKELGSSLASWTONLKELOTMKADLTHRVLVEDUWVLKGQTE HLHRQWEDLCLRVAIRKQEIBDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEBMIEKLQKDCMEEINLFSSENLLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFPVUJGGRVKKLKTFAPI QQLDKNMSNLRTWARIESELSKPVVYDVCDDQEIQKRLAEQOD LQRDIEGNSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFQRGIHBRLTQLELINKQY				SELMGRKLRVMRSVNKEKFKQQNSNPRLKNVSKPKQGLNFTSKT
MWNMLIVAMCLA\LIGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWGG\LFQLYILDEAGRGHSFSFHGAALITAPKQGQELMAKALES LSCPKDMAPSHCAEHKQPLQLGSQYRQKTAEDYQALNKD IEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYIGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYBEYGV IRDVLQNILITEVITLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNI. RWEGVPFILMSGKALDERVGYARLIFKNQACCVQSEKHWAAAQS QCLPRQLVHTIGHGJLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASNNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMSDFQVLRAKXRESSLVSAWSEELISKL ANDIEATAVRAVRRFQCFHLALSGGSSPVALFQQLATHYGFPW AHTHLWLDDERCYPLSDPBSNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQQAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGGQLVVLTTSPSQPHRMSLSLPLINRAKKV AVLWMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWMDY DAFIG  6138 4587 934 EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRTTCAL TLEAGEKLLLTTDLKYKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEGSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIRDRLNTWVFREKNELCAMLVQM ENKVLQTADISIEBMIEKLQKCMEBINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWGHLFDVIGSRVKKLETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQD LQRDIEQHSAGWSVFNICDVLLHDSDACARETECDSIQQTTRS LDRRWRICAMSMERRMKIEETWRLWQKPLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFQRQIHBRLTQLELINNGY				AEGHPKSLFIGEKAVLLKTKKKGQKKSGRPKKQRKQK
YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPKQQQELMAKALES LSCPRDMAPSHCAEHRDQFIQLGYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFFFSVPPFAYEDIARNINSSCRFGPGAMLRVV LEKSFGHDHFSAQQLATELGTFFQEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWRHHVERVEIIMKETVDAEGRTSFYBEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVREELQKPDSFHSLTPTFAGVLVHIDNI. RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASNNFWTPLLBSLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGQFHLALGGGSSPVALFQCLATHYGFPW AHTHLWLVDERCVPLSDPBSNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSFTGLDGEQLVVLTTSPSQPHRMSLSLPLINRAKKV AVLWMGRNKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFILS  6138 4587 934 EFSKLTDRWQNAVQGVQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKAGGERFSLYGTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETNDQCEKKIKELKSRLQVLKAGSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVYFMEKNKELCAMLVQM ENKVLQTADISIEBMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWGHLFDVIGSRVKKLKETFRFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQOD LQRDIEQHSAGVESVFNICDVLHDSDACARNETECDSIQQTTRS LDRRWRNICAMSMERRMKIELTWLHOKPLDDYSRFEDWILKSAB RTAACPNSSEVLYTSAKEELKRFEAFQRQIHERLTQLELINKQY	6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG
LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDTARNINSSCRPGPGAWLRVV LEKPFGDHPSAQQLATELGTFFQBEEMYRVDIYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYBETGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVPQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPFFAGVLVHIDNL RWEGYPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGAGAENGRLLDFEFSSGRIFFS QQQEQLVPGDFGFGPMPSDFOVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATHAYGFPW AHTHLWLVDERCVPLSDFBSNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG  EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRTTCAL TLEAGEKLLLITDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLOVLKAGSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELGTMKADLTRHVLVEDUMVLKEQIE HLHROWEDLCLRVAIRKQEIBDRLNTWVVPNEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQOD LQRDIEQHSAGVESVFNICODVLAHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLITSAKEELKRFEAFQRGIHERLTQLELINKQY	1			MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK
LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAMLRVV LEKPFGHDHFSAQQLATELGTFFQEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNILTEVLTLVAMELPHNVSSAEAVLRHKLQVPQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGLLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIFHGKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFOVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESMFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSFTGLDGEQLVVLTTSPSQPHRMSLSLPLLNRAKKV AVLWMGRMKREITTLVSRVGHEPKKWPISGVLDWYMDY DAFIG  6138 4587 934 EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYGYRSLHHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSSLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVNVLKEQIE HLHRQWEDLCLRVAIRRQEIBDRLNTWVVFNEKNKELGAWLOW ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLOLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQD LQRDIEQHSAGVESVFNICOVILHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWGKFLDDYSRFEDWLKSAB RTAACPNSSEVLITSAKEELKFFAFQRQIHERLTQLELINKQY	1			YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALES
LEKPFGHDHFSAQQLATELGTFFQEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHYEVEVEIIMKETVDAEGRTSFYBEYGV IRDVLQNHLTEVLTLVAMELPHNVSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTTTFAGULVHIDNI. RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPBDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGQFHLALSGGSSPVALFQQLATHAYGFPW AHTHLWLVDERCVPLSDEBSNFQGLQAHLLQHVRIPYYNIH,AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVILTTSFSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWMDY DAFLG  6138 4587 934 EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLVQTRSLIHELKNKEIHFQRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELGSLASWTQNLKELQTMKADLTRHVLVEDVAVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVFNEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQDD LQRDIEGHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETTWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFQRQIHBRLTQLELINKQY				
PFRDQNRKALDGWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLITEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRP9LPSSWKEMEGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGQFHLALSGGSSPVALFQQLATHAYGFPW AHTHLWLVDERCVPLSDERSNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSFDLVLLGWGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVWGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG  6138 4587 934 EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKBLEQSIASWTQNLKELQTMKADLTRHVLVEDVWVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQD LQRDIEGHSAGVESVFNICOVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKPLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFQRQIHBRLTQLELINKQY			1	<b>∮</b>
IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGFGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRPGGFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESMFQGLQAHLLQHVRIPYYNIH, AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVWGRMKREITTLVSKVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG  EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRITCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHROWEDLCLRVAIRKQEIEDRLNTWVVFMEKNKELCAMLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVYDVOCDDQEIQKRLAEQOD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLMQKFLDDYSRFFEDWLKSAE RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTQLELINKQY	1		}	
QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGYPFILMSGKALDBRVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGGFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPBSNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFIG  6138 4587 934 EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLHELKNKEIHFQRRRITCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLGVLKAGSEDPLEPLHEDLHNEK ELIKELEQSLASWTQNLKELGYMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIBDRLNTWVVFNEKNKELCAMLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQOD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEYLYTSAKEELKRFEAFQRQHERLTQLELINKQY	1	1	1	
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RKLAREMKIDIASKLKQMVHEGNQKWDNLQKKVIAVLKKLKHFI				
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	1 5 37 -b - 3	I bundlehad and	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	location	
NO:	nucleotide		Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			NOREEFEGTRESILVWLTEMDLOLTNVEHFSESDADDKMRQLNG
	ŀ	1	FOOEITLNTNKIDQLIVFGEQLIQKSEP\LDAVLIEDELEELHR
	1		YCOEVFGRVSRFHRRLTSCTPGLEDEKEASENETDMEDPREIQT
	1		DSWRKRGESEEPSSPQSLCHLVAPGHERSGCETPVSVDS\IPLE
	1		WDHTGRRGGPSSSH\EEDEBAQYY\SALSGKSISDGHSWHVPDS
i			PSCPEHHYKOMEGDRNVPPVPPASSTPYKPPYGKLLLPPGTDGG
			KEGPRVLNGNPQQEDGGLAGITEQQSGAFDRWEMIQAQEL\HNK
			LKIKQNLQQLNSDISAITTWLKKTEAELEMLKMAKPPSDIQEIE
	1		
	Ì		LRVKRLQEILKAFDTYKALVVSVNVSSKEFLQTESPESTELQSR
		İ	LRQLSLLWEAAQGAVDSWRGGLRQSLMQCQDFHQLSQNLLLWLA
			SAKNRRQKAHVTDPKADPRALLECRRELMQLEKELVERQPQVDM
			LQEISNSLLIKGHGEDCIEAEEKVHVI\EKKLKQLREQVSQDLM
•		'	ALQGTQNPASPLPSFDEVDSGDQPPATSVPAPRAKQFRAVRTTE
			GEEETESRVPGSTRPQRSFLSRVVRAALPLQLLLLLLLLLLACLL
		1	PSSEEDYSCTQANNF\ARSFYPMLRYTNGPPPT
6139	52	1131	LGDWVWSRTCGVLETPTSVLRRARARGPCPTDSKWALPRLREGE
			TERRPWEASSWKTL/LAGWIGGAASVIVGHPLDTVKTRLQAGVG
			YGNTLSCIRVVYRRESMFGFFKGMSFPLASIAVYNSVVFGVFSN
{			TQRFLSQHRCGEPKASPPRTLSDLLLASMVAGVVSVGLGGPVDL
		İ	IKIRLQMQTPPVSGRQPRFEVQGSGSCG\EPAYQGPVHCITTIV
		ļ	RNEGLAGLYRGASAMLLRDVPGYCLYFIPYVFLSEWITPEACTG
	ľ		PSPCAVWLAGGMAGAISWGTATPMDVVKSRLQADGVYLNKYKGV
			LDCISOSYOKEGLKVFFRGITVNAVRGFPMSAAMFLGYELSLQA
ļ	ì		IRGDHAVTSP
6140	694	136	RPELELWRLRSRSWRPLGVPRRCHRRNWKBPVRAQPLSVTVWAP
0140	1 334	150	RCORP/QPPAPEPSSPNAAVPEAIPTPRAAASAALELPLGPAPV
1			SVAPOAEAEARSTPGPAGSRLGPETFRQFRQFRYQDAAGPREA
Į.	1		FROLREL/SPROWLEPDI\RTKEQ\IVEMLVQEQLLAILPEAAR
		1	ARRIRRATOVRITG
			l
6141	2	984	AQVGPRSRPCKMPLKLRGKKKAKSKETAGLVEGEPTGAGGGSLS
		1	ASRAPARRLVFHAQLAHGSATGRVEGFSSIQELYAQIAGAFEIS
	ĺ		PSEILYCTLNTPKIDMERLLGGQLGLEDFIFAHVKGIEKEVNVY
			KSEDSLGLTITDNGVGYAFIKRIKDGGVIDSVKTICVGDHIESI
			NGENIVGWRHYDVAKKLKELKKEELFTMKLIEPKKAFEIELRSK
1			AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD
l			VLELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAFP
	}		DEFVFDVWGVIGDAKRRGL
6142	116	602	EAEGEQVCGAKCCGDAPHVENREEETARIGPGVMESKEERALNN
	1	1	LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR
			FRVRQPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMEKL
			REKQLSHSLRAVSTDPPHHDHHDEFC\LMP
6143	2802	270	FRMRIFLHCPWNQQMWKIWNLLETSLESCKAHLSIQKLLKER\Q
		1	\OLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED
			LLLNEWEASKCNIVCTOPRRISAVSLANRVCDELGCENGPGGRN
]		1	SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM
	1		FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE
			KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC
			QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK
	,		YSSRTOHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI
1			
			FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF
[			TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS
1			QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD
1			YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN
1			AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF
			GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL
1			TIYNAYLGWKKARQEGGYRSEITYCRRNFLNRTSLLTLEDVKQE

SEQ Predicted beginning nucleotide location nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seque
NO: nucleotide location corresponding corresponding to first amino acid residue of amino acid sequence
Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Correspondin
corresponding to first amino acid residue of amino acid residue of amino acid sequence S=Serine, T=Threonine, N=Asparagine, N=Dreine, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, N=Tryptophan, Y=Tyrosine, X=Unknown, *=Strine, S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quence S=Quenc
to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stopenstone amino acid sequence Codon, /=possible nucleotide deletion, '=possible nucleotide insertion)  LIKLVKAAGFSSSTTSTSWEGNRASQTLSFQEIALLKAVLVI YDNVCKI.YTKSVDVTEKI.ACIVETAQGKAQVHPSSVNRDLG GWLLYQEKIRYARVYLRETTLITPFFVLLFGGDIEVQHRERI IDGWIYFQAPVKIAVIFKQLRVLIDSVLRKKLENPKMSLENI LQIITELIKTENN  6144 1289 568 SGPGSMSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGF VSASGGARHGRGSGGPVICTYGPDLPPLVA\TIGAAFVAK VGDRTVTLGIWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDS FERAKFWVKELRSLEEGCQIYLCGTKSDLLEEDRRRRRVDFF QDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQW DKGVDLGQKPNPYFYSCCHH  6145 1109 196 GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEAGRGI GPMVYAICYCPLPRLADLEALKVADSKTLLESERERLFAKWH DFYGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYA QGYWYTQVVTVTVGMPETYQARLQOSFPGIEVTVKAKADALN VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDI
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=Stote Codon, /=possible nucleotide deletion, sequence LikuvkaAGFSSSTTSTSWEGNRASQTLSFQEIALLKAVLVI YDNVGKI!YTKSVDVTEKLACIVETAQGKAQVHPSSVNRDLG GWLLYQEKIRYARVYLRETTLITPFFVLLFGGDLEVQHRER; IDGWIYFQAPVKIAVIFKQLRVLIDSVLRKKLENPKMSLENI LQIITBLIKTENN  6144 1289 568 SGPGSMSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGFY VSASGGARHGGRGSGGPVICTYGPDLFPLVA\TIGAAFVAKV VGDRTVTLGIWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDS FERAKFWVKELRSLEEGCQIYLCGTKSDLLEEDRRRRVDFF QDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQVW DKGVDLGQKPNPYFYSCCHH  6145 1109 196 GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEAGRGI GPMVYAICYCPLPPLADLEBALKVADSKTLLESSERELFAKWM DFYGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYM QGYNVTQVTVTVGMPETYQARLQQSFPGIEVTVKAKADALN VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDI
residue of amino acid sequence    W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stephanino acid sequence   Codon, /=possible nucleotide deletion,    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide deletion,    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide deletion,    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide deletion,    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion)    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion)    -possible nucleotide insertion)    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion
residue of amino acid sequence
amino acid sequence Codon, /=possible nucleotide deletion,   =possible nucleotide insertion)
Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence
LIKLVKAAGFSSSTTSTSWEGNRASQTLSFQEIALLKAVLVI YDNVGKIIYTKSVDVTEKLACIVETAQGKAQVHPSSVNRDLQ GWLLYQEKIRYARVYLRETTLITPFPVLLFGGDIEVQHRERI IDGWIYFQAPVKIAVIFKQLRVLIDSVLRKKLENPKMSLENI LQIITELIKTENN  6144 1289 568 SGPGSMSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGP: VSASGGARHGGRGSGGPVICTYGPDLFPLVA\TIGAFVAKV VGDRTVTLGIWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDS FERAKFWVKELRSLEEGCQIYLCGTKSDLLEEDRRRRRVDFI QDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQVM DKGVDLGQKPNPYFYSCCHH  6145 1109 196 GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEAGRGI GPMVYAICYCPLPPRLADLEALKVADSKTLLESERERLFAKMI DFYGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYM QGYNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALM \VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDI
YDNVGKIIYTKSVDVTEKLACIVETAQGKAQVHPSSVNRDLQ GWLLVQEKIRYARVYLRETTLITPFPVLLFGGDIBVQHRERI IDGWIYFQAPVKIAVIFKQLRVLIDSVLRKKLENPKMSLENI LQIITELIKTENN  6144 1289 568 SGPGSMSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGPY VSASGGARHGGRGSGGPVICTYGPDLPPLVA\TIGAFVAKK VGDRTVTLGINDTAGSERYEAMSRIYYRGAKAATVCYDLTDS FERAKFWVKELRSLEEGCQIYLCGTKSDLLEEDRRRRRVDFI QDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQVM DKGVDLGQKPNPYFYSCCHH  6145 1109 196 GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEAGRGI GPMVYAICYCPLPPRADLEALKVADSKTLLESERERLFAKM DFYGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYM OGYNVTQVFVDTVGMPETYQARLQOSFPGIEVTVKAKADALM \VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDI
GWLLYQEKIRYARVYLRETTLITPFPVLLFGGDIEVQHRERI IDGWIYFQAPVKIAVIFKQLRVLIDSVLRKKLENPKMSLENI LQIITBLIKTENN  6144  1289 568 SGPGSMSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGP VSASGARHGGRGSGGPVICTYGPDLPPLVA\TIGAAFVAKV VGDRTVTLGIWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDS FERAKFWVKELRSLEEGCQIYLCGTKSDLLEEDRRRRVDFI QDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQVM DKGVDLGQKPNPYFYSCCHH  6145 1109 196 GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEAGRGI GPMVYAICYCPLPRLADLEALKVADSKTLLESERERLFAKMI DFYGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYA QGYNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALN \VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDI
GWLLYQEKIRYARVYLRETTLITPFPVLLFGGDIEVQHRERI IDGWIYFQAPVKIAVIFKQLRVLIDSVLRKKLENPKMSLENI LQIITBLIKTENN  6144  1289 568 SGPGSMSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGP VSASGARHGGRGSGGPVICTYGPDLPPLVA\TIGAAFVAKV VGDRTVTLGIWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDS FERAKFWVKELRSLEEGCQIYLCGTKSDLLEEDRRRRVDFI QDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQVM DKGVDLGQKPNPYFYSCCHH  6145 1109 196 GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEAGRGI GPMVYAICYCPLPRLADLEALKVADSKTLLESERERLFAKMI DFYGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYA QGYNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALN \VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDI
IDGWIYFQAPVKIAVIFKQLRVLIDSVLRKKLENPKMSLENI LQIITBLIKTENN  6144  1289  568  SGPGSMSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGP VSASGARHGGRGSGGPVICTYGPDLPPLVA\TIGAAFVAKV VGDRTVTLGIWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDG FERAKFWVKELRSLEEGCQIYLCGTKSDLLEEDRRRRRVDFI QDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQVM DKGVDLGQKPNPYFYSCCHH  6145  1109  196  GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEAGRGI GPMVYAICYCPLPRLADLEALKVADSKTLLESSRERLFAKMU DFVGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYM OGYNVTQVTVTVGMPETYQARLQQSFPGIEVTVKAKADALM \VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDI
LQIITELIKTENN  6144  1289  568  SGPGGMSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGPY VSASGGARHGGRGSGPVICTYGPDLFPLVA\TIGAAFVAKY VGDRTVTLGIWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDS FERAKFWVKELRSLEEGCQIYLCGTKSDLLEEDRRRRVDFY QDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQVW DKGVDLGQKPNPYFYSCCHH  6145  1109  196  GGMDLSELERDNTGRCRLSSPVPAVCRKBPCVLGVDEAGRGI GPMVYAICYCPLPRLADLEALKVADSKTLLESSRERLFAKWM DFYGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYX QGYNVTQVFVDTVGWPETYQARLQQSFPGIEVTVKAKADALX \VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDI
6144 1289 568 SGPGSMSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGPP VSASGGARHGGRGSGGPVICTYGPDLPPLVA\TIGAAFVAKY VGDRTVTLGIWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDS FERAKFWVKELRSLEEGCQIYLCGTKSDLLEEDRRRRRVDFY QDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQVN DKGVDLGQKPNPYFYSCCHH 6145 1109 196 GGMDLSELERDHTGRCRLSSPVPAVCRKEPCVLGVDEAGRGI GPMVYAICYCPLPRLADLEALKVADSKTLLESERERLFAKMI DFYGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYA QGYNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALX \VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDI
VSASGARHGGRGSGPVICTYGPDLFPLVA\TIGAAFVAKY VGDRTVTLGIWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDS FERAKFWVKELRSLEEGCQIYLCGTKSDLLEEDRRRRRVDFI QDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQVA DKGVDLGQKPNPYFYSCCHH 6145 1109 196 GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEAGRGI GPMVYAICYCPLPPLADLEALKVADSKTLLESERERLFAKMI DFVGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYA QGYNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALX \VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDI
VGDRTVTLGIWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDS FERAKFWVKELRSLEEGCQIYLCGTKSDLLEEDRRRRVDFI QDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQVN DKGVDLGQKPNPYFYSCCHH 6145 1109 196 GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEAGRGI GPMVYAICYCPLPRLADLEALKVADSKTLLESERERLFAKMI DFYGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYA QGYNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALX \VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDI
FERAKFWVKELRSLEEGCQIYLCGTKSDLLEEDRRRRRVDFT QDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQVM DKGVDLGQKPNPYFYSCCHH 6145 1109 196 GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEAGRGI GPMVYAICYCPLPPRLADLEALKVADSKTLLESERERLFAKMI DFVGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYA QGYNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALN \VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDI
FERAKPWVKELRSLEEGCQIYLCGTKSDLLEEDRRRRRVDFT QDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQVM DKGVDLGQKPNPYFYSCCHH 6145 1109 196 GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEAGRGI GPMVYAICYCPLPPLADLEALKVADSKTLLESERERLFAKMI DFYGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYA QGYNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALN \VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDI
QDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQVM DKGVDLGQKPNPYFYSCCHH  6145 1109 196 GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEAGRGI GPMVYAICYCPLPRLADLEALKVADSKTLLESERERLFAKMI DFYGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYX QGYNVTQVVVTVTVGMPETYQARLQQSFPGIEVTVKAKADALX \VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDI
DKGVDLGQKPNPYFYSCCHH  6145 1109 196 GGMDLSELERDNTGRCRLSSPVPAVCRKBPCVLGVDEAGRGI GPMVYAICYCPLPPRLADLEALKVADSKTLLESSRERLFAKMU DFVGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYX OGYNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALX \VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDI
6145 1109 196 GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEAGRGI GPMVYAICYCPLPRLADLEALKVADSKTLLESERERLFAKMI DFVGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQVI QGVNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALX \VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDI
GPMVYAICYCPLPRLADLEALKVADSKTLLESERERLFAKM DFVGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYX QGVNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALX \VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDI
DFVGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYA QGVNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALY \VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDI
QGVNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALY \VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDI
QGVNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALY \VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDI
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TOTAL CATALOGUE AND
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6146 428 781 LKKKGKEKAEAQQVEALPGPSLDQWHRSAGEEEDGPVLTDEC
R/YPGHEAHDQGG\WDARQSIIRKVVDPETGRTRLIKGDGEV
EIVTKERHREINKQATRGDCLAFQMRAGLLP
6147 1 2304 GTRQLPPPSPGSGPGDSPEGPEGEAPERRRKAHGMLKLYYGI
GEAAGRPAGPDPLDPTDLNGAHFDPEVYLDKLRRECPLAQIM
ETDMVRQIRALDSDMQTLVYENYNKFISATDTIRKMKNDFRK
DEMDRLATNMAVITDFSARISATLQDRHERITKLAGVHALLF
QFLFELPSRLTKCVELGAYGQAVRYQGRAQAVLQQYQHLPSF
IQDDCQVITARLAQQLRQRFREGGSGAPEQAECVELLLALGE
EELCEEFLAHARGRLEKELRNLEAELGPSPPAPDVLEFTDHO
SGFVGGLCQVAAAYQELFAAQGPAGAEKLAAFARQLGSRYFA
ERRLAQEQGGGDNSLLVRALDRFHRRLRAPGALLAAAGLADA
EIVERVARERLIGHHLQGLRAAFLGCLTDVRQALAAPRVAGKE
GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRG
CSQGVREGLIVGFVHSMCQTAQSFCDSPGEKGGATPPALLLL
RLCLDYETATISYILTLTDEOFLVQDQFPVTPVSTLCABARE
RRLLTHYVKVQGLVISQMLRKSVETRDWLSTLEPRNVRAVMK
VEDTTAIDVQVLPRLAGVALTQAGGTVPSRGAGAAEDHWQSL
GGDMCIWASHGASSVARASVREPQGNKSPRMNTKRAGECLCP
CSFSAQDYDIFAPILPVEKQRLRVTQEVRAGLVLVLKIRPQT
CILPLPHSTGSINSDHVPTK
6148 3056 353 VPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKR
KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPV
SYKAFSTRWNWNEWLKLPVKYPDLPRNAQVALTIWDVYGPGK
PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPG
SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMIN
VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDBSSPILTS
LVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPR
LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSV
DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAV.
LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSS
ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVP
ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRD.
THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVH
KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQ'
IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLR
QLILQIISLMDKLLRKENLDLKLTPYKYLATSTKHGFMOFIO
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Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   Libera   L	1			H=Histidine T=Isoleucine K-Lucine
to first amino acid residue of amino acid amino acid sequence    Periodine, Q-Glutamine, R-Arginine,   Sestine, T-Thireonine, V-Valine,   W-Tryptophan, Y-Tyrosine, K-Unknown, *=Stop   Codon, /=possible nuclectide deletion,   Possible nuclectide deletion,   Possible nuclectide deletion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible nuclectide timertion,   Possible	Ì	1		LeLeucine, Memethionine Newsparagine
### Amino acid residue of ### amino acid sequence ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino acid  ### amino ac			1	P=Proline, O=Glutamine P-Arginine
residue of amino acid sequence    N=Tryptophan, Y=Tyrocine, X=Unknown, *=Stop Coden, /=possible nuclectide deletion,  /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide insertion; /=possible nuclectide		1	1	
Sequence   Codon, /-possible nucleotide deletion,		residue of	1	
Nepossible nuclectide insertion			J ·	Codon. /=nossible nucleotide deletion
PVARVLDTGSTONFFRKYAPSENDINGISAEVMDTYVKSACY CVITYILGVGGRUKHPIDPGYTIGGDEKPLPPP MKLNKEMVEGMGGTGSEGYGEFRKGCYTAFHLIRAFSKILLIGAL SLAWDAN FDIALEDPUTVKKVOKYFHLLEDEAVHYMGALID ESVHALFAAVVEGIKFRAGVWEK  1 1413 PVDEFVREEMTAN FLOKRYSTAS KOOFTGKKTSVGGQVGKGND ESESDPESDPSPKSSEEERQDDEEVLOGEGGFINDDUTEPENL GERFLIMDSEDEEEEKHSSDDTGAAKNISMSSYVTRNSS GPTOOLDTILLITSAQLSSDVAVETPKGFEDVEAVKYFFAVRAGQ PQGSKRENLPORRFPAGAGSDVAVETPKGFEDVEAVKYFFAVRAGQ PQGSKRENLPORRFPAGAGSDVAVETPKGFEDVEAVKYFFAVRAGQ PQGSKRENLPORRFPAGAGSDVAVETPKGFEDVEAVFFAVRAGQ PQGSKRENLPORRFPAGAGSDVAVETPKGFEDVEAVFFAVRAGQ PQGSKRENLPORRFPAGAGSDVAVETPKGFEDVEAVFFAVRAGQ PQGSKRENLPORRFPAGAGSDVAVETPKGFEDVEAVFFAVRAGQ PQGSKRENLPORRFPAGAGSDVAVETPKGFEDVEAVFFAVRAGQ PQGSKRENLPORRFPAGAGSDVAVETPKGFEDVLSWFFAVRAGQ PQGSKRENLPORRFPAGAGSDVAVETPKGFEDVLSWFFAVRAGQ VGFBATTTGFTFAGAVYCHGSFSSADVETTAFFSKVAVVQCGT STKKTKFTTAFFAGATYCHGRAGSSSSSTETTSSEKDIS VALTDCKGGGNAVACHGFESTAGTTAFFSCATAVACA ALTICKGSVLANAVLIMLAQHALIATSSDLANAFGVCEFPWMDGND QEGGPPMGSBESTTDIDTSGIF FILMSVAGATATATAGAVCCEFPWMDGND QEGGPPMGSBESTTDIDTSGIF FILMSVAGATATATAGAVCCEFPWMDGND QEGGPPMGSBESTTDIDTSGIF FILMSVAGATATATAGAVCCEFPWMDGND QEGGPPMGSBESTTDIDTSGIF FILMSVAGATATATAGAVCCEFPWMACATATAGAVCCEFPWMDGND QEGGPPMGSBESTTDIDTSGIF KYTYAVTTROTOMPPTWESSEDDASLEHEARMALTAPPULDL REVYKHKKYKYLKXMAGKGAVYKPKEDTEFRATVQGAMCDL PRACASKAGATATATAGATAGAACATATAAAA ALATIALAFILLITAATALITATAATAATAAAAAAAAAAA		1		\=possible nucleotide insertion\
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KIYYYHUTROTOMDPPWESSGIDASLEHEARMDLGTPTYDEN PMK\ASKKPKTAEADTSSELAKKSKEVFRKEMSQFTVQCINPYR KPDCKVC\RITTTEDFKHLARKITHGVMNKBLKYCKNPE\DLEC NENVKHKTKEYIKYMQKFGAVYKPKEDTEFRVTVGPGWEDGWS GKTDSRERKSCGPPCSTPVSTVLINHHBGBFNPADVN GKTDSRERKSCGPPCSTPVSTVLINHHBGBFNPADVN  6152 1366 648 NRTWSTFSTMMGVALPPLCSTGPWPVTGOTTARTTCGAVPAKCP PWC/DVHEPRCQPPDCHGHGTCVDGHCQCTGHFWRGPGCDELDC GFSNCSOHGLCTETGCRCDAGWTGSNCSEECPLGWHGPGCORPC KCEHHCPCDPKTGNCSVSRVKQCLQPPEATLRAGELSFPTRTAW LALTLALAPLLLISTAANLSLLLSRAERNRRHGDYAYHPLQEW NGEPLAAEKEQPGGAHNPFKD  6153 2 3368 GRVGARSPGRAYALLLLICFNVGSGLHLQVLSTRNENKLLPKH PHLVRQKRAWITAPVALLEGEDLSKKNPIAKHSSLAEERGLKI TYKYTGKGITEPPFGIFVFNKDTGELNVTSILDREETPFFLLTG YALDARGNNVEKPLELRIKVLDINDNEPVFTQDVFVGSVEELSA AHTLVMKINATDADEPNFLNSKISYRIVSLEPAYPPVFLNKDT GEIYTTSVTLDREEHSSYTLTVEARDGNGEVTDKPVKQAQVQIR ILDVNDNIPVVENKVLEGMVEENQVNVEVTRIKVFDADEIGSDN WLANFTPASGNEGGYFHIETDAQTNEGIVTLIKEVDYEEMKNLD FSVIVANKAAPHKSIRSKYKPTPIPIKVNVKNVKSGIHFKSSVI SIVVSEMDRSSKGQIIGNFQAFDEDTGLPAHARYVKLEDRDNW ISVDSVTSEIKLAKLPDFESRYVQNGTYTVKIVAISEDYPPKTI TGTVLINVEDINDNCPTLIBEVQTICHDAEYVNVTAEDLDGHPN SGPFSFSVIDKPPGMAEKWKIARQESTSVLLQQSEKKLGRSEIQ FLISDNQGFSCPBKQVILTLTVCEVLHGS\GCREAQHDSYVGLGP AAALMILAPLLLLVPLLLLWCHGKGKAKGFTPIPGTIEMLPH WNNEGAPPEDKVVPSFLPVDQGGSLVGRNGVGGMAKEATMKGSS SASIVKGQHEMSEMDGRWEEHRSLLSGRATOFTGATGAI\MTTE TTITARATGASRDVAGAQAAAVALNEEFLKNYFTDKAASYTEED ENHTAKDCLLVYSQEETEESLNASIGCCSFIEGELDDRFLDDLGL KFKTLABVCLGQKIDINKEIFGQROKPATETSMYTASHSLCEQTM VNSENTYSSGSSFPVPKSLQEANAEKVTQEIVTERSVSRGAQK VATPLEDPMASRNVIATETSYVTGSTMPPTTVILGPSQPQSLIV				
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	L	L		TERVIAPASTLVDQPYANEGTVVVTERVIQPHGGGSNPLEGTQH

		1 5 13 15 1 2 2 3	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
l	ccdacase		LQDVPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL
		1	APASTLOSSYQIPTENSMTARNTTVSGAGVPGPLPDFGLEESGH
		Į.	SNSTITTSSTRVTKHSTVOHSYS
L		ļ	
6154	3660	2146	KKKTKMKNTLQKTVNFGAWPKPTISDKSHLLQMVSKLDLTDAKN
l	1	1	SDTAHIKSIEITSILNGLQASESSAEDSEQEDERGAQDMDNNGK
			EESKIDHLTNNRNDLISKEEQNSSSLLEENKVHADLVISKPVSK
1		ł	SPERLRKDIEVLSEDTDYEEDEVTKKRKDVKKDTTDKSSKPQIK
		1	RGKRRYCNTEECLKTGSPGKKEEKAKNKESLCMENSSNSSSDED
!			EEETKAKMTPTKKYNGLEEKRKSLRTTGFYSGFSEVABKRIKLL
		1	NNSDERLQNSRAKDRKDVWSSIQGQWPKKTLKELFSDSDTEAAA
i			SPPHPAPEEGVAEESLQTVAEEESCSPSVELEKPPPVNVDSKPI
ļ		1	EEKTVEVNDRKAEFPSSGSNFSA*IPLPYLHLNRLHQSL*QKGS
			ROOSSYTVSEPLAPNOEEVRSIKSETDSTIEVDSVAGELQDLQS
1		1	ERE*LASRF*CQCELEQ**SARTRTS*KSLYRSEKSERCSGRRK
			FIKKAEKKP*SNSGKQQKEGK
6155	869	121	HLLPELRGKSWITMKYVFYLGVLAGTFFFADSSVQKEDPAPYLV
	1	ı	YLKSHFNPCVGVLIKPSWVLAPAHCYLPNLKVMLGNFKSRVRDG
	1	1	TEQTINPIQIVRYWNYSHSAPQDDLMLIKLAKPAMLNPKVQALN
ì	1		P\PTTNVRPGTVCLLSGLDWSQENSGRHPDLRQNLEAPVMSDRE
	Ì	i	CQKTEQGKSHRNSLCVKFVKVFSRIFGEVAVATVICKDKLQGIE
1	1		VGHFMGGDVGIYTNVYKYVSWIENTAKDK
6156	5725	3984	GTSTVTMATKKHFSIILNLLGMLLKKDNQDTRKLLMTWALEVAV
0250			VMKKSETYAPLFCLPSFHKFCKGLLADTLVEDVNICLQACSSLH
1	1		ALSSSLPDDLLQRCVDVCRVQLVHRGTCIRQAFGKLLKSIPLGV
ŀ	1 -	·	FLSNNNHTEIQEISLALRSHMSKAPSNTFHPQDFSD/VISFILY
i	}		GNSHRTGKDNWLERLFYSCQRLDKRDQSTIPRNLLKTDAVLWQW
	1	ļ	AIWEAAQFTVLSKLRTPLGRAQDTFQTIEGIIRSLAGHTLNPDQ
	1	i	
1	}		DVSQWTTADNDEGHGNNQLRLVLLLQYLENLEKLMYNAYEGCAN
1	1	ļ	ALTSPPKVIRTFLYTNRQTCQDWLTRIRLSIMRVGLLAGQPAVT
1			VRHGFDLLTEMKTTSLSQGNELEVSIMMVVEALCELHCPEAIQG
1		ł	IAVWSSSIVGKHLLWINSVAQQAEGRFEKASVEYQEHLCAMTGV
1			DCCISSFDKSVLTLASAGCKSASLKHCLNGESRKSVLSKPTDSS
l			PEVINYLGNKACECYISTADWAAVQEWQNAIHDLKKSTSSTSLN
		1	LKADFNYIKSLSSFESGKFVECTEQLELLPGENINLLAGGSKEK
			IDMKKLLRNM
6157	946	329	MANRGPSYGLSREVQEKIEQKYDADLENKLVDWIILQCAEDIEH
0237	7.50	1 22	PPPGRAHFQKWLMDGTVLCKLINSLYPPGQEPIPKISESKMAFK
1		1	OMEQISQFLKAAETYGVRTTDIFQTVDLWEGKDMAAVQRTLMAL
		1	GSVAVTKDDGCYRGEPSWFHRKAQQNRRGFSEEQLRQGQNVIGL
			QMGSNKGASQAGMTGYGMPRQIM*DAASCP
6158	441	1482	LGSLIVLSLHCKVIFSSQSLERAMKEKAVDLVPILAQNPGLAQN
		1	PILEGKDHNQNTGVDPIIDHVQDRKTD/SRSKSPHKKRSKSRER
İ			RKSRSRSHSRDKRKDTREKIKEKERVKEKDREKEREREKEREKE
			KERGKNKDRDKBREKDREKDKEKDREREREKEHEKDRDKEKEKE
1			QDKEKEREKDRSKEIDEKRKKDKKSRTPPRSYNASRRSRSSSRE
			RRRRRSRSSSRSPRTSKTIKRKSSRSPSPRSRNKKDKKREKERD
İ			HISERRERERSTSMRKSSNDRDGKEKLEKNSTSLKEKEHNKEPD
1			SSVSKEVDDKDAPRTEENKIQHNGNCQLNEENLSTKTEAV
6159	53	84	AVIAPLHISLGDRARPYLKNTEKSSTTCSRRRNQSFPPVMSLTH
0123	33 .	"	RLHLCKYWGCAVSNVCRFWEGRPLPLMIVVPYTLPVSLPVGSCV
			IITGTPILTFVKDPQLEVNFYTGMDEDSDIAFQFRLHFGHPAIM
			NSCVPGIWRYEEKCYYLPFEDGKPFELCIYVRHKEYKVMVNGQR
1			IYNFAHRFPPASVKMLQVFRDISLTRVLISD*GRCVRITAVQEF
			DVSVSCDCTTAYQPG
6160	1626	1790	AGAKPFP*F*KVADAQPTESEKEIYNQVNVVLKDAEGILEDLQS
			YRGAGHEIREAIQHPADEKLQEKAWGAVVPLVGKLKKFYEFSQR
l			TOTAL TANKEN TO THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF TH

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1 1			
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1 1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LEAALRGLLGALTSTPYSPTQHLEREQALAKQFAEILHFTLRFD
j			ELKMTNPAIQNDFSYYRRTLSRMRINNVPAEGENEVNNELANRM
Ì			SLFYAEATPMLKTLSDATTKFVSENKNLPIENTTDCLSTMASVC
1			RVMLETPEYRSRFTNEETVSFCLRVMVGVIILYDHVHPVGAFAK
			TSKIDMKGCIKVLKDQPPNSVEGLLNALRYTTKHLNDETTSKOI
ł i			KSMLQ*QLLTLVNKG
6161	455	1660	
9191	455	1569	PVSGSESSLRRAWASILRLMLGPRVAVSILCEDGISH*LLEKH*
l i			KSHVLEPLSSLALEBQCLALSLDWSTGKTGRAGDQPLKIISSDS
i			TGQLHLLMVNETRPRLQKVASWQAHQFEAWIAAFNYWHPEIVYS
			GGDDGLLRGWDTRVPGKFLFTSKRHTMGVCSIOSSPHREHILAT
		ĺ	GSYDEHILLWDTRNMKQPLADTPVQGGVWRIKWHPFHHHLLLAA
			CMHSGFKILNCQKAMEERQEATVLTSHTLPDSLVYGADWSWLLF
			RSLQRAPSWSFPSNLGTKTADLKGASELPTPCHECREDNDGEGH
			ARPQSGMKPLTEGMRKNGTWLQATAATTRDCGVNPEEADSAFSL
1 1		ł	LATCSFYDHALHLWEWEGN
6162	1	586	RTIHATGRAGASPMHRLIVWRLAEANKOHVRCOKCLEFGHWTYE
	_		CTGKRKYLHRPSRTAELKKALKEKENRLLLOOSIGETNVERKAK
į į		ļ	KKRSKSVTSSSSSSDSSASDSSSESEETSTSSSSEDSDTDESS
1			SSSSSASSTTSSSSSDSDSDSSSSSKQ*HQHR*QL*R*TTKEE
		1	
			EKEIELLHSYWTDGLKTLM
6163	1081	785	RIRSTTEGCAVRLHPTQNTGKARIMILLSVSLGRHWAFTYKFFL
		i	TPVVFVFFFFFFHRKE*VMQKNPMKSREDEWMEKLNNLHVQRAD
			MNRLIMNYLVTEGFKEAAEKFRMESGIEPSVDLETLDERIKIRE
1			MILKGQIQEAIALINSLHPELLDTNRYLYFHLQQQHLIELIRQR
ŀ			ETRAALEFAQTQLAEQGEESRECLTEMERTLALLAFDSPEESPF
		[	GDLLHTMQRQKVWSEVNQAVLDYENRESTPKLAKLLKLLLWAQN
}			ELDQKKVKYPKMTDLSKGVIEEPK
6164	90	406	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKKR
	-		SCISRTAPRLLCTLEPGVDTKLKFTLEPSLGONGFOOWYDALKA
i			VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFTFNERS
		i	NPDDDSMGIQIVKDLHRTGCSSYCGQEAEQDRVVLKRVLLAYAR
Į l			WNKTVGYCQGFNILAALILEVMEGNEGDALKIMIYLIDKVLPES
1			
			YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTANKESGG
			GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL
1		i	RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSHE
1	<b>\</b>	1	LMQTVYSMAPFPFPQLAELREKYTYNITPFPATVKPTSVSGRHS
1 1			KARDSDEENDPDDEDAVVNAVGCLGPFSGFLAPELQKYQKQIKE
1			PNEEQSLRSNNIAELSPGAINSCRSEYHAAFNSMMMERMTTDIN
			ALKRQYSRIKKKQQQQVHQVYIRADKGPVTSILPSQVNSSPVIN
1	1	1	HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVPYEDLKTKLNS
1			PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEQNEASKTNGLGAA
1			EAFPSGCTATAGREGSSPEGSTRRTIEGOSPEPVFGDADVDVSA
1	i		VQAKLGALELNQRDAAAETELRVHPPCQRHCPEPPSAPEENKAT
1			SKAPQGSNSKTPIFSPFPSVKPLRKSATARNLGLYGPTERTPTV
1			HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEYORN
1			_ = _ /
63.65			GGERFG
6165	90	406	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKKR
1			SCISRTAPRLLCTLEPGVDTKLKFTLEPSLGQNGFQQWYDALKA
1			VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFTFNERS
1			NPDDDSMGIQIVKDLHRTGCSSYCGQEAEQDRVVLKRVLLAYAR
1 .	[		WNKTVGYCQGFNILAALILEVMEGNEGDALKIMIYLIDKVLPES
1	1		YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTANKESGG
1		1	
1			GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL
1			17
,			RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSHE
			17

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NO:	SEQ			
Cortisponding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffreshonding   Coffr		1 2		
to first amino acid residue of amino acid residue of amino acid sequence  Perfoline, G-Glutamine, R-Augharne, Seserine, T-Threonine, V-Valine, amino acid sequence  W-Trytpothan, Y-Trytosine, V-Unknown, *-Stop Codon, /-possible nucleotide deletion, \possible nucleotide insertion)  PNEEDSLESSINIAELSPOAINSCRSETHARNSHMMERHYTDIN ALKROYSRIKKKOQOVAIQVIRADKOWTSILPSOWDISSPVIN HILLIKKMMKNINRAAKNAYIHIPGKTOSKISPVYEDLATKIANS PHRTHIRVHKKMMERHYKSHOCODTVUCLIDEQNEASYIKTSIGGAA EAPPSGCTATAGREGSSPEGSTRRTIEGGSPEVYGDADVDVSA VOAKIGALEINGRAAMTSILAVIPGKTOSKISPVYEDLATKIANS SKAPQOSNISKTIFSSPSVKEHKRSATARNICHIGYPTERTPTV HFPONSRSFSKFSGGOSSP-KWYESSGTHARNSHVANGLOGAN SKAPQOSNISKTIFSSPSVKEHKRSATARNICHIGYPTERTPTV HFPONSRSFSKFSGGOSSP-KWYESSGTHARNSHVANGLOGAN SKAPQOSNISKTIFSSPSVKEHKRSATARNICHIGYPTERTPTV HFPONSRSFSKFSGGOSSP-KWYESSGTHARNSHVANGLOGANIT SULPHAPVARQUSAHRRIKATIVEVANGCOSHITERGPETTY GERKAMIGDFEVTGFTAVNICYGRHERIMMINYSINGARIFIKTSHIPSVODINTSTYTM BEGNICHHVPROTOFGRIAVNICYGRHERIMMINYSINGARIFIKTSHIPSVODINTSTYTM BEGNICHHVPROTOFGRIAVNICYGRHERIMMINYSINGARIFIKTSHIPSVODINTSTYTM BEGNICHHVPROTOFGRIAVNICYGRHERIMMINYSINGARIFIKTSHIPSVODINTSTYTM BEGNICHHVPROTOFGRIAVNICYGRHERIMMINYSINGARIFIKTSHIPSVODINTSTYTM BEGNICHHVPROTOFGRIAVNICYGRHERIMMINYSINGARIFIKTSHIPSVODINTSTYTM BEGNICHHVPROTOFGRIAVNICYGRHERIMMINYSINGARIFIKTSHIPSVODINTSTYTM BEGNICHHVPROTOFGRIAVNICYGRHERIMMINYSINGARIFIKTSHIPSVODINTSTYTM BEGNICHHVPROTOFGRIAVNICYGRHERIMMINYSINGARIFIKTSHIPSVODINTSTYTM BEGNICHHVPROTOFGRIAVNICYGRHERIMMINTSHIPSVODINTSTYTM BEGNICHHVPROTOFGRIAVNICYGRHERIMMINTSHIPSVODINTSTYTM BEGNICHHVPROTOFGRIAVNICYGRHERIMMINTSHIPSVODINTSTYTM BEGNICHHVPROTOFGRIAVNICYGRHERIMMINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIPSVODINTSHIP	NO:			
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residue of amino acid sequence  amino acid sequence  Codon, '-possible nucleotide deletion, '-possible nucleotide deletion, '-possible nucleotide deletion, '-possible nucleotide deletion,'  PRESSIGERSHINELEPGAINSCRSE PHARANSHMMERMYTDIN ALKROYSRIKKKOQOVIQVYTRADKOPYTSILPSONSSPVIN HILLICKKMCHTMRANANVIHTPERTORISTSPYPYEDLATKINS PHATHIRVHKKNMPRYKSHPOCODTVCLIDEOMERSKTHOLGAN BAPPSGCTATAGRESSPESTRENTER IEOSPESVPOLDATVINS SPRENKAT SKAPOGOSNKTFISPSPSPSVELERKERARNSHMOODAVDVS-NUCKLGALELMORDAAASTELRVHPPOGHFCPFPSAPEERKAT HIPPOMSRSFSKROGGOSNKTFISPSPSVELERKARTARNLGLIGOPTRETTY HIPPOMSRSFSKROGGOSNKTPSPSVELERKARTARNLGLIGOPTRETTY HIPPOMSRSFSKROGGOSNGF*NWVFSSGTMLSRQLPGYPQEYORN GGERTO COMMENT OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATEMAN OF THE PROMISE STATE				
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Appossible nucleotide insertion	1			
PNEOSLESNITABLISFORINSCRSEYHALPISMMERNITUR ALKRYSRITAKUQQQVQHQVI YARDKQFYSTILENGSVONSSPVIN HLLLGKKMMTHRARNAVIHIPOHTOGKI SPVPYEDLKTKINS PHETHIRVHKUMPHTSKIPHOGDTYGLIBONARSTGIGAA BAPPSCCTAYAGROSS PROSTRETT EGGJSPEPVFODADVDVSA VQAKLGALEINQRDAAAETELRVEPPCQRICCEPPSPEEVKAT SKAPQOSNSKIT I FSP FP SVRURIKSATARNILGLYGPTERTPTV HFPQMSRSFSKPGGGNSGP * NOVESSGTHLSRQLPGYPQEPCRYC GGSRG  6166 2 1206 HKLMETVAKAGAEWSLEECLEKHLPLPDLQEVKRVLYGSKELRK LDLPEARFARASREDFELGVAFFACAGAECHERIUNGVON IPLPANARVAGOVSALHRI KATVEVAAMGOVII I CPGBAWHP PACTTEELLPHTERASBADDGTHRPLOKVAFTUGUNGN IPLPANARVAGOVSALHRI KATVEVAAMGOVII I CPGBAWHP PACTTEELLPHTERASBADDGTHRPLOKUMPUVSPILE RDSEHIDDVLNNTAVUTISNSGAVLGKTRINHI PRVODENSSTYM BGNLGHPVFOTOPGRILVANI CYGRHIPLANIAVIS INSGALIGKTRINHI PRVODENSSTYM BGNLGHPVFOTOPGRILVANI CYGRHIPLANIAVIS INSGALIGKTRINHI PRVODENSSTYM BGNLGHPVFOTOPGRILVANI CYGRHIPLANIAVIS INSGALIGKTRINHI PRVODENSSTYM BGNLGHPVFOTOPGRILVANI CYGRASSTOFIGLSSRIDGLUARLDI. NLCQOVINDVANFKMTGRYEMYARELABAVSSNYSPTIVKEY PAS VPALIG 6167 1220 1844 YGTVTOPELCAGDKOPKKOEKNPVLVSPEYODALCACEEYIS. LAHMDIDDCLEAPLYLTYPESWSLEPLGYPVOVHEGAELBHLDTO VQSCEDILOOLOAVYPOIDMSCORIN IN VKGGAKSGRGINGM HLERMIKLIVAGDPVMDCKWVVVS Y ISPILLI FORTFOLLOOW HLERMIKLIVAGDVMDCKWVVV I SPILLI FORTFOLLOOW HLERMIKLIVAGDVMDCKWVVV I SPILLI FORTFOLLOOW UVCKVI SEPILLI POTKYDLINGRACH SIENDAV TORTFOLLOOW UVCKVI SEPILLI POTKYDLINGROUN TORTFOLLOOW UVCKVI SEPILLI POTKYDLINGROUN TORTFOLLOOW VORKUM BERKKEPKTOTUCKIFILEAI ENNINGMPWUVGGGGOI CMYRAKI BARKKEPKTOTUCKIFILEAI ENNINGMPWUVGGGGOI CMYRAKI BARKKEPKTOTUCKIFILEAI ENNINGMPWUKGGGGOT CMYRAKI BARKKEPKTOTUCKIFILEAI ENNINGMPWUKGGGOOT CMYRAKI BARKKEPKTOTUCKIFILEAI ENNINGMPWUKGGGOOT CMYRAKI BARKKEPKTOTUCKIFILEAI ENNINGMPWUTGGGOOT CMYRAKI BARKKEPKTOTUCKIFILEAI ENNINGMPWUTGGGOOT CMYRAKI BARKKEPKTOTUCKIFILEAI ENNINGMPWUTGGGOOT CMYRAKI BARKKEPKTOTUCKIFILEAI ENNINGMPWUTGGGOOT CMYRAKI BARKKEPKTOTUCKIFILEAI ENNINGMPWUTGGGOOT CMYRAKI BARKKEPKTOTUCKIFILEAI ENNINGMPWOTKHELDAT BARKKEPKTOTUCKIFILEAI ENNINGMPWOTKHELDAT BEGGLEREEDEN NEGETVAPKVUTLEMBRATCHOOT VORCHELDANDATISCH TYLLOON SA	l		sequence	
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HPPOMSRSPSKPGGNSGP*MVFSSGIMLSRQLPGYPQEYORN GGRRFG  6166  2 1206  HKIMETVAMAGAEWKSLEECLEKHLPLPDLQEVKRVLYGKELRK LDLPRRAPEAASREDPBLQGYAPRAABEQLERPRILYHGUVQRR IPLPANAPVAGQVSALHRRIKAIVEVAMAGOVII ICPQEAWTHP PACTTEKLPHTEPABSAEDGPTTRCCKLAKHHDWVVSFILE RDSHENDVLHMTAVVISSAGAVLGKTRRINVGYGHHPDESTYYM EGNLGHPVFQTQFGRTAVNICYGRHPLNWIMYSINGBEITFN SATIGALGSESUPIERANAATANICCTGCHHPLNWIMYSINGBEITFN GDKKAHQDFGYFYGSSVVAAPDSSRTPGLSRSRDGLLVASLDL NLCQQVNDVWHFWTGRYEWYARPLAEAVKSNYSPTIVKE*PAS VPALG  6167  1220  1844  YGIVTGPSLCAGDKQPKKQEKNPVLVSPEFVDEALCACEEYLSN LAHMDIDKDLEAPLYLTFEGMSLFLCRYYQVVHEGAERHLDTQ VQRCEDILQQLQAVVQQIDMSGORNINIVKGGAKSRGINCHD HLEEMIKLIVANOPVVWKGDKWVQKYIERPLLIFGTKFDLEQW LVTDWHPLTVWFYRBSYTRFSTQPFSLKNLDK*APLYLTFEGMS LFPLGRYGVVYEGGAERHLDTQOVCCGDLQAVVQDIDMSG DRNINIVKRGAKSRGGIMCMDHLEEMIKLUNGNPVVWKDGKWV VQXYIERPLLIFGTKFDLRQWFLVTDWHPLTVFFYRDSYIRFST QPFSLKNLDK VQXYIERPLLIFGTKFDLRQWFLVTDWHPLTVWFYRDSYIRFST QPFSLKNLDK VQXYIERPLLIFGTKFDLRQWFLVTDWHPLTVWFYRDSYIRFST QPFSLKNLDK  6168  84  1392  WWFVFSVSAMPFKKOQAGGGSKKAEQKKKEKIIEDKTFFEKNKK GARKQKFIKAATHQVKFGQGNPRQVAQSEAEKKLKKDDKKKELQ ELNELFKPVVAAQKISKGADPKSVVCAFFKQGCTKGGKKKFELG ELNELFKPVVAAQKISKGADPKSVVCAFFKQGCTKGGKKKFELG ELNELFKPVVAAQKISKGADPKSVVCAFFKQGCTKGGKKKFELG DLTLERKCEKRSYVIDARBEELBKDTMDNVKKHGELEDVNTKHG EAEKKPKTQTVCKHFLBAIENNKVGWFWVCPGGGICMYRHAL PDGFVLKKKKKKKKENSIS.SI-DLIERERSALGFNVTKITLESP LAWKKKRQEKIDKLEGDMERRKADFKAGKALVISGRSVFEFRR ELVNDDEEADDTRYTQCTGGDEVDDSVSVDIDLISLSYIPEFRR ELVNDDEEADDTRYTQCTGGDEVDDSVSVDIDLISLSYIPEFRR ELVNDDEEADDTRYTQCTGGDEVDDSVSVDIDLISLSYIPEFRR ELVNDDEEADDTRYTQCTGGDEVDDSVSVDIDLISLSYIPEFRR ELVNDDEEADDTRYTQCTGGDEVDDSVSVDVIDLISLSYIPEFRR ELVNDDEEADDTRYTQCTGGDEVDDSVSVDVDIDLSLSYIPEFRR ELVNDDEEADDTRYTQCTGGDEVDDSVSVDVDIDLSLSYIPEFRR ELVNDDEEADDTRYTTQCTGGDEVDDSVSVDVDIDLSLSYIPEFRR ELVNDDEEADTRYTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT		İ		
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1206   HKLWERVARGABEWSLEECLEKHLELDDLGEVERVLYGKELEK   LDLPRABPEABSREDFELGGYAPRABEOLER PILVYGKELEK   LDLPRABPVARGVSALHARIKAIVEVAMCGVNII CPÇBAWTHP   FAPCTEEKLPHTEFABSAEDDPTTRECKLAKHHDWVSFILE   RDSEHDUYLMTAVVISSAGAVLGKTRKMINEVGSTEESTYM   EGNLGHPVFOTOPGRIAVNICYGRHEPLNMIMYSINGABITFN   SATIGALGSESWPIEARNAATANHCETCAMVETSHEPNEFTS   GDGKKAHQDFGYFYGSSYVAAPDSSRTPGLSRSRDGLLVAKLDL   NLCQQVNDVMFFKMTGRYEMYARELABAVKSNYSPTIVKE* PAS   VPALG   VPALG   VPALG   VPALG   LAMMDIDKOLBEPLYLUTPEGMSJFLORTYQVVIEGGACEEYLSN   LAMMDIDKOLBEPLYLUTPEGMSJFLORTYQVVIEGGACEEYLSN   LAMMDIDKOLBEPLYLUTPEGMSJFLORTYQVVIEGGACEEYLSN   LAMMDIDKOLBEPLYLUTPEGMSJFLORTYQVVIEGGACEEYLSN   LAMMDIDKOLBEPLYLUTPEGMSJFLORTYQVVIEGGACEEYLSN   LAMMDIDKOLBEPLYLUTPEGMSJFLORTYQVVIEGGACEEYLSN   LAMMDIDKOLBEPLYLUTPEGMSJFLORTYQVVIEGGACEEYLSN   LAMMDIDKOLBEPLYLUTPEGMSJFLORTYQVVIEGGACEEYLSN   LAMMDIDKOLBEPLYLUTPEGMSJFLORTYQVVIEGGACEEYLSN   LAMMDIDKOLBEPLYLUTPEGMSJFLORTYQVVIEGGACEEYLSN   LAMMDIDKOLBEPLYLUTPEGMSJFLORTYQVVIEGGACEEYLSN   LAMMDIDKOLBEPLYLUTPEGMSJFLORTYQVVIEGGALRHIDTQVQRCEDILQQUQAVVPQIDMBG   DRININIVKEGASKSRGGIMCMDPVVIEGGABURTUNDFVVIEGGAB   LAMMDIDKOLBEPLYLUTPEGMSJFLORTYQVIEGGABURTUNDFVVIEGGABURTUNDFVVIEGGABURTUNDFVVIEGGABURTUNDFVVIEGGABURTUNDFVVIEGGABURTUNDFVVIEGGABURTUNDFVVIEGGABURTUNDFVVIEGGABURTUNDFVVIEGGABURTUNDFVVIEGGABURTUNDFVVIEGGABURTUNDFVVIEGGABURTUNDFVVIEGGABURTUNDFVVIEGGABURTUNDFVVIEGGABURTUNDFVVIEGGABURTUNDFVVIEGGABURTUNDFFTELMSTALLUTGBEVDFFFR   LAMKKKRKGBEISL*POLVERHAG   SAEKKPKTQVIVCHHELASINNIVGAWFWVOEGGGGICMYRHALL   PPGGVUKKKKKKKKKKKKKKBGBISL*POLVERHAGABURTUTABSELFATULDLEE   LAMKKKRKGBEIDAVPUDEBLITFGGELDELBEERSCHLEEDN   ETGITVASLERFSTYTSDKDRNKLSBASGGABNGSGBLEEDN   LAMKKKRKGBEIDAVPUDEBLITFGGELDTEBEBERSLITBLEEN   LAMKKKRKGBEIDAVPUDEBLITFGGELDTEBEBERSLITBLEEN   LAMKKKRKGBEIDAVPUDEBLITFGGELDTEBEBERSLITBLEEN   LAMKKBRGGABURTUNDFVATTAT   LAMKKBRGGABURTUNDFVATTAT   LAMKKBRGGABURTUNDFVATTAT   LAMKKBRGGABURTUNDFVATTAT   LAMKKBRGGABURTUNDFVATTAT   LAMKKBRGGABURTUNDFVATTAT   LAMKKBRGGABURTUNDFVATTAT   LAMKKBRGGABURTUNDFVATTAT   LAMKKBRGGABURTUNDFVATTAT   LAMKKBR		1	}	
LDLPRAYPASERDPELQYAPRAAECLIRREITUHQUVQNR IPLDANAPVAGVOSALHRIKAIYUEVAAMCOVNI I CPQEAMTMP PAPCTREKLWWTEPAESAEDGPTTRPCQKLAKNHDMVVVSPILE RDSEHGDVLMNTAVVISNSGAVIGKTRKNHIP RVGOFRESTYYM EGKIGHPVOTQ GRITAVHI CYGRHPLWHMIMTS INGAE II FMP SATIGALESSLW PI EARNAAIANHCTCAINRVGTHEPREFTS GDCKKAHQDFGYFYGSSTVAAPADDSSRTDGLSRSKDGLLVAKLDL NLCQQVIDVWMFKMTGRYEMYARELAEAVKSNYSPTIVES + PAS VPALG  6167  1220  1844  YGIVTGPSLCAGDXQFKKQEKNPVLVSPEFVDEALCACEEYLSN LAHMDIDKDLEAPLYLTFEGMSLFLQRYYQVVEGGERHIDTO VQRCEDILQOLQAVVPQ IDMEGRNINIVKGGAKSRGKGIMCMD HLEEMIKKLVNGNPVVMKDGKWVQKY I ERPLLI FGTKFDLEQWF LVTONWPLTVHYFYRDSY I FSTQP FSLKNOPAPLYLTFEGMS LFLQRYYQVVEGGELRHIDTOVACCEDILQOLQAVVPQ IDMEG DRNIN VIXEARASRGGGIMCHDHEMKLKAPAPLYLTFEGMS LFLQRYYQVVEGGELRHIDTOVACCEDILQOLQAVVPQIDMEG DRNIN VIXEARASRSGGGIMCHDHEMKLKAPAPLYLTFEGMS LFLQRYYQVVEGGELRHIDTOVACCEDILQOLQAVVPQIDMEG DRNIN VIXEARASRSGGGIMCHDHEMKLKAPAPLYLTFEGMS LFLQRYYQVVEGGABRHUNTOVACCEDILQOLQAVVPQIDMEG DRNIN VIXEARASRSGGGIMCHDHEMKLKAPAPLYLTFEGMS LFLQRYYQVVEGGABRHUNTOVACCEDILQOLQAVVPQIDMEG DRNIN VIXEARASRSGGGIMCHDHUNTOVATYPORY YRDSYIRFST QPFSLINNLDK GAKQNFIKAVTHQVKFQGQDMRQVAQSEAKKIKKOKNDVAMCKWW VQXYIERPLLIFGTKFDLRQWFLVTDWNPYTMDYYRDSYIRFST QPFSLINNLDK GAKQNFIKAVTHQVKFQGQMPRQVAQSEAKKIKKOKKKE GAKQNFIKAVTHQVKFQGQMPRQVAQSEAKKIKKOKKKE EARKKKRYKTQIVCKHFLEAIENNNYCHPWCGGGGICMYMFHGL PPGFVLKKKKKKKKKKKBGISI-DLIERERSALGPNVTKITLESF LAMKKRXQERIDKLEQDMERRKADF KAGKALVISGRSFFFRR ELVNDDZEBADDTRYTQGTGGDEVDDSYVQTDILGLIVITRDVD STGITVASLERFSTYTSDKDENKLISASGGRANGRSGLEEN ERGSTENGAIDAVPUDENLIFTGGEDEDLISEENVTDLEEN ERGSTENGAIDAVPUDENLIFTGGEDEDLISEENVTDLEEN ERGSTENGAIDAVPUDENLIFTGGEDLDEISEENTIDLEEN ERGSTENGAIDAVPUDENLIFTGGEDLDEISEENTIDLEEN PREGTEMGAIDAVPUDENLIFTGGEDLOSEENTIDLEEN PREGTEMGAIDAVPUDENLIFTGGEDLOSEENTIDLEEN PREGTEMGAIDAVPUDENLIFTGGEDLOSEENTIDLEEN PREGTEMGAIDAVPUDENLIFTGGEDLOSEENTIDLEEN PREGTEMGAINFYGENTAVCHLIFTGGELDSCHEENTIDLEEN PREGTEMGAINFYGENTAVCHLIFTGGELDSCHEENTIDLEEN PREGTEMGAINFYGENTAVCHLIFTGGELDSCHEENTIDLEEN PREGTEMGAINFYGENTAVCHLIFTGGELDSCHEENTIDLEEN PREGTEMGAINFYGENTAVCHLIFTGGELDSCHERATORTQCCGGRAVAV PRAKKTERED				
IPLDAMAPVASQUSALHRIKATIVEVAAMGGVNII CFGEAWTHP FAPCTREKLPWTEFAESAEDGPTTFFCQKLANHDMUVVSPILE RDSEHDDVLMNTAVVISNSGAVLGKTRKNHIPRVGDFNESTYYM EGNEGHDVLMNTAVVISNSGAVLGKTRKNHIPRVGDFNESTYYM EGNEGHPVEQTGGRIAVNICVGRHHPLANHLMYSINGAEIIFMP SATIGALSESLW PIEARMAAIANHCTARWGTEHPEFFS GDGKKAHQDFGYFYGSSYVAAPDSSRTGGLSRSRDGLLVAKLDL NLCQQVMDUWNFKHTGRYEMYARELAEAVKSNYSPTIVKE*PAS VPALG  6167 1220 1844 YGTVTGPSLCAGDKQPKKQEKNPVLVSPEFVDEALCACEEYLSN LAHMDIDKDLEAPLYLTPEGWSLFLQRYYQVVHEGAELRHLDTO VQRCEDILQQLQAVPQUDMEGGRINIVVKFGAKSRGRGIMCMD HLEEMLKLUNGNPVVMADGKWVVQKYFLLIFTGKFDLINGFKGHLGHTDTO VQRCEDILQQLQAVVPQUDMEG DRNINIVKRGAKSRGRGIMCMD HLEEMLKLUNGNPVVMKDGKWVVQKYFLDILIFGTKFDLINGFK DLAVLTPEGWS LFLQRYYQVVHEGAELRHLDTO VQRCEDILQQLQAVVPQUDMEG DRNINIVKRGAKSRGRIMCMD VQXYIERPLLIFGTKFDLAVPOLUMBE DRNINIVKRGAKSRGRIMCMD LEWHLKLUNGNPVVMKDGKWV VQXYIERPLLIFGTKFDLRQWFLVTDWNPLTWFYRDSYIRFST QFFSLINLDK  6168 84 1392 WWFVPSVSAMPPKKQAQAGSKKAEQKKKEKI IEDKTFGLINKK GAKQOKFI KANTHOWKSGQNRGRQVAQSAEAKKLKEUDKKKELQ ELNELFFRVVAAQKISKGADPKSVVCAFFKQQCTKGDKCKFSH DLTLEKKCKKSVYIDARDEELEKUTMDNNDEKKLEVVKKRIG EARKKKEKFTQTVCKHIFLEAIENNKYMGPWVCPGGGDICMYKHALD PPGFVLKKKKKKKKEBEISL*DLIERESALGPBVTKITLESF LAMKKRRGEKIDKLEGDMERRKADFWWVCFGGGDICMYKHALD PPGFVLKKKKKKKKKEBEISL*DLIERESALGPBVTKITLESF LAMKKRRGEKIDKLEGDMERRKADFARAVTSGARSFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	6166	2	1206	
FAPCTREKL,PHTEPABSABGETTRFCQKLAKNHUMVVSPILE RDSHGDVLWNTAVVISNSGAVLGKTRKNHIPRVGDFNESTYYM BGMLGHPVPQTQFGRIAVNICYGRHPLAWLHYSINGABITFNP SATIGALSESLWPIEARNAAIANHCFTCAINAVETHEPREFTS GDKKKAHQCFGYFYGSSYVAAPDSSRTPGLISRSRDGLLVAKIDL NLCQQVNDWNFKMTGRYEMYARBLAEAVKSNYSPTIVKE*PAS VPALG  6167 1220 1844 YGIVTGPSLCAGDKQPKKQEKNPVLVSPEFVDEALCACEEYLSN LAHMDIDKDLEAPLYLTPEGMSLFLQRYYQVVHEGAELRHLDTQ VQRCEDILGQLQAVVPQIDMEGGRINIVTVKPGAKSSRGGIMCMD HLEEMLKLUNGNPVMKDGKWVQKY1ERPLLIFGTKFDLRQMF LVTDWNPLTVWFYRDSY1RFSTQPFSLKNLDK*APLLY1PGFGS DRNIWIVKPGAKSRGRGIMCMDHLEEMLKLVNGNPVVMKDGKWV VQXY1ERPLLIFGTKFDLRQWFLVTDWNPLTVWFYRDSY1RFST QPFSLKNLDK VWFVFSVSAMPPKKQAQAGGSKKAEQKKEKIIEDKTFGLKNKK GAKQQKTIKAVTHQWFLVTDWNPLTVWFYRDSY1RFST QPFSLKNLDK  6168 84 1392 VWFVFSVSAMPPKKQAQAGGSKKAEQKKEKIIEDKTFGLKNKK GAKQQKTIKAVTHQWFLVTDWNPLTVWFYRDSY1RFST QPFSLKNLDK  LITLERKCKRSVYIDADRDELEKUTHOMPEKKLEEVVIKKHG EARKKRYROKINCHFLEATENNKYGHFWCQGCTKGDKCKFSH DLTLERKCKRSVYIDADRDELEKUTHOMPEKKLEEVVIKKHG EARKKKPKTQTVCKHFLEATENNKYGHFWCQGGCTKGDKCKFSH LAMKKRRQEKIDKLEQDMERRKADFKRGALVISGREVFEFFP ELWDDDDEEADDTRYTGGTGGDEVDDSVSVNIDLDLSLYIFRDVD STGITVASLERFSTYTTSDDENKLSAAGGRABNGEKSDLEENN ERGSTENGAIDAVFVDENLFTGGDLDBLEEELMTDLEE TGTTVASLEFSTYTTSDDENKLSAAGGRABNGEKSDLEENN ERGSTENGAIDAVFVDENLFTGGDLDBLEEELMTDLEE AASAVFVLYATSCANNFAMKGKRKTLASDVLSAMEEMEFGRFVT PLKEALEAYRRQKGKKEASEGKKKDKKKTOBEQDVSSRDBIN DEDEBRLDEEERGNEEEEVN*KGRETVAPWKVFLEMRRATCFCE APPCWAE  6170 62 667 STKVMLPNTGRLAGCTVFITGASRGIGKATALKARAGANIVIA AKTAQPHPKLLGTIYTAABEIEAVGGKALPCIVDVRDEQQISAA VEKAIKKFGGIDILVNNASAISLTNTLDTFTKRLDLMMVNTTGG TYLLSKACTPYLKKSVKAH PNISPPLINAFVWFKQHCGRW*VV G*GGLCLLCFELMLCMSDVITICT  MAEAFSKTTSEEDDSIGEFREANSNTAAKGKK*GLEGGRRTHAN SGGIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSWRDILLD RIATFAGHLAHYSKCVTITSRDIRMAVGKK*GLEGGRRTHAN SGGIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSWRDILLD RIATFAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESGGT NATLRYTKSK  6172 651 54 GLCRAGGAHRSRTHVEAALKMLREARLARGEYLYKRAREBAQG				1 - 1
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LAHMDIOKDLEAPLYITPEGWSLFLQRYYQVVHEGAELRHLDTO VQRCEDILQQLQAVVPQIDMEGGRNIHIVKPGAKSRGRGIMCMD HLEEMIKLIVKGNPVVMKDGKWVQKYIERPLLIFGTKFDLRQWF LVTDWNPLTTWFYRDSYIRFSTQDFSLKNLDK*APLYLTPEGWS LFLQRYYQVVHEGAELRHLDTQVQRCEDILQQLQAVVPQIDMEG DRNIHIVKPGAKSRGRGIMCMDHLEEMLKLVNONPVVMKDGKWV VQXYIERPLLIFGTKFDLRQWFLVTDWNPLTVWFYRDSYIRFST QPFSLKNLDK  6168 84 1392 VWPVPSVSAWPPKKQAQAGGSKKAEQKKKEKIIEDKTFGLKNKK GAKQQKFIKAVTHQVKRGQQNPRQVAQSBAEKKLKKDDKKKELQ ELNELFKPVVAAQKISKGADPKSVVCAFFKQGQCTKGDKCKFSH DLTLERKCEKRSVYIDARDEELEKDTMDMWDEKKLEEVVNKKHG EAEKKKPKTQIVCCHFLEAIENNKYGGFWCVGGCFGICMYRHAL PPGFVLKKKKKKKENDE ISDLIERERSALGPNVTKITLESF LAWKKRKQEKIDKLEQDMERRKADFKAGKALVISGREVFEFRP ELVNDDDEEADDTRYTQGTGGDEVDDSVSVNDLDLSLYIFRDVD ETGITVASLERFSTYTSDKDENKISBASGGRARNGRSDLEEDN EREGTENGAIDAVPVDENLFTGEDLDELEELNTLDLEE APAAAMAERPEDLINENNVITRIIKRADPGVNISKEARSAISR AASVYULYATSCANNFAMKGKRTLNASDVLSAMEEMEPQRFVT PLKEALEAYRRQKGKKEASEQKKKDKDKKTDSBEQDKSRDBDN DEDEBERLEEEEQNBEEEVDN*KGRETVAPWKVPLEMRRATCFCE AFPCWAE  6170 62 667 STKVMLPNTGRLAGCTVFITGASRGIGKAIALKAAKDGANIVIA AKTAQPHPKLLGTIYTAAEEIEAVGKALPCIVDVRDEQQISAA VEKKIKKFGGITLIVNNASAISLTNTLDTPTKRLDLMMVNTTRG TYLASKACIPYLKSKVAHIPNISPPLILDLYDVRVDQCOISAA VEKKIKKFGGITLIVNNASAISLTNTLDTPTKRLDLMMVNTTRG TYLASKACIPYLKSKVAHIPNISPPLILDLYDVRVPKQHCGRW*VV G*GDGLCLICFELNLCMSDVITICT  6171 382 941 HFMGSDVELDCDIEFFCGHTKFFPTLEISTTVIVCSCHPVATAST MAEAFSKTTSEEDGSIQE PKEANSMTAQKQKK*GLRGSRRRHAN SGGDIFGDSFAAYFPRVLKQVQHQALSLSQEAVSVMDSMVDDLDL RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT NATLRYYKSK  6172 651 54 GLCRAGGAHRFSRTHVEAALKMLRREARLEKSLLYRKREEAQR SAQERKERLRRALEENLITEELRREALALQGSLEFDDAGGEGV				
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QPFSLKNLDK  OPFSLKNLDK  OPFSLKNLDK  OWPVPSVSAMPPKKQAQAGGSKKAEQKKREKIIEDKTFGLKNKK GAKQQKFIKAVTHQVKFGQQNPRQVAQSEAEKKLKKDDKKKELQ ELNELFKPVVAAQKISKGADPKSVVCAFFKQGCTKGDKCKFSH DLTLERKCEKRSVYIDARDEELEKDTMDNWDEKKLEEVVNKKHG EAEKKKPKTQIVCKHFLEAIENNKYGWFWVCPGGGDICMYRHAL PPGFVLKKKKKKKKEBEISL*DLIERERSALGPNVTKITLESF LAWKKRKRQEKIDKLEQDMERRKADFKAGKALVISGREVFEFRP ELVNDDDEEADDTRYTQGTGGDEVDDSVSVNDIDLSLYIFRDVD ETGITVASLERFSTYTSDKDENKLSEASGGRAENGERSDLEEDN EREGTENGAIDAVVVENLFTGEDLDBLEEELNTLDLEE  6169  112  662  APAAAMAERPEDLNLPNAVITRITKEALPDGVNISKEARSAISR ASVPVLYATSCANNFAMKGRKTLNASDVLSAMEEMEFQAFVT PLKEALEAYRREÇKGKKEASEQKKDKDKKKTDSBEQDKSRDEDN DEDEERLEEBEQNEEEEVDN*KGRETVAPWKVPLEMRRATCFCE AFPCWAE  6170  62  667  STKVMLPNTGRLAGCTVFITGASRGIGKAIALKAAKDGANIVIA AKTAQPHPKLLGTIYTAABEIEAVGGKALPCIVDVRDEQQISAA VEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMVNTRG TYLASKACIPYLKKSKVAHIPNISPPLNLNPVWFKQHCGRW*VV G*GDGLCLICFELNLCMSDVITICT  6171  382  941  HFMQSDVELDCDIEPCGHTKFFPTLPLSTTVIVCSCHPVATAST MAEAFSKTTSEEDQSIQEPKEANSMTAQKQKK*GLRGSRRHAN SGGDIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSMVRDILD RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT NATLRYTKSK SGGDIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSMVRDILD RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT NATLRYTKSK SQGDIFGDSFAAYFPRVLKQVHQALSLSGEAVSVMDSMVRDILD RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT NATLRYTKSK SQGDIFGDSFAAYFPRVLKQVHQALSLSGEAVSVMDSMVRDILD RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT NATLRYTKSK SQGDIFGDSFAAYFPRVLKQVHQALSLSGEAVSVMDSMVRDILD RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT NATLRYTKSK SQGDIFGDSFAAYFPRVLKQVHQALSLSGEAVSVMCSHVFRAEEAQR SAQERKERRRAEEENRALEENRLIPTELRREALALQGSLEFDDAGGEGV				
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DEDEBRLEEEQNEEEEVDN+KGRETVAPWKVPLEMRRATCFCE AFPCWAE  6170 62 667 STKVMLPNTGRLAGCTVFITGASRGIGKAIALKAAKDGANIVIA AKTAQPHPKLLGTIYTAABEIEAVGGKALPCIVDVRDEQQISAA VEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTRG TYLASKACIPYLKKSKVAHIPNISPPLNLNPVWFKQHCGRW+VV G*GDGLCLICFELNLCMSDVITICT  6171 382 941 HFMQSDVELDCDIEPCGHTKFPPTLPLSTTVIVCSCHPVATAST MAEAFSKTTSEEDQSIQEPKEANSMTAQKQKK*GLRGSRRHAN SGGDIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSMVRDILD RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT NATLRYTKSK 6172 651 54 GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR SAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGV	1	1		
AFPCWAE  6170  62  667  STKVMLPNTGRLAGCTVFITGASRGIGKAIALKAAKDGANIVIA AKTAQPHPKLLGTIYTAABEIEAVGGKALPCIVDVRDEQQISAA VEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTRG TYLASKACIPYLKKSKVAHIPNISPPLNLNPVWFKQHCGRW*VV G*GDGLCLICFELNLCMSDVITICT  6171  382  941  HFMQSDVELDCDIEPCGHTKFPPTLPLSTTVIVCSCHPVATAST MAEAFSKTTSEEDQSIQEPKEANSMTAQKQKK*GLRGSRRHAN SGGDIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSMVRDILD RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT NATLRYTKSK  6172  651  54  GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR SAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGV				
6170 62 667 STKVMLPNTGRLAGCTVFITGASRGIGKAIALKAAKDGANIVIA AKTAQPHPKLLGTIYTAAEEIEAVGGKALPCIVDVRDEQQISAA VEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTRG TYLASKACIPYLKKSKVAHIPNISPPLNLNPVWFKQHCGRW*VV G*GDGLCLICFELNLCMSDVITICT 6171 382 941 HFMQSDVELDCDIEPCGHTKFPPTLPLSTTVIVCSCHPVATAST MAEAFSKTTSEEDQSIQEPKEANSMTAQKQKK*GLRGSRRHAN SGGDIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSMVRDILD RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT NATLRYTKSK 6172 651 54 GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR SAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGV				
AKTAQPHPKLLGTIYTAAEEIEAVGGKALPCIVDVRDEQQISAA VEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTRG TYLASKACIPYLKKSKVAHIPNISPPLNLNPVWFKQHCGRW*VV G*GDGLCLICFELNLCMSDVITICT 6171 382 941 HFMQSDVELDCDIEPCGHTKFPPTLPLSTTVIVCSCHPVATAST MAEAFSKTTSEEDQSIQEPKEANSMTAQKQKK*GLRGSRRRHAN SGGDIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSMVRDILD RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT NATLRYTKSK 6172 651 54 GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR SAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGV				
VEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTRG TYLASKACIPYLKKSKVAHIPNISPPLNLNPVWFKQHCGRW*VV G*GDGLCLICFELNLCMSDVITICT 6171 382 941 HFMQSDVELDCDIEFCGHTKFFPTLPLSTTVIVCSCHPVATAST MAEAFSKTTSEEDQSIQEPKEANSMTAQKQKK*GLRGSRRHAN SGGDIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSMVRDILD RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT NATLRYTKSK 6172 651 54 GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR SAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGV	6170	62	667	
TYLASKACIPYLKKSKVAHIPNISPPLNLNPVWFKQHCGRW*VV G*GDGLCLICFELNLCMSDVITICT 6171 382 941 HFMQSDVELDCDIEPCGHTKFPPTLPLSTTVIVCSCHPVATAST MAEAFSKTTSEEDQSIQEPKEANSMTAQKQKK*GLRGSRRRHAN SGGDIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSMVRDILD RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT NATLRYTKSK 6172 651 54 GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR SAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGV				
G*GDGLCLICFELNLCMSDVITICT  6171  382  941  HFMQSDVELDCDIEFCGHTKFPPTLPLSTTVIVCSCHPVATAST  MAEAFSKTTSEEDQSIQEPKEANSMTAQKQKK*GLRGSRRHAN SGGDIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSMVRDILD RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT NATLRYTKSK  6172  651  54  GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR SAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGV	İ			1
6171 382 941 HFMQSDVELDCDIEPCGHTKFPPTLPLSTTVIVCSCHPVATAST  MAEAFSKTTSEEDQSIQEPKEANSMTAQKQKK*GLRGSRRRHAN  SGGDIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSMVRDILD  RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT  NATLRYTKSK  6172 651 54 GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR  SAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGV				
MAEAFSKTTSEEDQSIQEPKEANSMTAQKQKK*GLRGSRRRHAN SGGDIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSMVRDILD RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT NATLRYTKSK 6172 651 54 GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR SAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGV				
SGGDIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSMVRDILD RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT NATLRYTKSK 6172 651 54 GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR SAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGV	6171	382	941	
RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT NATLRYTKSK  6172 651 54 GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR SAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGV				
NATLRYTKSK  6172 651 54 GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR SAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGV				
6172 651 54 GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR SAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGV		}	}	
SAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGV				
	6172	651	54	
TSHVDDEYRWAGVEDPKVMITTSRDPSSKLKMFAKBLKLVFPGA	1			
	L		1	TSHVDDEIRWAGVEDPKVMITTSRDPSSKDAMFAABBALVFPGA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:		location	
NO:	nucleotide		Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	amino acid	sequence	Codon, /=possible nucleotide deletion,
1		sequence	
	sequence	<u> </u>	\=possible nucleotide insertion)
		İ	QRMNRGRHEVGALVRACKANGVTDLLVVHEHRGTPVGLIVSHLP
1		1	FGPTAYFTLCNVVMRHDIPDLGTMSEAKPHLITHGFSSRLGKRV
	1		SDILRYLFPVPKDDSHRVITFANQDDYISFRHHVYKKTDHRNVE
	i		LTEVGPRFELKLYMIRLGTLEQEATADVEWRWHPYTNTARKRVF
Į.			LSTE*AAPRPLGOLL
6173	3	288	SVDHREVQVLSQSMPLTPHQAVLRGERPYMCVECGKCFGRSSHL
01/3	] 3	200 .	
1			LQHQRIHTGEKPYVCSVCGKAFSQSSVLSKHRTIHTGEKPYECN
	İ	İ	ECGKAFRVSSDLAQHHKIHTGEKPHECLECRKAFTQLSHLIQHQ
ì	1	1	RIHTGERPYVCPLCGKAFNHSTVLRSHQRVHTGEKPHRCNECGK
			TFSVKRTLLQHQRIHTGEKPYTCSECGKAFSDRSVLIQHHNVHT
1			GEKPYECSECGKTFSHRSTLMNHERIHTEEKPYACYECGKAFVO
	1		HSHLIQHQKVHRKL*PTCVLSVGSALAGVPTSFSISVSTLERSP
1			
			MCAVYVGRPSARAQSLVNTGQFTQVRSPMSVMSVEKPLE
6174	1060	959	PRPPGKRWMVAGLGNPGLPGTRHSVGMAVLGQLARRLGVAESWT
		1	RDRHCAADLALAPLGDAQLVLLRPRRLMNANGRSVARAAELFGL
		1	TAEEVYLVHDELDKPLGRLALKLGGSARGHNGVRSCISCLNSNA
	}	ł	MPRLRVGIGRPAHPEAVQAHVLGCFSPAEQELLPLLLDRATDLI
	1		LDHIRERSQGPSLGP*H*WFSKKA
6175	2204	334	<u> </u>
67/3	2204	334	RYFRADPRSRSGQPRAEGLGAFAEGPLRAMAAPVKGNRKQSTEG
ł	ľ		DALDPPASPKPAGKQNGIQNPISLEDSPEAGGEREEEQEREEEQ
1			AFLVSLYKFMKERHTPIERVPHLGFKQINLWKIYKAVEKLGAYE
Į		1	LVTGRRLWKNVYNELGGSPGSTSGATCTRRHY*RLVLPYVRHLK
İ	!	1	GEDDKPLPTSKPRKQYKMAKENRGDDGATERPKKAKEERRMDOM
ĺ	1	(	MPGKTKADAADPAPLPSQEPPRNSTEQQGLASGSSVSFVGASGC
			PEAYKRLLSSFYCKGTHGIMSPLAKKKLLAOVSKVEALOCOEEG
			CRHGAEPQASPAVHLPESPQSPKGLTENSRHRLTPQEGLQAPGG
}		1	
1		}	SLREEAQAGPCPAAPIFKGCFYTHPTEVLKPVSQHPRDFFSRLK
}	1	}	DGVLLGPPGKEGLSVKEPQLVWGGDANRPSAFHKGGSRKGILYP
			KPKACWVSPMAKVPAESPTLPPTFPSSPGLGSKRSLEEEGAAHS
1			GKRLRAVSPFLKEADAKKCGAKPAGSGLVSCLLGPALGPVPPEA
1	i		YRGTMLHCPLNFTGTPGPLKGQAALPFSPLVIPAFPAHFLATAG
Į.	l		PSPMAAGLMHFPPTSFDSALRHRLCPASSAWHAPPVTTYAAPHF
			FHLNTKL
-6176	1040	402	
.01/8	1040	402	PLSALRAMAEVHVIGQIIGASGFSESSLFCKWGIHTGAAWKLLS
	1		GVREGQTQVDTPQIGDMAYWSHPIDLHFATKGLQGWPRLHFQVW
İ	1		SQDSFGRCQLAGYGFCHVPSSPGTHQLACPTWRPLGSWRBQLAR
			AFVGGGPQLLHGDTIYSGADRYRLHTAAGGTVHLEIGLLLRNFD
		1	RYGVEC*GTLPPTSPPSTPRTPSDGGGWHSGQEHRL
6177	1400	992	VPIESLVGKVHNFPLIAFYCCEKGKROPHKSLHDRCFGEALDPN
1			CSHCYLDQIKRSDFLGFSGYSPHFVAISTNSEHKMQPSSMQQAL
	1	1	
			PSQ*PYWTDPRPALVPCCSHRPDVHRSRPGPGLPGTSGCSDRPP
			VCPI
6178	1027	254	STORGGIKGVARAASLVGRRRAGTGMALLLCLVCLTAALAHGCL
			HCHSNFSKKFSFYRHHVNFKSWWVGDIPVSGALLTDWSDDTMKE
}		1	LHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELR
1		1	NIFREQVHLIQNAIIESRIDCQHRCGIFQYETISCNNCTDSHVA
			CFGYNCESSAQWKSAVQGLLNYINNWHKQDTSMRPRSSAFSWPG
<del></del>			THRAAPAFLVLPALRCLEPPHLANLSLEDAA*CLKQH
6179	806	276	RGETREMAGNLLSGAGRRLWDWVPLACRSFSLGVPRLIGIRLTL
	]	J	PPPKVVDRWNEKRAMFGVYDNIGILGNFEKHPKELIRGPIWLRG
			WKGNELQRCIRKRKMVGSRMFADDLHNLNKRIRYLYKHFNRHGK
1			FR*KRKLRTSEKAHLSPWRRETVLFPVRKRLCIFSVIKWGFFGI
6100	150	1023	
6180	156	1833	DHHILKAASTTHVCARGNIFAIPNTRCLEC*ATATPSSLECQN*
	1	ļ	SHLSLCPLPATTSGLTPNSMIPEKERQNIAERLLRVMCADLGAL
	1	[	SVVSGKEFLKLAQTLVDSGARYGAFSVTEILGNFNTLALKHLPR
			MYNQVKVKVTCALGSNACLGIGVTCHSQSVGPDSCYILTAYQAE
	<del></del>	L	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
j	amino acid	residue of	
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
}			W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			GNHIKSYVLGVKGADIRDSGDLVHHWVQNVLSEFVMSEIRTVYV
1			TDCRVSTSAFSKAGMCLRCSACALNSVVQSVLSKRTLQARSMHE
1			VIELLNVCEDLAGSTGLAKETFGSLEETSPPPCWNSVTDSLLLV
1			HERYEQICEFYSRAKKMNLIQSLNKHLLSNLAAILTPVKQAVIE
			LSNESQPTLQLVLPTYVRLEKLFTAKANDAGTVSKLCHLFLEAL
1			KENFKVHPAHKVAMILDPQQKLRPVPPYQHEEIIGKVCELINEV
		1	KESWAEEADFEPAAKKPRSAAVENPAAQEDDRLGKNEVYDYLQE
			PLFQATPDLFQYWSCVTQKHTKLAKLAFWLLAVPAVGARSGCVN
			MCEQALLIKRRRLLSPEDMNKLMFLKSNML
6181	169	1032	TRTLLSPVLLPGPRWKPWRRRPMGPLALPAWLOPRYRKNAYLFI
	1		YYLIQFCGHSWIFTNMTVRFFSFGKDSMVDTFYAIGLVMRLCQS
			VSLLELLHIYVGIBSNHLLPRFLQLTERIIILFVVITSOEEVOE
			KYVVCVLFVFWNLLDMVRYTYSMLSVIGISYAVLTWLSQTLWMP
	]		IYPLCVLAEAFAIYQSLPYFESFGTYSTKLPFDLSIYFPYVLKI
[	1	ļ	
İ			YLMMLFIGMYFTYSHLYSERRDILGIFPIKKKKM*STAFQCDTR
6182	1760	1224	KDRLWIQCSK*NTGSILVEKFLVF
0102	1769	1224	AS*IDYQLNTLLKEFQLTEENTKLRYLTCSLIEDMAAAYFPDCI
	,	ļ	VRPFGSSVNTFGKLGCDLDMFLDLDETRNLSAHKISGNFLMEFQ
-			VKNVPSERIATQKILSVLGECLDHFGPGCVGVQKILNARCPLVR
1			FSHQASGFQCDLTTNNRIALTSSELLYIYGALDSRVRALVFSVR
		•	CWARAHSLTSSIPGAWITNFSLTMMVIFFLQRRSPPILPTLDSL
			KTLADAEDKCVIEGNNCTFVRDLSRIKPSQNTETLELLLKEFFE
ļ	}		YFGNFAFDKNSINIRQGREQNKPDSSPLYIQNPFETSLNISKNV
l	ļ		SQSQLQKFVDLARESAWILQQEDTDRPSISSNRPWGLVSLLLPS
ł			APNRKSFTKKKSNKFAIETVKNLLESLKGNRTENFTKTSGKRTI
1			STQT
6183	1118	452	HLDRYIKSPGSGSSTPAPPSHLLLYLLHPQSTRTMGCCGCSRGC
ļ			GSGCGGCGSSCGGCGSGCGGCGSGCGGCSSCGGCGS
1			RCYVPVCCCKPVCSWVPACSCTSCGSCGGSKGGCGSCGGSKGGC
i			GSCGCSQSSCCKPCCCSSGCGSSCCQSSCCKPCCCQSSCCVPVC
	1	]	CQSSCCKPCCCQSNCCVPVCCQCKI*GSGPRPSGFSCLVKAFLM
			VP
6184	1	2191	IVTVREEDGAPAVAPPGVVVSRANKRSGAGPGGSGGGGARGAEE
	1		EPPPPLQAVLVADSFDRRFFPISKDQPRVLLPLANVALIDYTLE
			FLTATGVQETFVFCCWKAAQIKEHLLKSKWCRPTSLNVVRIITS
	1		ELYRSLGDVLRDVDAKALVRSDFLLVYGDVISNINITRALEEHR
	1		LRRKL*KNVSVMTMIFKESSPSHPTRCHEDNVVVAVDSTTNRVL
	1		HFQKTQGLRRFAFPLSLFQGSSDGVEVRYDLLDCHISICSPQVA
1			QLFTDNFDYQTRDDFVRGLLVNEEILGNQIHMHVTAKEYGARVS
1	1		
			NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD
			\
1			NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL
1			TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK
1	1	1	DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEBELQQNLWGLKI
	1		NMEEESESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR
1	}		GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ
1			MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED
			FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ
L	]		QLRKNQQLQRFIQWLKEAEEESSEDD
6185	791	44	PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG
			IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFFFOR
	1		HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF
			GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK
	1		REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR
			GCQEAEMQTPRRLGWGWYHTLTLYLWBEK
1 61 66	569	238	VYGIDSSNTNTHGAEERNRKLKKHWKLCHAOSRLDVNGLALKMA
6186			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	sequence	<del> </del>	KERKVKNKVKNKADTEEVPNNSPTNQEKMPTSAILPDFSGSVIS
		1	NIRNOMETLHSOPHOEENLCFENSFSLINLLPINAVEPTSSOOI
	i	1	PNRETSEANKERRKMTSKSSESNIYSPLTSFITADSELHDIIKD
		1	
		1	LEDCLMVGLHTCGDLAPNTLRIFTSNSEIKGVCSVGCCYHLLSE
			EFENQHKERTQEKWGFPMCHYLKEERWCCGRNARMSACLALERV
	1.7		AAGQGLPTESLFYRAVLQDIIKDCYGITKCDRHVGKIYSKCSSF
			LDYVRRSLKKLGLDESKLPEKIIMNYYEKYKPRMNELEAFNMLK
	1	ì	VVLAPCIETLILLDRLCYLKEQEDIAWSALVKLFDPVKSPRCYA
	1	ľ	VIALKKQQ*FPLKQIIRCISL*DSAGCAEEVSVGDGGPALRDAP
	1		PSGSRVGSRYD
6107	1701	771	DAWGPETRLARILNPDSFIEPRPGRLPBLEATRPHMEPKASCPA
6187	1/01	'/1	AAPLMERKFHVLVGVTGSVAALKLPLLVSKLLDIPGLEVAVVTT
		1	ERAKHFYSPODIPVTLYSDADEWEMWKSRSDPVLHIDLRRWADL
			LLVAPLDANTLGKVASGICDNLLTCVMRAWDRSKPLLFCPAMNT
			AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGDEGLGAMAEVG
			TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSEWVQAKSVKMDV
	1	1	GKIGGYPHLLNGGPALSLPRGQACSRLNWTEGPGLSFFQPGEAA
			A
6188	238	1534	KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHPSA*GPRWASW
0100			NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCMQEMG
			NGKANRLYEAYLPETFRRPOIDPAVEGFIRDKYEKKKYMDRSLD
	1	1	INAFRKEKDDKWKRGSEPVPEKKLEPVVFEKVKMPQKKEDPQLP
	1		RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTLEKDLDLLASV
	1		
	1	1	PSPSSSGSRKVVGSMPTAGSAGSVPENLNLFPEPGSKSEEIGKK
		1	QLSKDSILSLYGSQTPQMPTQAMFMAPAQMAYPTAYPSFPGVTP
	1		PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGYMGGMQASMMG
			VPNGMMTTQQAGYMAGMAAMPQTVYGVQPAQQLQWNLTQMTQQM
	1		AGMNFYGANGMMNYGQSMSGGNBQAANQTLSPQMWK
6189	1297	793	LGEPLGDLCELIPGDVQQLQMGEVHPGTGAQGSAAQSVAGEVQL
			TOLSHARQRPSCQGSQLIALDLQHMDISRQPRWQHVQPVARQVQ
	1	1	RAOOAOLAEGVAVHLWAGDAVVAEVELLQEVGGGKVFAANACDL
	1	1	VVODHEGAHAARQATGHALQRVIVQVRRVQPLEAL*RVPSGLPR
			RVRAFMILHNQITGIGREDFATTYFLEELNLSYNRITSPQVHRD
İ			AFRKLRLLRSLDLSGNRLHMLPPGLPRNVHVLKVKRNBLAALAR
1			GALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQ
1	1		
1			LTEIPEGLPESLEYLYLQNNKISAVPANAFDSTPNLKGIFLRFN
1			KLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKDRGRLGKEKE
L			EEEEDEVEREETR
6190	66	1309	ILVGNVSFLLSFAEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQ
1			GLHCETCKEGFYLNYTSGLCQPCDCSPHGALSIPCNSSGKCQCK
			VGVIGSICDRCQDGYYGFSKNGCLPCQCNNRSASCDALTGACLN
		1	CQENSKGNHCEECKEGFYQSPDATKECLRCPCSAVTSTGSCSIK
1		1	SSELEPECDQCKDGYIGPNCNKCENGYYNFDSICRKCQCHGHVY
1		1	PVKTPKICKPESGECINCLHNTTGFWCENCL*GYVHDLEGNCIK
	1		KVILPTPEGSTILVSNASLTTSVPTPVINSTFTPTTLQTIFSVS
			TSENSTSALADVSWTQFNIIILTVIIIVVVLLMGFVGAVYMYRE
		1	
1			YONRKLNAPFWTIELKEDNISFSSYHDSIPNADVSGLLEDDGNE
			VAPNGQLTLTTPIHNYKA
6191	1212	1511	VNLCHGGLLHLSTHHLGIKPSMH*LFFLMLSFPHLTPQQPKCPS
	}		MIDWIKKIWYIYTMEYYATIKRNEIMFFAGTWMEMEAIILSKLM
		}	ODYMFSLISGS
6192	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
0137	,	350	KGGLVSDAYGEDDFSRLGGDEDGYEBEEDENSRQSEDDDSETEK
		1	
	•		PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
			RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI
1_	.1		QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK
<u></u>			

	Predicted	Predicted end	Amino acid segment containing signal peptide
1 25 1	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO: 1	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1 1			
l L	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l .	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1 1		sequence	
	sequence		\=possible nucleotide insertion)
l i		1	AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
1			DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
			IVKKAKQ
6193	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
0133	3	330	KGGLVSDAYGEDDFSRLGGDEDGYEEEEDENSRQSEDDDSETEK
		1	-
		1	PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
] !			RCSNHLQDKIQKLYBRKIKEGMDMNYIIQRKKEFRNPSIYEKLI
			QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK
1			AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
			DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
1 1			-
<u> </u>		ļ	IVKKAKQ
6194	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
		1	KGGLVSDAYGEDDFSRLGGDEDGYEEEEDENSRQSEDDDSETEK
			PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
1			RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI
		1	QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK
l i			AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
1		1	DSAIPVTTIAOPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
1 1		i	
			IVKKAKQ
6195	736	235	VANGLQSNMPKFYCDYCDTYLTHDSPSVRKTHCSGRKHKENVKD
		1	YYQKWMEEQAQSLIDKTTAAFQQGKIPPTPFSAPPPAGAMIPPP
1			PSLPGPPRPGMMPAPHMGGPPMMPMGPPPPGMMPVGPAPGMRP
l i			PMGGHMPMMPGPPMMRPPARPMMVPTRPGMTRPDR
6100	1510	623	KTGKRRSAAYVRNILDNAEQVISNLEARNLGPRLTPLLQEEDSH
6196	1512	623	1
1		1	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC
1 [			HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL
		1	FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL
{ <b>1</b>		ſ	MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR
		4	NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS
!!			NOALYPFEGHDNVDAEFVBEAALKHTAMLLGL
6197	3	819	ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG
019/	3	) 613	1
1 1		l .	PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG
			RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS
1 1		1	RSSSWGRNRRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ
1 1			SRTPRRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS
1 1			RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS
1 .			YRHKNSW
6198	111	1912	SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE
0130	T T T	1312	l :
1		1	RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLQDSQ
			REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL
		1	LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW
1		1	
			GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV
			GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV SRQPSFTYSEWMBEKIEDDFLDLDPVPBTPVFDCVMDIKPEADP
			SRQPSFTYSEWMBEKIEDDFLDLDPVPBTPVFDCVMDIKPEADP
			SRQPSPTYSEWMBEKIEDDFLDLDPVPBTPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES
			SRQPSPTYSEWMBEKIEDDFLDLDPVPBTPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY
			SRQPSPTYSEWMBEKIEDDFLDLDPVPBTPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRXNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG
			SRQPSPTYSEWMBEKIEDDFLDLDPVPBTPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRMVWQEHTPIIVMITNIEEMN
			SRQPSPTYSEWMBEKIEDDFLDLDPVPBTPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRXNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG
			SRQPSPTYSEWMBEKIEDDFLDLDPVPBTPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRMVWQEHTPIIVMITNIEEMN
			SRQPSFTYSEWMBEKIEDDFLDLDPVPBTPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRMVWQBHTPIIVMITNIEEMN EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVBEAAQQEGPHCAPII
			SRQPSPTYSEWMBEKIEDDFLDLDPVPBTPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYLATQGPIVSTVADFWRMVWQBHTPIIVMITNIEEMN EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVEEAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG
6100			SRQPSPTYSEWMBEKIEDDFLDLDPVPBTPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDFLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRMVWQBHTPIIVMITNIEEMN EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVEEAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE
6199	144	1211	SRQPSPTYSEWMBEKIEDDFLDLDPVPBTPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNEHSRVCLTSPDPDDPLSSYINANYIRG YGGEKVYIATQGPIVSTVADFWRMVWQBHTPIIVMITNIEEMN EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVEEAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA
6199	144	1211	SRQPSPTYSEWMBEKIEDDFLDLDPVPBTPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYLATQGPIVSTVADFWRMVWQBHTPIIVMITNIEEMN EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVBEAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY
6199	144	1211	SRQPSPTYSEWMBEKIEDDFLDLDPVPBTPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNEHSRVCLTSPDPDDPLSSYINANYIRG YGGEKVYIATQGPIVSTVADFWRMVWQBHTPIIVMITNIEEMN EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVEEAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA
6199	144	1211	SRQPSPTYSEWMBEKIEDDFLDLDPVPBTPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYLATQGPIVSTVADFWRMVWQBHTPIIVMITNIEEMN EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVBEAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY
6199	144	1211	SRQPSPTYSEWMBEKIEDDFLDLDPVPBTPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYLATQGPIVSTVADFWMWWQBHTPIIVMITNIEEMN EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVBEAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY ESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV

CEC	I Dec 24 3	Predicted end	
SEQ	Predicted		Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			FYDENDSKLFEQILKAEYBFDSPYWDDISDSAKDFIRNLMEKDP
1			NKRYTCEQAARHPWIAGDTALNKNIHESVSAQIRKNFAKSKWRQ
			AFNATAVVRHMRKLHLGSSLDSSNASVSSSLSLASQKDCASGTF
ł		{	HAL*
6200	702	96	LPEVPHSLRPRVKPHLCCAQPAVRVMARLPKLAVFDLDYTLWPF
0200	702	1	
1			WVDTHVDPPFHKSSDGTVRDRRGQDVRLYPEVPEVLKRLQSLGV
i			PGAAASRTSEIEGANQLLELFDLFRYFVHREIYPGSKITHFERL
l			QQKTGIPFSQMIFFDDERRNIVDVSKLGVTCIHIQNGMNLQTLS
			QGLETFAKAQTGPLRSSLEESPFEA
6201	2809	2383	GOTPRVRWKMRRSLRAGKRRQTAGRKSKSPPKVPIVIQDDSLPA
			GPPPQIRILKRPTSNGVVSSPNSTSRPTLPVKSLAQREAEYAEA
1			RKRILGSASPEEEQEKPILDRPTRISQPEDSRQPNNVIRQPLGP
			DGSQGFKQRR
6202	2	426	INADRAAVASSLLSRPTRKMAPQKDRKPKRSTWRFNLDLTHPVE
1			DGIFDSGNFEQFLREKVKVNGKTGNLGNVVHIERFKNKITVVSE
ĺ			KQFSKRYLKYLTKKYLKKNNLRDWLRVVASDKETYELRYFQISO
1	}		DEDESESED
6203	419	2550	RCPRPPATAGAAASRPDRSPPSGISGSEAAAGAGAAAAPASQHPA
0203	419	2550	
1			TGTGAVQTEAMKQILGVIDKKLRNLEKKKGKLDDYQERMNKGER
			LNQDQLDAVSKYQEVTNNLEFAKELQRSFMALSQDIQKTIKKTA
			RREQLMREEAEQKRLKTVLELQYVLDKLGDDEVRTDLKQGLNGV
1	1		PILSEEELSLLDEFYKLVDPERDMSLRLNEQYEHASIHLWDLLE
ļ	1		GKEKPVCGTTYKVLKEIVERVFQSNYFDSTHNHQNGLCEEEEAA
1	1		SAPAVEDQVPEAEPEPAEEYTEQSEVESTRYVNRQFMAETQFTS
1	1		GEKEQVDEWTVETVEVVNSLQQQPQAASPSVPEPHSLTPVAQAD
	1		PLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPAIVSAOPM
ļ.	<u> </u>		NPTQNMDMPQLVCPPVHSESRLAQPNQVPVQPEATQVPLVSSTS
			EGYTASQPLYQPSHATEQRPQKEPIDQIQATISLNTDQTTASSS
İ			LPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFNMNAPVP
Ì	ł		PVNEPETLKQQNQYQASYNQSFSSQPHQVEQTELQQEQLQTVVG
	İ		
l			TYHGSPDQSHQVTGNHQQPPQQNTGFPRSNQPYYNSRGVSRGGS
			RGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYTQSQFSAP
			RDYSGYQRDGYQQNFKRGSGQSGPRGAPRGRGGPPRPNRGMPQM
ļ <u>.</u>			NTQQVN
6204	2933	787	CTHNLISLLGGRALIHFNRFLNLKIQEGEAHNIFCPAYDCFQLV
			PGDIIKSVVSKEMDKRYLQFDIKAFVENNPAIKWCPTPGCDRAV
			RLTKQGSNTSGSDTLSFPLLRAPAVDCGKGHLFCWECLGEAHEP
1	ļ		CDCQTWKNWLQKITEMKPEELVGVSEAYEDAANCLWLLTNSKPC
1	1		ANCKSPIQKNEGCNHMQCAKCKYDFCWICLEEWKKHSFVHWEVI
ŀ			YRCTRYEVIQHVEEQSKEMTVEAEKKHKRFQELDRFMHYYTRFK
	1		NHEHSYQLEQRLLKTAKEKMEQLSRALKETEGGCPDTTFIEDAV
1	1		HVLLKTRILKCSYPYGFFLEPKSTKKEIFELMQTDLEMVTEDL
	1		AQKVNRPYLRTPRHKIIKAACLVQQKRQEFLASVARGVAPADSP
	1		
			EAPRRSFAGGTWDWEYLGFASPEEYAEFQYRRHRQRRRGDVHS
			LLSNPPDPDEPSESTLDIPEGGSSSRRPGTSVVSSASMSVLHSS
			SLRDYTPASRSENQDSLQALSSLDEDDPNILLAIQLSLQESGLA
1			LDEETROFLSNEASLGAIGTSLPSRLDSVPRNTDSPRAALSSSE
	1		LLELGDSLMRLGAENDPFSTDTLSSHPLSEARSDFCPSSSDPDS
			AGQDPNINDNLLGNIMAWFHDMNPQSIALIPPATTEISADSQLP
			CIKDGSEGVKDVELVLPEDSMFEDASVSEGRGTQIEENPLEBNI
			PGGGKQHPQAW
6205	1	1200	RAHRGKMALEVGDMEDGQLSDSDSDMTVAPSDRPLQLPKVLGGD
1			SAMRAFQNTATACAPVSHYRAVESVDSSEESFSDSDDDSCLWKR
	[		KRQKCFNPPPKPBPFQFGQSSQKPPVAGGKKINNIWGAVLQEQN
1			
	1		QDAVATELGILGMEGTIDRSRQSETYNYLLAKKLRKESQEHTKD
1	1	l	LDKELDEYMHGGKKMGSKEEENGQGHLKRKRPVKDRLGNRPEMN

PCT/US00/34263

Predicted   Predicted and   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection   Incolection		•		
Note	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
corresponding	ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
to first amino acid residue of amino acid residue of amino acid aequence    Poptoline_Goldutamine_RAPgimine_   Sestine_TThreonine_Vavaline_   Sequence	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
to first anino acid residue of anino acid residue of anino acid anino acid sequence  #TYPTODIAIN, YTYYTODIAN, X-UNKNOWN, *-Stop codon, /-possible nucleotide deletion,possible nucleotide insertion)  #TYPTODIAIN, YTYYTODIAN, Y-TYYTODIAN, X-UNKNOWN, *-Stop UND YKREVETARBOSEVADE ISFALDEVEKOLIARVYRTIONKA  #ILLIMETAREVENGELPTMNSSRRTTGGVPLHALLENTPEISES	ĺ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
anino acid residue of anino acid aequence  Sequence  WTTPLOPAIN, VTTYPOSIAN, KUNDKNOWN, **Stop Codon, /=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion V=possible nucleotide deletion V=possible nucleotide deletion V=possible nucleotide delet	Į.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
amino acid		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
amino acid		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence		amino acid	1	
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amino acid sequence  Codon, /-possible nucleotide deletion, /-possible nucleotide desertion)  FLSSCNONRISIMDCKNNOMGGLTCHYREAKITCSAHREPRIV, GGDIPCSGREVEKIGDTWGSILGNSFSILABAVCRELCGGTVV SILGABIGERONG IMAGEPCCEGRESHLISLCPWAPPREGICES SREVEKIGDTWGSILGNSFSILABAGSICHSHM IEDAHVLCOOLKCVALSTPGGARPOKKONG) TREMPHICTOTEG HEMOCPYTALGABLCPSBQVASVICSKNOGITERSSILAPP RPTIPESAVACIESGGLESHLISLCPWAPPREGICES HEMOCPYTALGABLCPSBQVASVICSKNOGITERSSILAPP RPTIPESAVACIESGGLESHVICSKNOGITERSSILAPP RPTIPESAVACIESGGLESHVICSKNOGITERSSILAPP RPTIPESAVACIESGGLESHVICSKNOGITERSSILAPP RPTIPESAVACIESGGLESHVICSKNOGITERSSILAPP RPTIPESAVACIESGGLESHVICSKNOGITERSSILAPP RADARASTER PREVIOUND REPORT ACAGRIEVY YNAHAGTVCKSSMSZTTUVVCQLGCOALKGKISSSILAPP ACAGRIEVY YNAHAGTVCKSSMSZTTUVVCQLGCOALKGKISSSILAPP ACAGRIEVY YNAHAGTVCKSSMSZTTUVVCQLGCOALKGKISSSILAPP ACAGRIEVY YNAHAGTVCKSSMSZTTUVVCQLGCOALKGKISSSILAPP ACAGRIEVY YNAHAGTVCKSSMSZTTUVVCQLGCOALKGKSSSILAPP ACAGRIEVY YNAHAGTVCKSSMSZTTUVVCQLQCGOALKGKSSSSILAPP ACAGRIEVY YNAHAGTVCKSSMSZTTUVVCQLQCGOALKGKSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	1			
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ASJDKAMSIPWUDNVQCPKGPDTIMQCPSSPRERILASPSEET WITCDNKIRLQEGFTSCGRVEIWHGGSWGTVCDDSWDLDDAQU VCQUGCGPALKAPKEABEPGGTGFINLNEVKCKGNESSLWDCP ARRWGHSECHKEDAAVNCTDISVQKTPQKATTGRSSRQSSFIA VGLGGVULLAIFVALFITIKKRRQRQRLAVSSRGENLYHQTQVR EMNSCLANADDLDLMNSSGGHSBPH  176WSKLRWILLEDSGADFRHFVNISPFTITVVLLLSACFVY SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV SVICNQLGCPTAIKAPGWANSSAGSGRIMMDHYSCRGNESALMM CKHEGWGKHSNCTHQDAGAVTCSDGSMLERRITRGGNNCSGRIE IKRQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGGG SGPIWFDDLICNNGSSALMNCKHGGWKHCDHAEDDAGVICSS ADLISLRLVDGWTECSGRLEVRRQGEWGTICDDGWDSYDAAVACK QLGCPTAVTAIGRVNASKGFGHIWLDSVCQGHEPAVWQCKHHE WGKHTCNNNEDAGVTCSDGSDLEURLRGGGSRCAGTVEVEIQRL LGKVCDRGWGLKEADVVCRQLGCSSALKTSYQVYSKIQATNTWI PLSSCNGNETSLMDCKNWGWGGLTGUBEAKTTCGANTSFERFRLV GGDIPCSGRVEVKHGDTWGSICDSDFSLEASSVLCRELQCGTVV SILIGAHHVLCQLKGSVALSTPGGAFFGKGNGQ URRIMFHFCTGTEG HMDGCPVTALGASLCSSEQVASVICSGNGSGTLSSCNSSLGFT RPTIPESSAVACIESGGLELVNGGGRCAGRVEIYHEGSWGTICD DSDLSDBAHVVCRQLGCGSALMTSPCGYTSKUGHTWFBCTGTEG HMDGCPVTALGASLCSEEQVASVICSGNGSGTLSCNSSSLGFT RPTIPESSAVACIESGGLELVNGGGRCAGRVEIYHEGSWGTICD DSDLSDBAHVVCRQLGCGEALNATSHFGGTGFIHWDEMKCN GKSSTWQCHSHGWGQONCRHKEDAGVICSEFMSIRLTSSAGGT RPTIPESSAVACIESGGLELVNGGGRCAGRVEIYHEGSWGTICD DSDLSDBAHVVCRQLGCGEALNATSHFGGTGFIHWDEMKCN GKSSTWQCHSHGWGQONCRHKEDAGVICSEFMSIRLTSSASSEFT WITCDNKIRLGGGFTSCSGRVEIWHGGSWGTVCDDSWDLDDAQV VCQULGGPALKAFREABFGGGTGFIHWFVKKGKNESSLWDCC ARRWGHSECGHKEDAAVNCTDISVCKTPGKSTTGRSSRQSSFIA VGILGVYLLAFFVALFFIHKKRRGGNGTVCDDSWDLDDAQV VCQULGGPALKAFREABFGGGTGFIHWFVKKGKNESSLWDCC ARRWGHSECGHKEDAAVNCTDISVCKTPGKSTTGRSSRQSSFIA VGILGVYLLAFFVALFTIKKSRGRGAGTGAPRSCCCCTNTPGPPSSLRRAFR RELPFPACHEIGLGABAGSGPPPAPARESSRRAMEEBASSPGI GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERRIMISSWE OKNICVWREDVKKFYLTMTNGPHMWSVKLDEHIPLGRALVYHEPIT DTTTAYTYLLLTHILGJCPQNVAFTSYGISFQAKQNSWYKPITY NTHLLTEETDSFVNKLDPSKVFKSRNIVIYFKKGPVQPAGGGK GSGSGSPSTSSTSKSSSGSSGSTFALABDTSLRRAFFR RELPFPACHEIGLGABAGSGPPPAARESSRRAMEEBASSPGI GGSKPPILKKLTLGITTLESSPGTTEVTIIEKPAARRHMISSWE GGSGSGSGFSTSSTSKSSSSGSSGSTFALTHESSPGTTTIEKPARAMEEBASSFGC GGSGPGFSTSSTSKSSSSSGSNGTPTTIEKPTIIEKPAARHTHI	}		1	
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	1			QKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI
SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPBKPHFDSRS		1		SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS

| SEQ   Predicted   Predicted   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclection   Inuclectide   Inuclectide   Inuclectide   Inuclectide   Inuclection   Inuclectide                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
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| Noticetide   Cortion corresponding to first amino acid residue of amino acid residue of amino acid sequence   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February    | SEQ      | Predicted  | Predicted end | Amino acid segment containing signal peptide                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| Corresponding   Corresponding   Corresponding   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirs   |          |            |               | (A=Aldning, C=Cysteine, Danapartit Acta, E=                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| to first amino acid residue of amino acid residue of amino acid sequence    Pepcline, O-Golutamine, N-Asparagine,   Pepcline, O-Golutamine, N-Valine,   Sestine, T-Threonine, V-Valine,   Sestine, T-Threonine, V-Valine,   W-TryPoplan, Y-Tyrosine, V-Valine,   W-TryPoplan, Y-Tyrosine, V-Valine,   W-TryPoplan, Y-Tyrosine, V-Valine,   W-TryPoplan, Y-Tyrosine, V-Valine,   W-TryPoplan, Y-Tyrosine, V-Valine,   W-TryPoplan, Y-Tyrosine, V-Valine,   W-TryPoplan, Y-Tyrosine, V-Valine, V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide deletion,   V-Popsible nucleotide delet | NO:      |            |               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| to first. amino acid amino acid amino acid amino acid amino acid amino acid sequence    Seferie, T-Thireonine, V-Valline,   Seferie, T-Thireonine, V-Valline,   Sequence   Seferie, T-Thireonine, V-Valline,   Sequence   Seferie, T-Thireonine, V-Valline,   Sequence   V-Valline, V-Tyrosine, X-Unknown, *-Stop   Sequence   V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline, V-Valline,  |          |            |               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| amino acid residue of amino acid sequence whytpothan, y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, EDTEIMFLORALYWHLIT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |          |            |               | L=Leucine, M=Methionine, N=Asparagine,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| menica edid sequence  amino acid sequence  codon, /=possible nucleotide deletion,  vpossible e nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible nucleotide deletion,  vpossible |          | to first   |               | P=Proline, Q=Glutamine, R=Arginine,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| antino acid sequence Codon, /=possible nucleotide deletion, /=possible nucleotide sequence V=possible nucleotide insertion)  VIFELDSCNOSGKVCLVYKSGKRALABDTEIMFLORALYMHELT DTFPAYVRLLITHLEOPKGVVATSISSPAKOKVSKYKPTTY NTHLILIEETDSFVAKLDPSKYKSKRNIVIEKKKGPVOPAGGGK OPSEPSGTSTSTSKSSGSGNTPUKTSTYKNIVIEKKKGPVOPAGGGK OPSEPSGTSTSTSKSSGSGNTPUKTSTYKNIVIEKKKGPVOPAGGGK OPSEPSGTSTSTSKSSSGSGNTPUKTSTYKNIVIEKKKGPVOPAGGGK OPSEPSGTSTSTSKSSSGSGNTPUKTSTYKTYPTUKTSTYRUKTSTYKTYPTUKTSTYRUKTSTYKTYPTUKTSTYKTYPTUKTSTYKTYPTUKTSTYKTYPTUKTSTYKTYPTUKTSTYKTYPTUKTSTYKTYPTUKTSTYKTYPTUKTSTYKTYPTUKTSTYKTYPTUKTSTYKTYPTUKTSTYKTYPTUKTSTYKTYPTUKTSTYKTYPTUKTSTYKTYPTUKTSTYKTYPTUKTSTYKTYPTUKTSTYKTYPTUKTSTYKTYPTUKTSTYKTYPTUKTSTYKTYPTUKTSTYTTTUKTSTYKTYPTUKTSTYTTTYPTUKTSTYTTTYPTUKTSTYTTTYPTUKTSTYTTYPTUKTSTYTTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYPTUKTSTYTTYTTYTTYTTYTTYTTYTTYTTYTTYTTYTTYTTY                                                                                                                                                                                                                                                                                                |          | amino acid | residue of    | S=Serine, T=Threonine, V=Valine,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| Sequence   V-possible nuclectide insertion                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |          | residue of | amino acid    | W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence    |          | amino acid | sequence      | Codon, /=possible nucleotide deletion,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| VIFELDSCNGSGKVCLVYLSGKPALAEDTEINFLDRALLWHEPT   DPTPAYTHLLITHILDFDQWOYAFTSYGLSGAQAGVSMYKPTY    NTHLLITESTDSFVNLDPSKVPKSRKKIVJPKKGPVQPAGGGK    GPSGPGGPTSTSSKSSSGSGNFTRK    6214   2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 1        |            | •             | \=possible nucleotide insertion)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| NTILLITETIDSFVINLIDPSKYPKSRKKIVIPKKKEPYQPAGGQK   CPSCPSGPSTSKSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | ļ        |            |               | VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| NTILLITETIDSFVINLIDPSKYPKSRKKIVIPKKKEPYQPAGGQK   CPSCPSGPSTSKSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | İ        |            | Į.            | DTFTAYYRLLITHLGLPOWOYAFTSYGISPQAKQRVSMYKPITY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| GPSCPSGPTSSTSKSSSGNPTRK  2 460 HELBPSATERJARJELJGPARGSBAAAFYFVRGFRTGMSFVOWV VLGTSAKSTRLFFFLSKMAASSRAQVLALYRAMLEBEKRPSVOWV VLGTSAKSTRLFFFLSKMAASSRAQVLALYRAMLEBEKRPSVOWV VLGTSAKSTRLFFFLSKMAASSRAQVLALYRAMLEBEKRPSVOWV VLGTSAKSTRLFFFLSKMAASSRAQVLALYRAMLEBEKRPSVOWV VRTYAVRSILDARFRINDWXDVEIQTLAVKKKRCLGVIRQVH IQQLYSTOKLI I ENROMPRT  2 1849 FVAGGFRGSGSABETMEETRTFLGAGQDVGRSCTLVSLAGKNV MLDCGMHGMFUNDRFFPDRSYTTONGRITDFLOVI ISHFHLDH CGALPYFSEWVGYDDEI YMTHFTQALCPILLBUTKKLAVVKKUGA ANFOLKVOS BSVVYTGDYMMFDGHLGAANIDKCRPHLLLTSHFHLDH CGALPYFSEWVGYDDEI YMTHFTQALCPILLBUTKKLAVVKGUGA ANFOLKVOS BSVVYTGDYMMFDGHLGAANIDKCRPHLLLTSHFHLDH CGALPYFSEWVGYDDEI YMTHFTQALCPILLBUTKALAVAGHULGA ANFOLKVOS BSVVYTGDYMMFDGHLGAANIDKCRPHLLST YAATTI ADSKRCERSPDLKKWHETVERGGKVLLI PVALGRAQELC LLLETTWERSPLKKVOYTHYTGRAGVIDVAGCELOF FVGRMFEPKHLAARDPAARANDFOMPVVFATPGHLGAGSLOLF RKWAGNERNWY IMPGVCVQGTVGHKILLSGGRKLEBEGROULGE RKWAGNERNWY IMPGVCVQGTVGHKILLSGGRKLEBEGRFOLLE MOVYTMSSCHALANGSBEGAMVGVGSPESVLLIVGBERKMEFILK KEDELRVNCYMPANGETVTLJTSPSI PVGISLGLKREMGGEL LLEAKFRELLIGHLIMKDNSHFLAVSSEQALKELLGRENGRFTC RVHLHIDTTRKSGCTALRVVSHLSSTLKGHLGASPS LAALAPSBEDDTAVLJUSMYTVDGELGSFUTSLLKKGLPQASPS LAALAPSBEDDTAVLJUSMYTVDGELGSFUTSLLKKGLPQASPS LAALAPSBEDDTAVLJUSMYTVDGELGSFUTSLLKKGLPQASPS LAKLFTGLGSFETTDOLERHEREKRGTLTDCVVMDPQTTRSRG GARGEGGGARMWKTLTFFVALDGUAVMLAVVLKMPDGTFTRSRG GCPVTTSCVEEVDAAMCARPHKVDGRVVSFRRAVSREDSVKPG RGGTGGGGGGGYNGFGGGGNTGGGGFTVARDPGTGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | <b>\</b> |            |               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 6214 2 460 HELAPSATERARICALDRANGSRAADYPVRGPFTCHSFYOWY VLOTSAKTERLPFTISKMANASSRAQVALAYMAR.BBSKRPSANY VLOTSAKTERLPFTISKMANASSRAQVALAYMAR.BBSKRPSANY VRTYAVERIRDAPERNGVKDPVEIQTLVNKAKROLGVIRRQVH IGQLYSTOKLIENROMPRT 6215 2 1849 FVAGGPRGSGARETMFEIRVTPLGAGQDVGRSCILVSIAGKNV MLDCGHMSTRIDDRRFPDFSYTIQNGGRITDFLDCVIISHFLDH GALPYSEMVGVGDFINMFPDGALFFILLDEVRKIAVDKKGE ANFOIKVGSSVVYTODNHTPDGALFFILDEVRISHFLDH GALPYSEMVGVGDFINMFPDGALFFILDEVRISHFLDH GALPYSEMVGVGDFINMFPDGALFFILDEVRISHFLDH GALPYSEMVGVGDFINMFPDGALFFILDEVRISHFLDH GALPYSEMVGVGDFINMFPDGALFFILDEVRISHFLDH GALPYSEMVGANGFUNG GALPYSEMVGVGDFINMFPDGALFFILDEVRISHFLDH GALPYSEM ANFOIKVGSSVVYTODNHTPDGALFGALBURKAVDKKGE ANFOIKVGSSVVYTODNHTPDGALFGANDKENDLITEST YATTIGDSKCRERDFLKKVHETVERGGKVLIPVFRAGASLCI ILLETYMERNILKVFIYSTOTHERANNFYKHFIFFTWANGFIKKT FVQRNMFPEKKINAPPAFADNGFMVVFATFOMLHAGGSLCIF RRWAGHENNIKVFPTAFFADNGFMVVFATFOMLHAGGSLCIF RRWAGHENNIKVFPTAFFADNGFMVFATFOMLHAGGSLCIF RRWAGHENNIKVFTPAFADNGFMVVFATFOMLHAGGSLCIF RRWAGHENNIKVFTPAFADNGFMVVFATFOMLHAGGSLCIF RRWAGHENDARFTKLLVSTAMVGANGFMANGFALKFTSSVALKSCAMGA LLFTKKTPAMAGETALRVSSHLKSVLKARCVQHLEPDGSVTVSVL LAGARFGANGANTAVSSSVALLGRSRFQLARFFTLAMSKALAGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSSLKARGANTAVSTRAGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGANTAVSKLKARGA |          |            | }             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| ULGTSAKTTLLFFTS.KMAASSRAQVLALIRAMLRESKEPSAYN YRTYAVREI IDAPERENKYVLOPDE QTLVNKAKRLGVIRQVH IQQLYSTOKLI IENROMPRT  6215  2 1849 FVAGGRGSGSARETHFFIRVTPIGAGQDVGRSCILVSIAGRUV MLDCGHHEMYRDDRFFPSYTTOMGRLTDFLDCVIISHFHLDH CGALPYFSEMVGTOGF IYMTHPTQAICPILLEDYRKIAVACHUGA ANFGIKUGSBSVYYTNODYNMTPDRHLGAGATDKCRPHLLITEST YATTIRDSKGCREEDFLKKVHLGTVQVDDELBIKNYYACHVUGA ANFGIKUGSBSVYYTNODYNMTPDRHLGAAGINCKCPHLLITEST YATTIRDSKGCRERDFLKKVHLGTVQNDELBIKNYYACHVUGA ANFGIKUGSBSVYYTNODYNMTPDRHLGAAGINCKCPHLLITEST YATTIRDSKGCRERDFLKKVHLFVERGGKVLHYFFPALGAGAGLEC LILETTWEENMILKVPIYFSTGILBKANHYKLFIFFWINGKIKT FVQGNMFBFRHIKAPDAFADNGGPHVYPATFOMLHAGGSLGIF RKHAGNEKMVIMPGYCVGGTVGHKILLSGGRKLEMEGRGVLEVK MCVEYNFSFRHADAKGINQLVGQABPESVILLVHGEAKMEFIKAV KIEGELRVNCVMPANGBTVTLPTSPSIFVGISLGLIKRERRAGGI LPBAKKPRLILBGTLIMKOSNFRLVSSEGALKBIGLARHGLRFTC RVHHENTRKREPALLRGTLIMKOSNFRLVSSEGALKBIGLARHGLRFTC RVHHENTRKFPRLILBGTLIMKOSNFRLVSSEGALKBIGLARHGLRFTC RVHHENTRKFPRLILBGTLIMKOSNFRLVSSEGALKBIGLARHGLRFTC RVHHENTRKFPRLILBGTLIMKOSNFRLVSSEGALKBIGLARHGLRFTC RVHHENTRKFPRLILBGTLATHVONGVSVSVSLLGERSFFQLGRFMSS GAHGEESSARWKTLIFFVALDGVAVSKINVVLKSHHGHERPE FIAPPHLBIRTKFPPHGGGNAVGVSVSVSLLGERSFPLGKFMFSS GAHGEESSARWKTLIFFVALDGVAVSKINVVLKSHHGHERPE FIAPPHLBIRTKFPPHGGGNATUFFSVSTLLENGLERGGERDFKERE GESTAGRGGGGGALKBEVESFFFRRGDESGGRERRRGEEGHDFKEPEQ LRKLFIGGISFETTDDSLREHFEKWGTLTVVLKSHGOFTSCHERPE FIAPPHLBIRTKFPPHGGGGNAVGSFGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |          |            |               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| ### STYANGRIPDAFRENKNYKDEVETQTLVNKAKRDLGVTRRQVH    TOQUYSTOKLI ERROMPET                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 6214     | 2          | 460           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| IGQLYSTOKILIENROMPRT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ŀ        |            | 1             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 1849   VYÄÄGERGSARÄTHEERTYELÄÄGODVORSCILVSIAGKON                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |          | ļ          | •             | 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| MLDCGHMGFNDDRFPPFSYITONGELTDFLOCVILSFHELDE   CGALPPYSEMWCYDGITUMTPOTAL CPILLEDYRKIADVAKGE     ANFFISQMI KDCMKKVVAVHLHCTVQVDDELBIKAYYAGHVLGA     AMFOIKVGSESVYTTGDYMMTPDRHLGAMIDKCRPNLLITEST     YATTIRDSRGCREDPLKKVHETVERGGKVLIFVFAGRAGELC     ILLETFWERMILKVPIYFSTGLITEKANHYYKLFIPWINGKIKK     FVORIMFERSHIIKAPDRAFANDOPMYVETGHLINGGSLGIF     RYMAGNEKMMYIMPGVCVGGTVGHKILSGORKLEMEGROVLEVK     MQVEYMSFSAHADAKGIMQLVGAPEPSLHJMGGAGLEC     REMAGNEKMMYIMPGVCVGGTVGHKILSGORKLEMEGROVLEVK     MQVEYMSFSAHADAKGIMQLVGAPEPSLHJMGHAKHPIKL     KIEGELRVNCTMPANGETVILPTSPSIPVGISLGLIKREMAQGIL     LPEAKKRILLHGTLIHKOSNFRLHVSEQALKBICLHGHAPTOR     RVHHIDTIREGGTALRVYSHLKSVLKDHCOQHEDDGSVTVESVL     LQAAAPSEDPGTKVLLVSHTVQDEBLGSFLITSLLKKRLPQAPS     RVHHIDTIREGGTALRVYSHLKSVLKDHCOQHEDDGSVTVESVL     LQAAAPSEDPGTKVLLVSHTVQDEBLGSFLITSLKKRLPQAPS     CATTPEFERSALRGSRSKANVOVGSVSTALGSRFPQLGFMSS     GAHGEEGSARMKKTLTFYALDGVAVSMLNVYLKSHHGBHERPE     FIAYPHHRIRTIKFPMGOINTLIFHNPHVNPLPTGYFEDS     GAHGEEGSARMKKTLTFYALDGVAVSMLNVYLKSHHGBHERPE     FIAYPHHRIRTIKFPMGOINTLIFHNPHVNPLPTGYFEDS     CARLEL FOR STANDARD     FIAYPHHRIRTIKFPMGOINTLIFHNPHVNPLPTGYFEDS     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLEL FOR STANDARD     CARLES FOR STAND   |          | i          |               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| CGALPYSERMYGYDGP IYMTHPTQAICPILLEDTRIADVKSGE ANPTTSGNIKOMKKVVAVAHLHGTQVOUPDELEIKAYYAGHVLGA AMPQIKVGSESVVYTGDYNMTPDEHLGAAMIDKCRPNILITEST YATTIRDSKRCRERDELKKVIETVERGKVLIPTVPALGRAQELC ILLETTWERMALKVPITYSTGLTEKANHYYKLFIPWTNGKIRKT FVQRNMFEPKHIKAPDRAFADNPOPMVPATFGHLIAHGGSLQIF RKWAGMEKNMYIMPGYCVGGTVGHKILISGGKLEMBGRQVLEVK MQVEYMSFSAHADAKGIMQLVGQAEPSVLLVHGEAKMEFIKQ KIEGLERVACVMPANGETVTLTF951PUTGISLGLLKREMAGGL LPEAKKPRLLHGTLIMKOSNPELVSSEQALKRLGLAEHGLRFTC RVHHHDTRKEQETALRVYSHLKSVLKDHCVQHLPGGSVTVESVL LQAAAPSEDPGTKVLLVSSTVQDERLGSFLTSLLKKGLEQAPS  6216 11 393 GTTEPEPRISALRGSRSKMAVVGYSSVSRLGGSRPGVGAPMSS GAGGEGSGARMWKTLTFPAALPGVAVSMUTLSSHGBHERPE FIAYPHHRITRTKPPFMGDONHTLFHNPHVNPLPTGYSDB TYVGRGESGLKMEVVEPPGPOPPOGRERGEGGGDGPYGE GAHGEGSGARMWKTLTFPAALPGVAVSMUTLSSHGBHERPE FIAYPHLRITRTKPPMGDONHTLFHNPHVNPLPTGYSDB TRVGRGESGLKMEVVEPPGPPOPPGGRERGEGGGDFYEPEQ LRKLFIGGLSPETTDDSLREHFEKMGTLTDCVVRRDPGTKSEG GGFVTYSCUERVDAAMCARPHKVDGRVDFKFEGEGDPFNEGG ASSGRGGGGRIKMEVGENFOFPOPPGGSGRAFGEGGGDFOFKEGG ASSGRGGGGGNFGGGGGNFGGGGGGGGGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 6215     | 2          | 1849          | FVAGGPRGSGSAAETMPEIRVTPLGAGQDVGRSCILVSIAGKNV                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| ANPTISMI KDOMKKUVAVHLIGTUQVDDELBIKAYYAGHVLGA AMPOIKVGGESUVTORDINTPORHLGANIDKCRPNLITEST YATTIRDSKRCRERDFLKKVHETVERGGKULIPYFALGRAQELC ILLETFWERMILKVPITFSTGLITEKANHYYKLFIPWTNQKIRKT FVQRNMFERKHIXAFDAFADNEGMVVFATFOMLHAGGSLQIF RKWAGNEKNNVIMPGYCVQGTVGHKILSGGRKLEMGRGVULVGV MQVEYMFSSAHADAKGIMQLUGQABESVLLUVKGEAKKMEFIKQ KIEGELRUNCYMPANGETVTLLPTSPSIPVGISLGLIKRERMAGGL LPEAKKPRILHGTLIMKOSNFRLUVSSEQALKEIGLAERDLRTC RVHHDITRKEGSTALRVYSHLKSVLKDHCVQHLPDGSVTVESVL LQAAAPSEDPGTKVLLVSWTYQDEBLGSFITJSLLKKGERQAPS GAHGEGSARMWKTLTFFVALDGVAVSHLNVLKSHKGHERPE FIAPHLHAITRTKPFPEMGOGNTLFINHPWNPLPTGYEDB  6216  11  393  GTTRFEFRNSALRGSRSKMVVVSSYSRLLGRSRFOLGRFMSS GAHGEGSARMWKTLTFFVALDGVAVSHLNVLKSHKGHERPE FIAPHLHAITRTKPFPEMGOGNTLFINHPWNPLPTGYEDB  6217  9  1178  TRVGRGESGLKMEVKPFPGRPQPDSGRRRRRGEEGHDKEPEQ LRKLFIGGLSFETTDDSLRSHFEKWGTITDCVVMRPQTKRSR FGFVTYSCWEDVAAMCARPHKVDGAVVBFRRAVSREDSVKEGA HLTVKKIFVGGIKEDTETYBLRDYFEKYGKTETTIFVMEDROSGK KRGPAFVTSCWEDVAAMCARPHKVDGAVVBFRRAVSREDSVKEGA HLTVKKIFVGGIKEDTETYBLRDYFEKYGKTETTIFVMEDROSGK KRGPAFVTSCWEDVAAMCARPHKVDGAVVBFRRAVSREDSVKEGA GASRGSGGGGGYNGFGGGGGGNTGGGGRGGGGGGGGGGGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |          | Ì          |               | MLDCGMHMGFNDDRRFPDFSYITQNGRLTDFLDCVIISHFHLDH                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| AMPOIXVGSESVVTGDYMTPDRHIGAAMIDKCRPNLLITEST YATTIRDSKRCRERDFLKKWHETVERGAELC ILLETTWEEMMILKYP 17FSTGLTEKANHYYKLFIPWINQKIRKT FVQRNMFERKHI KAPDRAFADWGPMVVFATPEMULIAGGSLQIE RKWARGHEKMIVIMEGYCVGTVGHKLISGGRKLEMEGRGVLEVK MQVEYMSFSAHADAGIMQLVGQAEPESVLLVHGEAKKMEFIKQ KIEQELRVNCYMPANGETVVLPTSSICULSGGRKEMEMGRULEVK MQVEYMSFSAHADAGIMQLVGQAEPESVLLVHGEAKKMEFIKQ KIEQELRVNCYMPANGETVTLPTSSICULSGGLKEMEMAGGL LPEAKKPRILHGTLIMKOSNFRLVSSEQALKELGLAEHQLRFTC RVHHHDTRKEQSTALRVYSHLKSVLKDDKCVQHLPDGSVTVESVL LQAAAPSEDPGTKVLLVSMTYQDEELGSFLTSLLKKGLPQAPS  6216 11 393 CTTRPEFRINSALKGSRSMMVUVGVSSVSRLIGRSRPGLGFPMSS GAHGEEGSAMMKTLTFVALPGAVANVVKNSHGEMERPE FIAPPHLRIRTKPFPWGDQNHTLFHNPHVNPLPTGYEDB GAHGEEGSAMMKTLTFVALPGAVANVVKNSHGEMERPE FIAPPHLRIRTKPFPWGDQNHTLFHNPHVNPLPTGYEDB LRKLFIGGLSFETTDGLSREHFEKWGRVYEPGRAVSEDSVKPG LRKLFIGGLSFETTDGLSREHFEKWGRTTDCVVMRDPQTKRSRG RGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSEDSVKPG HATVKLFIVGGIKEDTEFYNLRDYSKJEGSTGAGGGGGG GGSRGSGGGGGGGGGGGGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | i        | i          | İ             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| VATTIRDSKRCKERDFLKKYHETVERGGKVLIPPALGRAĢELC   ILLETFWERMILKVPIYPSTGITEKANHYKKPIFPHTNÖKIRKT   FVQRNMFERKHIKAFDRAFADNPGPMVVFATPGMLHAGQSLQIF   RKWAGNEKMNVIMPGYCVQGTVGHKILSGQRKLEMGBRQVLUSKY   MQVEYMFSSAHADAKGIMQLVGQABFBESVLLVHGEAKKMEFIKQ   KIEGELRUNCYMPANGETVTLIPTSPSIPVGISLGLIKREMAGGL   LPEAKKPRILHGTLIMKOSNFRLVSSEQALKELGLAEHGLRFTC   RVHLHDTRKEQSTALRVYSHLKSULKDEVQHLPDGSVTVESVL   LQAAAPSEDPGTKVLLVSNTYQDEELGSFLITSLLKKGLPQAPS   CATREFERNSALKQSSKMAVVGVSKSLLGKSRPGLGAFPMSS   GAHGEEGSARMWKTLTFPVALDGVAVSMLNVYLKSHGGHERPE   FIAYPHHRIRTKFPFWGDGNHTLHFNNYLPTGYEDB   FIAYPHHRIRTKFPFWGDGNHTGHFKNGTTDCVVMRDPQTKRSRG   GAHGEEGSARMWKTLTFPVALDGVAVSMLNVYLKSHGGHERPE   FIAYPHHRIRTKFPFWGDGNHTGHFKNGTTDCVVMRDPQTKRSRG   PGFVTYSCVEEVDAAMCAPHRVLOGAVERPKAVSKEDSVKGA   AGSQRGSGIKNFWFPGGRPGPDSGRRRRRRGEEGHDPKEPEQ   LEKLFIGGLSFETTDDSLREHFEKNGTTDCVVMRDPQTKRSRG   PGFVTYSCVEEVDAAMCAPHRVLOGAVVEPKRAVSKEDSVKGA   AGSQRGSGGKNAMCAPHRVLOGAVVEPKRAVSKEDSVKGA   AGSQRGSGGSGNAMCAPHRVLOGAVVEPKRAVSKEDSVKGA   AGSGRGSGGSGNAMGRGNFGGGGGNTGRGGNFGGGGGGGGGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |          | i          |               | ANFFTSQMIKDCMKKVVAVHLHQTVQVDDELEIKAYYAGHVLGA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| VATTIRDSKRCKERDFLKKYHETVERGGKVLIPPALGRAĢELC   ILLETFWERMILKVPIYPSTGITEKANHYKKPIFPHTNÖKIRKT   FVQRNMFERKHIKAFDRAFADNPGPMVVFATPGMLHAGQSLQIF   RKWAGNEKMNVIMPGYCVQGTVGHKILSGQRKLEMGBRQVLUSKY   MQVEYMFSSAHADAKGIMQLVGQABFBESVLLVHGEAKKMEFIKQ   KIEGELRUNCYMPANGETVTLIPTSPSIPVGISLGLIKREMAGGL   LPEAKKPRILHGTLIMKOSNFRLVSSEQALKELGLAEHGLRFTC   RVHLHDTRKEQSTALRVYSHLKSULKDEVQHLPDGSVTVESVL   LQAAAPSEDPGTKVLLVSNTYQDEELGSFLITSLLKKGLPQAPS   CATREFERNSALKQSSKMAVVGVSKSLLGKSRPGLGAFPMSS   GAHGEEGSARMWKTLTFPVALDGVAVSMLNVYLKSHGGHERPE   FIAYPHHRIRTKFPFWGDGNHTLHFNNYLPTGYEDB   FIAYPHHRIRTKFPFWGDGNHTGHFKNGTTDCVVMRDPQTKRSRG   GAHGEEGSARMWKTLTFPVALDGVAVSMLNVYLKSHGGHERPE   FIAYPHHRIRTKFPFWGDGNHTGHFKNGTTDCVVMRDPQTKRSRG   PGFVTYSCVEEVDAAMCAPHRVLOGAVERPKAVSKEDSVKGA   AGSQRGSGIKNFWFPGGRPGPDSGRRRRRRGEEGHDPKEPEQ   LEKLFIGGLSFETTDDSLREHFEKNGTTDCVVMRDPQTKRSRG   PGFVTYSCVEEVDAAMCAPHRVLOGAVVEPKRAVSKEDSVKGA   AGSQRGSGGKNAMCAPHRVLOGAVVEPKRAVSKEDSVKGA   AGSQRGSGGSGNAMCAPHRVLOGAVVEPKRAVSKEDSVKGA   AGSGRGSGGSGNAMGRGNFGGGGGNTGRGGNFGGGGGGGGGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |          | 1          |               | AMFOIKVGSESVVYTGDYNMTPDRHLGAAWIDKCRPNLLITEST                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| ILLETPHERMILKVPIYFSTGLITEKANHYYKLFIPHTNOKIRKT   FVQRNMFEPKHIKAPDRAFADNOFOMVVPARPOMLIHAGGSLQIF   RKWAGNEKMWIMEGYCYGOTYGHKILSGGRKLEMEGRQVLEVK   MQVEYMFSSAHADAGIMQLVGQABPESVLLVKGEAKKMEFIKG   KIEGLEKVNCYMPANGETVILTSPS IPVGISLGLKKEMEPIKG   LPBAKKPRILHGTLIMKOSNFRLVSSEQALKELGLAEHQLRFTC    RVHLHDTRKBQETALRVYSHLKSSUKJOVHDEDGSYVTESVL   LQAAAPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGLPQAPS   CTTRPEPRISALRQSRSKMAVVGVSSVSRLIGSRSPGLGFPMSS    GAHGEEGSARMKKILTPVALPGAVASMLNYYLKSHHGEHERPE    FIAYPHARIRTKPPWGDGNHTLFINPHVNPLPTGYEDB    GAHGEEGSARMKKILTPVALPGAVASMLNYYLKSHHGEHERPE    FIAYPHARIRTKPPWGDGNHTLFINPHVNPLPTGYEDB    ARKLFIGGLSFETTDDSLRHFFKKMGTITDCVMRDPQTKRSRG    RGFYTYSCUEBVDAMACARPHKVDGRVVEPKRAKASEDSVKPGA    HLTVKKITYGGIKEDTESYNLRDYFSKYGKLETIFVMERPQSK    KRGRAFVTFDDHDTVDKIVVGVKHTINGHICEVKKALSKORMOS    AGSQRGRGGGSGNFMRGGGGNFGGGGNGFGGGGGGGGGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Ì        |            | Į.            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| FYQRIMPERKHI KARDRAFADNPOPMVPATPOMILIAGOSLQIF RKWAGNEKNAVIMPGYCVQGTVGHKILSGQRKLEMEGRQVLEVK MQVEYMSFSAHADAKG INQLVGQAEPESVLLVHGEAKKMEPLKQ KIEQELEVNCYMPANGETVTLPTS PS TPUSISLGLLKRENAQGL LPEAKKPRLHGFLIMKONNFRLVSSEQALKBIGLABEHQLRFTC RVHLHDTRKEQETALRVSHLKSVLKDHCVQHLPDGSVTVESVL LQAAAPSEDPGTKVLLVSWTYQDELGSFLTSLLKKGHQAPS GTTREFERNSALKQSRSKMAVVGVSSVSRLLGRSRPQLGRPMSS GAHGEGSARMWKTLTFFVALDGVAVMLNVYLKSHHGEHERPE FLAYPHRIETKTSPPROGONITLENHVAVLPTYSEDR 6217 9 1178 TRVGRGESGLKMEVKPFPGROPNDSGRRRRRGEEGHDPKEPEQ LRKLFIGGLSFETTDDSLREHFEKWGTLTDVVMRDPGTKRSRG RGFVTYSCVEEVDAAMCARPIKKVDCRVVBFKRAVSREDSVKFGA HLTVKKIFVGGIKEDTESFULRDVFKRAVSREDSVKFGA HLTVKKIFVGGIKEDTESFULRDVFKRAVSREDSVKFGA AGSQRGRGGGSGNFMGRGGNTGGGGGSTGGGGGGGGG GGSRGSVGGGGGGGGGGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |          |            |               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| RKMAGNEKINNTIMPGYCVOGTVGHKILISGGRKLEMEGRGVUEVK MQVEYMSFSAHADAKGIMQLVGQAPBESVLLVHGEAKKMEFIKQ KIEGELRVNCYMPANGETVTLPTSPSIPVGISLGLLKREMAGGIL LPEAKKPRLIHGTLIMKDSNFRLVSSEQALKBLGLAREHQLBFTC RVHLHDTRKBGETALRAVISHLKSVLKDHCVGHLPDOSVTVESVL LQAAAPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGLPQAPS  6216  11 393 GTTRFEFRNSALRQSSKMAVVGSSVSRLLGRSRFQLGRFMSS GAHGEGSARMWITLTFVALBGGVAVSMLNVYLKSHGGHERPE FIAYPHLRIETKFFPPGDONHTLEHNPHVMPLDFTGYEDB 6217 9 1178 TRVGRGESGLKMEVKPPFGRPQDDSGRRRRRRGEEGHDPKEPEQ LRKLFIGGLSFETTDDSLREHFEKMGTLTDCVVMRDPQTKSSRG PGFVTYSCVEBVDAAMCARPHKVDCRVVEFKRAVSREDSVKPGA HLTVKKIFVGGIKEDTEEYNLEDVFEKYGKTETIEMEDROGSK KRGFAFVTFDDHDTVDKLVVQKYHTINGHNCEVKKALSKQEMQS AGSQRGGGGSGNFGGGGGGFGGGGGGGGGGGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 1        |            |               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| MOVEYMSFSAHADAGIMQLVGQABPESULUWGEAKKMEFIKQ KIEQELRVNCYMPANGETVTLDTS PS I PVGISIGLIKEMEMQGI LPEAKKPRLHGTLIMKDSNFRJVSSEQALKBLGLAEHQLRFTC RVHLHDTRKBQETALRVYSHLKSVLKDHCVQHLPDGSVTYTESVL LQAAAPBEDPGTKVLLVSWTYQDEBLGSFUTSLIKKGUPQAPS  6216  11 393 QTTRPEPRNSALRQSRSKMAVVGVSSVSRLLGSRFPQLGRPMSS GAHGEGGSARMKTLTFFVALPGVAVSMLNVTLKSHHGHERPE FIATPHHRIRTKFPFPGDONITLIHNPHVNPLPTGYEDB  6217 9 1178 TRVGRGESGLKMEVKPPPGRPOPDSGRRRRRGESGHDFKEPE LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQTKRSRG RGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSREDSVKPGA HLTVKKIFVGGIKEDTESYNLRDVFEKYGKETITEVMEDROSGK KGRPAFVFTPDHDTVDKLVVQKYKHINGHNCEVKKALSKOEMOS AGSQRGGGGGNFGRGGGTNGRGGONFGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Į.       | 1          | İ             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| KIEGELRVNCYMPANGETVILPTSPS 19VGISLGILKREMAGGI LPEAKKPRLIHGTLIMKDSNFRLVSSEQALKBLIABEIQLRFTC RVHLHDTRKRGETALRVYSHLKSVLKDHCVGHLPGSVTVESVL LQAAAPSEDPGTKVLLVSMTYQDEBLGSFLTSLLKKGLPQAPS  6216  11 393 QTTRPEPRNSALRQSRSKMAVVOVSSVSALLGRSRPOLGRPMSS GAHGEEGSARMKTLTFFVALPGVAVSMLNVYLKSHHGEHERPE FIAYPHURIRTKFPPMGDGNHTLFHNPHVNILPTGYEDB  6217 9 1178 TRVGRGESGLKMEVVEPPGRFDQDGGRRPRRRGESGHDPKEPEQ LRKLFIGGLSFETTDDSLREHPEKWGTLTDCVVMRDPQTKRSRG RGFVTYSCVEEVDAAMCARPHKVDGRVVPSKRAVSREDSVKPGA AGSQRGGGGGGTGKGRGFGGGGGGGGGGGGGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 1        |            |               | MOVENMEET AND DESCRIPTION OF DESCRIPTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF TH |
| LPEAKKPRILHGTLIMKOSNFRIVSSEOALKSIGLAERIOLEFTC RVHLHDTRKEQETALRVYSHLKSVLKCHCVQHLPDGSVTVESVL LQAAAPSEDECTKYLLVSMTYQDEBLGSFLITSLLKKKGLPQAPS 6216 11 393 GTTRPEPRISALRQSRSKMAVVGVSSVSLGGRSRPQLGRPMSS GAHGEEGSARMWKTLTFYVALPGVAVSMLNVYLKSHGEHERPE FIAYPHRIRIKKPPMGDOMHTLFINPHVNIPTGYSDB 6217 9 1178 TRVGRGESGLKMEVKPPFGRPQDESGRRRRRGEGHIDPKEPEQ LRKLFIGGLSFETTDDSLREHPEKWGTLTDCVVMRDPQTKRRG FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSREDSVKPGA HLTVKKIFVGGIKEDTEEYMLRDYFFKYGKLETIEVMEDROSGK KRGPAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSKQBMQS AGSQRGRGGGSGNFWGRGGNFGGGGGPTGGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 1        | i          |               | MOVE THIS PORTAGE PROPERTY DECRET DIVETEL CLI KDEMACCI.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| RVHLHDTRKBQETALRVSHLKSVLKDHCVQHLPDGSVTVESVL LQAAAPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGLPQAPS  GTTRPEPRNSALRQSRSRMAVWGVSSVSRLIGRSRPQLGRPMSS GAHGEEGSARMWKTLTFVALDFGVAVSMLNVYLKSHGEHERPE FLAYPHLRIRTKPFPWGGNITLHINPHVNPLPTGYEDB  6217  9 1178 TRVGRGESGLKMEVKPPFGRPQPDSGRRRRRGEEGHDPKEPEQ LRKLFIGGLSFETTDDSLREHFEKWGTTDCVVMRDPQTKRSRG PGFVTYSCVEEVDAMCARPHKVDGTVDEFKRAVSREDSVRGA HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVMEDRQSGK KRGPAFVTFDDHDTVDKLVVQKYHTINGHNCEVKKALSKQEMQS AGSQRGGGGSGNFMGRGGGGGGGGFGGRGGRGGRGGGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |          |            |               | KIEGELKVNCYMPANGETVILPISPSIPVGISLGLDKKENAQGD                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| LQAAAPSEDPOTKVLLVSWTYQDELGSFLTSLLKKGLPQAPS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 1        |            | 1             | LPEAKKPRLINGTLIMKDSNFKIVSSEQAIRBIGHAANQDRFTC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| 6216  11  393  QTTREPENSALRQSRSKMAVVGVSSVSRLLGRSRPQLGRPMSS GAHGEEGSARMWKTLTFFVALDGVAVSMLNVYLKSHHGEHERPE FIATYPHLRIRTKPFPWGDGNTTLFHNPHVPPLPTGYEDB  6217  9  1178  TRVGRGESGLKMEVKPPPGRPQDDSGRRRRRGEEGHDPKEPEQ EKKLFIGGLSFETTDDSLREHFERWGTTTDCVVMRDQTKRSRQ EGFYTYSCUSEWDAMAMCARPHKVDGRVVEPKRAVSREDSVKPGA HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVMEDRQSGK KRGFAFVTFDDHDTVDKLVVQKYHTINGHNCEVKKALSKQEMQS AGSQRGRGGGSGSNFMGRGGGGGSGNFGRGGGNGGRGGGGGGGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |          |            |               | RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSVTVESVL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| GAHGEGSARMMKTLTFFVALPGVAVSMLNVYLKSHHGEHERPE FLAYPHLRIRTKPFFWGDGNHTLFHNPHVNPLPTGYEDB TRVGRGESGLKMEVKPPFGGPQPDSGRRRRRGEEGHDFKEPEQ LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQTKRSRG PGFVTYSCVEEVDAAMCARPHKVDGRVEFKRAVSREDSVKPGA HLTVKKIFVGGIKEDTEEVNLRDYFEKYGKIETIEVMEDRQSGK KRGPAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSKQEMQS AGSQRGGGGGGHTGGGGNTGGGGGFGGGGGFGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |          |            |               | LOAAAPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGLPQAPS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| FIAYPHLRIRTKPFPEGGONHTLEHNPHWNPLPTGYEDE   1178                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 6216     | 11         | 393           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 1178   TRVGRGESGLKMEVKPPPGRPQPDGSGRRRRRGEEGHDPKEPEQ LRKLFIGGLSFETTDDSLREHFERWGTLTDCVVMRDPQTKRSRG FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSREDSVKPGA HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVMEDRQSGK KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSKQEMQS AGSQRRGGGGGNFMGRGGGGGGGGGGGGGGGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |          |            | 1             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| LRKLFIGGLSFETTDDSLREHFEKMGTLTDCVVMRDPCTKRSRG FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSREDSVKPGA HLTVKKIFVGGIKEDTEYNLRDVFEKYGKIETIEVMEDRQSGK KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSKQEMQS AGSQRGGGGSGNFMGRGGNFGGGGNFGGGGYGGGGPYG NGGGYGGGGGYNGFGGGGNFGGGGNFGGGGPGYGGGGPYG NGGGYGGGGGYNGFGGGGGYNGFGGGNYGGGPYNDFGNYSGQQQS NYGPMKGGSFGGRSSGSPYGGGYGSGGGGGGYGSYNDFGNYSGQQQS NYGPMKGGSFGRSSGSPYGGGYGSGGGGGGGYGSYRFF SCERRGFIMADDLKRFLYKKLPSVEGLHAIVVSDRDGVFVIKVA NDNAPBHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFBELRQVVEVS VQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFBELRQVVEVS IGVSGGTASGKSTVCEKIMELLGQNEVBQRQRKVVILSQDRFYK VLTARGKAKALKGQYNFDHPDAFDNDLHHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFBGILVFYSQEIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFEEFCLP TKKYAPDVI FRGVDNMVAINLIVOHIQDILNGDICKWHRGGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH EQNISLEMSCTIEKALADAKALVERLENDHDDAESLIEQTTALN KRYAPANLGYQEEIQELNEVARHRPRSTLVMGIQQENRQIRELQQ ENKELRTSLEEHGSALELIMSKYREDMFALLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH  6221 98 916 RWINDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NUGAGLSWGLYFVFYNNIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVXIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYBLLKLKYNQHINRLPE AQLSTUEYISVAALSKIFAVAATYPQVVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |          |            | i             | FIAYPHLRIRTKPFPWGDGNHTLFHNPHVNPLPTGYEDB                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| LRKLFIGGLSFETTDDSLREHFEKMGTLTDCVVMRDPCTKRSRG FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSREDSVKPGA HLTVKKIFVGGIKEDTEYNLRDVFEKYGKIETIEVMEDRQSGK KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSKQEMQS AGSQRGGGGSGNFMGRGGNFGGGGNFGGGGYGGGGPYG NGGGYGGGGGYNGFGGGGNFGGGGNFGGGGPGYGGGGPYG NGGGYGGGGGYNGFGGGGGYNGFGGGNYGGGPYNDFGNYSGQQQS NYGPMKGGSFGGRSSGSPYGGGYGSGGGGGGYGSYNDFGNYSGQQQS NYGPMKGGSFGRSSGSPYGGGYGSGGGGGGGYGSYRFF SCERRGFIMADDLKRFLYKKLPSVEGLHAIVVSDRDGVFVIKVA NDNAPBHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFBELRQVVEVS VQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFBELRQVVEVS IGVSGGTASGKSTVCEKIMELLGQNEVBQRQRKVVILSQDRFYK VLTARGKAKALKGQYNFDHPDAFDNDLHHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFBGILVFYSQEIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFEEFCLP TKKYAPDVI FRGVDNMVAINLIVOHIQDILNGDICKWHRGGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH EQNISLEMSCTIEKALADAKALVERLENDHDDAESLIEQTTALN KRYAPANLGYQEEIQELNEVARHRPRSTLVMGIQQENRQIRELQQ ENKELRTSLEEHGSALELIMSKYREDMFALLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH  6221 98 916 RWINDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NUGAGLSWGLYFVFYNNIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVXIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYBLLKLKYNQHINRLPE AQLSTUEYISVAALSKIFAVAATYPQVVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 6217     |            | 1178          | TRYGRGESGLKMEVKPPPGRPQPDSGRRRRRGEEGHDPKEPEQ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSREDSVKPGA HLITVKKIFVGGIKEDTESYNLRDYFEKYGKIETIEVMEDRQSGK KRGPAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSKQEMQS AGSQRGGGGGSGSTMGRGGGFGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 0217     | 1          |               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVMEDRQSGK KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSKQEMQS AGSQRGRGGGGGNFMGRGGNFGGGGNFGGRGGYGGGG GGSRGSYGGGDGYNGFGGDGNYGGGGNFGRGGRGGYGGGG NQGGYGGGGYDGYNGGGGNYGGGGNYDFGNYSGQQS NYGPMKGGSFGGRSSGSFYGGGYGGGGNYDFGNYSGQQS NYGPMKGSFGGRSSGSFYGGGYGGGGYGSRF  6218  1305  906  SCERRFIMADDLKRFLYKKLPSVEGLHAIVVSDRDQVPVIKVA NDNAPBHALRFGYLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIASSANTGLIVSLEKELAPLFEELRQVVEVS  6219  2  890  AGFGEGAGAGTRCAGAEAEMASAGGEDCESPAPRADRPHGRPFL IGVSGGTASGKSTVCEKIMELLGQNEVBQRQRKVVILSQDRFYK VLTABQKAKALKQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQVTTFVKPAFEBFCLP TKKYADVIIPRGVDRMVAINLIVQHIQDILMGDICKWHROGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH EONISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEAMKQYQEEIQELNEVARHRPRSTLVMGIQQENRQIRELQQ ENKELRTSLEEHQSALELIMSKYREMFRLIMASKKDDFGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH  6221  98  916  RHIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK YEGURGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE GQURGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | İ        | 1          |               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| RRGFAFVTFDDHDTUKIVVQKYHTINGHNCEVKKALSKQEMQS AGSQRGRGGGSGNFMGRGGNFGGRGNFGGRGYGGGG GGRGSYGGGGGSGNFMGRGGNFGGGGNFGRGGNFGGGGGGGGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 1        | l .        |               | HUTUKKI FUGGI KEDTEEYNI RDYFEKYGKIETIEVMEDROSGK                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| AGSQRGRGGGGNFMGRGGNFGGGGGNFGGRGSYGGGG GGSRGSYGGGDGYNGFGGDGGNYGGGPGYSSRGYYGGGPGYS NQGGYGGGGGYGYNGGGGPGYSSRGGYGGGPGYN NYGPMKGGSFGGRSGSPYGGGYGGGGSGYGSRF  6218 1305 906 SCERRGFIMADDLKRFLYKKLPSVEGLHAIVVSDRDGVPVIKVA NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFEELRQVVEVS 1GVSGGTASGKSTVCEKIMELLGQNEVEQRQRKVVILSQDRFYK VLTAEQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAPEEFCLP TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHRGGSNG RSYKRTTSEPGDHPGMLTSGKRSHLESSSRPH 6220 227 764 EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEAMKQYQEEIQELMEVARHEPRSTLVMGIQQENRQIRELQQ ENKELRTSLEEHQSALELIMSKYPEQMFRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH 6221 98 916 RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NIMGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 1        | į.         |               | VPGPA FVTFTDHDTVDKTVVOKYHTINGHNCEVKKALSKORMOS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| GGSRGSYGGDGGYNGGGGRYSSRGGYGGGPGYG NQGGYGGGGGYYDEGGNYGGGGNYGDGGNYGDGGNYSGQQQS NYGPMKGGSFGGRSSGSPYGGGYGSGGGGYGRRF  6218 1305 906 SCERRGFIMADDLKRFLYKKLPSVEGLHAIVVSDRDGVPVIKVA NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFEELRQVVEVS  6219 2 890 AGPGEGAGAGTRCAGAEAEMASAGGEDCESPAPEADRPHQRPFL IGVSGGTASGKSTVCEKIMELLGQNEVBQRQRKVVLLSQDRFYX VLTAEQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAPEEFCLP TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHRGGSNG RSYKRTFSEPGDHFGMLTSGKRSHLESSSRPH  6220 227 764 EONISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEAMKQYQEEIQELNEVARHRPRSTLVMGIQQENRQIRELQQ ENKELRTSLEEHQSALELLMSKYREGMFRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH  6221 98 916 RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFYYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNOHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHPL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 1        |            |               | ACCORCECCECUEMCECCUECCCCCUECCCCCCCCCCCCCCCCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| NQGGYGGGGYDGYNEGGNYGGGGNYNDFGNYSGQQQS NYGPMKGGSFGGRSSGSYGGGYGSRRF  6218 1305 906 SCERRGFIMADDLKRFLYKKLPSVEGLHAIVVSDRDGVPVIKVA NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFBELRQVVEVS 6219 2 890 AGPGEGAGAGTRCAGAEAEMASAGGEDCESPAPEADRPHQRPFL IGVSGGTASGKSTVCEKIMELLGQNEVEQRQRKVVILSQDRFYK VLTAEQKAKALKGQYNFTHPDAFDNDLMHRTLKNIVEGKTVEVY TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKRAPEEFCLP TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHRGGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH 6220 227 764 EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEAMKQYQEEIQELNEVARHRRRSTLVMGIQQENRQIRELQQ ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH 6221 98 916 RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFYYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 1        | į          | 1             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| NYGPMKGGSFGGRSSGSPYGGGYGSGGSGYGSRRF  6218 1305 906 SCERRGFIMADDLKRFLYKKLPSVEGLHAIVVSDRDGVPVIKVA NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIASSANTGLIVSLEKELAPLFEELRQVVEVS 6219 2 890 AGPGEGAGAGTRCAGAEAEMASAGGEDCESPAPEADRPHQRPFL ULTAEQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAPEEFCLP TKKYADVIIPRGVDNMVAINLIVQHIQDILMGDICKWHROGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH 6220 227 764 EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEAMKQYQEEIQELNEVARRRPRSTLYMGIQQENRQIRELQQ ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH 6221 98 916 RHIWDLNPYSDGLELRPKYNGILHCLTTTWKLDGLRGLYQGVTP NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 1        | Į.         | 1             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 6218 1305 906 SCERRGFIMADDLKRFLYKKLPSVEGLHAIVVSDRDGVPVIKVA NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIASSANTGLIVSLEKELAPLFEELRQVVEVS 6219 2 890 AGPGEGAGAGTRCAGAEAEMASAGGEDCESPAPEADRPHQRFFL IGVSGGTASGKSTVCEKIMELLGQNEVEQRQRKVVILSQDRFYK VLTAEQKAKALKGQVNFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFEEFCLP TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHRGGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH 6220 227 764 EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEAMKQYQEEIQELNEVARHRPRSTLVMGIQQENRQIRELQQ ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH 6221 98 916 RWIWDLNPVSDGLELRFKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK YEGVGRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1        | 1          | 1             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIASSANTGLIVSLEKELAPLFBELRQVVEVS 6219 2 890 AGPGEGAGAGTRCAGAEARMASAGGEDCESPAPEADRPHQRFFL IGVSGGTASGKSTVCEKIMELLGQNEVBQRQRKVVILSQDRFYK VLTABQKAKALKGQVNFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAPEEFCLP TKKYADVIIPRGVDMMVAINLIVQHIQDILNGDICKWHROGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH 6220 227 764 EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEAMKQYQEEIQELIMEVARHRPRSTLVMGIQQENRQIRELQQ ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH 6221 98 916 RWIWDLNPVSDGLELRFKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMPDTLVKIYK YEGGYRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |          |            |               | NYGPMKGGSFGGRSSGSPYGGGYGSGGSGGSGKF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| VQFNRLPLVVSFIASSANTGLIVSLEKELAPLFEELRQVVEVS  AGPGEGAGAGTRCAGAEAMASAGGEDCESPAPRADRPHQRPFFL IGVSGGTASGKSTVCEKIMELLGQNEVEQRQRKVVILSQDRFYK VLTAEQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFEEFCLP TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHRGGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH  6220 227 764 EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEAMKQYQEEIQELNEVARHRPRSTLVMGIQQENRQIRELQQ ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH  6221 98 916 RWIWDLNPVSDGLELRFKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK YEGYRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 6218     | 1305       | 906           | SCERRGFIMADDLKRFLYKKLPSVEGLHAIVVSDRDGVPVIKVA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| 6219 2 890 AGPGEGAGATRCAGAEAEMASAGGEDCESPAPEADRPHQRPFL IGVSGGTASGKSTVCEKIMELLGQNEVEGRQRKVVILSQDRFYK VLTAEQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAPEEFCLP TKKYADVIIPRGVDMWAINLIVQHIQDILMGDICKWHROGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH 6220 227 764 EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEAMKQYQEEIQELNEVARHRPRSTLVMGIQQENRQIRELQQ ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH 6221 98 916 RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |          |            |               | NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| 6219 2 890 AGPGEGAGATRCAGAEAEMASAGGEDCESPAPEADRPHQRPFL IGVSGGTASGKSTVCEKIMELLGQNEVEGRQRKVVILSQDRFYK VLTAEQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAPEEFCLP TKKYADVIIPRGVDMWAINLIVQHIQDILMGDICKWHROGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH 6220 227 764 EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEAMKQYQEEIQELNEVARHRPRSTLVMGIQQENRQIRELQQ ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH 6221 98 916 RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |          |            |               | VQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFEELRQVVEVS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| IGVSGGTASGKSTVCEKIMELIGQNEVBQRQRKVVILSQDRFYK VLTAEQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFEEFCLP TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHRGGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH 6220 227 764 EONISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEAMKQYQEEIQELNEVARHRPRSTLVMGIQQENRQIRELQQ ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH 6221 98 916 RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 6219     | + - 2      | 890           | AGPGEGAGAGTRCAGAEAEMASAGGEDCESPAPEADRPHQRPFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| VLTAEQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFEEFCLP TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHRGGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH 6220 227 764 EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEAMKQYQEEIQELNEVARHRPRSTLVMGIQQENRQIRELQQ ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH 6221 98 916 RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | """      | 1 ~        |               | IGVSGGTASGKSTVCEKIMELLGQNEVEQRQRKVVILSQDRFYK                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFEEFCLP TKKYADVIIPRGVDMWAINLIVQHIQDILMGDICKWHRØGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH  6220 227 764 EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEAMKQYQFEIQELMEVARRRPRSTLYMGIQQENRQIRELQQ ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH  6221 98 916 RHIWDLNPYSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |          |            |               | VLTAEQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFEEFCLP TKKYADVIIPRGVDMWAINLIVQHIQDILMGDICKWHRGGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH 6220 227 764 EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEAMKQYQEEIQELNEVARHRPRSTLVMGIQQEMRQIRELQQ ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH 6221 98 916 RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQQVTP NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMPDTLVKIYK YEGYRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |          |            | j             | TYDEVTHSRIDETTVVYPADVVLFEGILVFYSOEIRDMFHLRLF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHROGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH  6220 227 764 EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEAMKQYQEEIQELNEVARHRPRSTLVMGIQQENRQIRELQQ ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH  6221 98 916 RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMPDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYBLLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |          |            | 1             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH  6220 227 764 EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEAMKQYQEEIQELNEVARHRPRSTLYMGIQQEMRQIRELQQ ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH  6221 98 916 RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMPDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYBLLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |          |            | {             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 6220 227 764 EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEAMKQYQEEIQELNEVARHRPRSTLVMGIQQENRQIRELQQ ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH  6221 98 916 RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYBLLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |          |            |               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| KRVEAMKQYQEEIQELNEVARHRPRSTLVMGIQQENRQIRELQQ ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH  6221 98 916 RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |          |            |               | NOTARTTSBYGUNFUNGIAGARANDE TOURS ARCT TROUBLE TO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH  6221 98 916 RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 6220     | 227        | 764           | EQNISCENSCTIERALADARALVERDRUDDAAESHIEQTTALN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH  6221 98 916 RMIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMPDTLVKIYK YEGVYGGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |          |            |               | KRVEAMKQYQEEIQELNEVARHRPRSTLVMGIQQENKQIRELQQ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| NVH 6221 98 916 RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYELIKLKKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |          |            |               | ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| NVH 6221 98 916 RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYELIKLKKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | }        |            | 1             | LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYBLLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | i        |            |               | NVH                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYBLLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 6221     | OQ.        | 916           | RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 1 3221   |            | 1             | NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| YEGVRGLYKGFVPGLFGTSHGALQFMAYBLLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |          |            |               | AMTICITAPI WVTKTRLMLOYDAVVNSPHROYKGMFDTLVKIYK                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI<br>DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |          |            |               | VEGUECL VYGEVEGLEGTSHGALOFMAYRLLKLKYNOHINRI.PE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |          |            |               | ACT CAMENT CALVE SELECT ENVIOLEMENT ADDOMMENS CALL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |          |            |               | MUDDIVE I ISVMMDSTIMANTI I I TV TOSCOVERNIVENI TOUT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| LDLREKRK                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |          |            |               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | L        |            |               | LDEKEKRK                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |

	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID			
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence	sequence	\=possible nucleotide insertion)
		2116	MARELRALLLWGRRLRPLLRAPALAAVPGGKPILCPRRTTAQLG
6222	2	2116	
			PRRNPAWSLQAGRLFSTQTAEDKEEPLHSIISSTESVQGSTSKH
	1	j	EFQAETKKLLDIVARSLYSEKEVFIRELISNASDALEKLRHKLV
1		[	SDGQALPEMEIHLQTNAEKGTITIQDTGIGMTQEELVSNLGTIA
	l .		RSGSKAFLDALQNQAEASSKIIGQFGVGFYSAFMVADRVEVYSR
1			SAAPGSLGYOWLSDGSGVFEIAEASGVRTGTKIIIHLKSDCKEF
			SSEARVRDVVTKYSNFVSFPLYLNGRRMNTLQAIWMMDPKDVRE
I			WOHEEFYRYVAQAHDKPRYTLHYKTDAPLNIRSIFYVPDMKPSM
	ĺ		FDVSRELGSSVALYSRKVLIQTKATDILPKWLRFIRGVVDSEDI
1			-
İ	1		PLNLSRELLQESALIRKLRDVLQQRLIKFFIDQSKKDAEKYAKF
1		1	FEDYGLFMREGIVTATEQEVKEDIAKLLRYESSALPSGQLTSLS
			EYASRMRAGTRNIYYLCAPNRHLAEHSPYYEAMKKKDTEVLFCF
l	I	1	EQFDELTLLHLREFDKKKLISVETDIVVDHYKEEKFEDRSPAAE
		1	CLSEKETEELMAWMRNVLGSRVTNVKVTLRLDTHPAMVTVLEMG
	1	!	AARHFLRMOOLAKTOEERAOLLOPTLEINPRHALIKKLNOLRAS
}			EPGLAQLLVDQIYENAMIAAGLVDDPRAMVGRLNELLVKALERH
6222	<del> </del>	715	DAWARTMAGMVDFQDEEQVKSFLENMEVECNYHCYHEKDPDGCY
6223	3	/15	
			RLVDYLEGIRKNFDEAAKVLKFNCEENQHSDSCYKLGAYYVTGK
			GGLTQDLKAAARCFLMACEKPGKKSIAACHNVGLLAHDGQVNED
}	}		GQPDLGKARDYYTRACDGGYTSSCFNLSAMFLQGAPGFPKDMDL
i	•	1	ACKYSMKACDLGHIWACANASRMYKLGDGVDKVEAKAEVLKNRA
			QQVHKEQQKGVQPLTFG
6224	1	133	LRTISSMAWGPLLLTLLAHCTGSWAQSVLTQPPSVSGARIPHBK
6225	3259	938	LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT
6223	3233	550	OKEWRLLSPAORALYREVTLENYSHLVSLGILHSKPELIRRLEQ
1	ľ		GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD
1	l		QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES
1	I .		
1		1	
1			SQGQRENPTEIDKVLKGIENSRWGAFKCABRGQDFSRKMMVIIH
			SQGQRENPTEIDKVLKGIENSRWGAFKCABRGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG
			SQGQRENPTEIDKVLKGIENSRWGAFKCABRGQDFSRKMMVIIH
			SQGQRENPTEIDKVLKGIENSRWGAFKCABRGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG
			SQGQRENPTEIDKVLKGIENSRWGAFKCABRGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH
			SQGQRENPTEIDKVLKGIENSRWGAFKCABRGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT
			SQGQRENPTEIDKVLKGIENSRWGAFKCABRGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST
			SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK FFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC
			SQGQRENPTEIDKVLKGIENSRWGAPKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH
			SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE
			SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH
			SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN
			SQGQRENPTEIDKVLKGIENSRWGAPKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSGEKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHWRIHSKE
			SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN
			SQGQRENPTEIDKVLKGIENSRWGAPKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSGEKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHWRIHSKE
6226		266	SQGQRENPTEIDKVLKGIENSRWGAPKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFRDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS
6226	29	266	SQGQRENPTEIDKVLKGIENSRWGAPKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KFFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS
_			SQGQRENPTEIDKVLKGIENSRWGAPKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA
6226	29	266 890	SQGQRENPTEIDKVLKGIENSRWGAPKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCQGFSWKRSLTRHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLBEKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA
_			SQGQRENPTEIDKVLKGIENSRWGAPKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMBGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS
_			SQGQRENPTEIDKVLKGIENSRWGAPKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCRGYTTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSFSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS
_			SQGQRENPTEIDKVLKGIENSRWGAPKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK FPACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCRGFJILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFQQPGALGSTPFLQQHGFNFPPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL
_			SQGQRENPTEIDKVLKGIENSRWGAPKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGGSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI
_			SQGQRENPTEIDKVLKGIENSRWGAPKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK FPACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCRGFJILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFQQPGALGSTPFLQQHGFNFPPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL
			SQGQRENPTEIDKVLKGIENSRWGAPKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGGSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI
			SQGQRENPTEIDKVLKGIENSRWGAPKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRYTTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSGEKPFVCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMBGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLQQHGFNFFPSGIDFS AWGNNSSQGQSTQSSGYSNYAPPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPFIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG
			SQGQRENPTEIDKVLKGIENSRWGAPKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSGEKPFVCRCGCGRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLBEKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLQQHGFNFFPSGIDFS AWGNNTSQGGSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATLAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPQPAQLSVQQQAAQPTRWV
			SQGQRENPTEIDKVLKGIENSRWGAPKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRFRENKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLBEKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFFEYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFQQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVFVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPPPADLSVQQQAAQPTRWV APRNRGSGFGHNGVDGNVGQSQAGSGSTPSEPHPVLEKLRSIN
_			SQGQRENPTEIDKVLKGIENSRWGAPKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK FPACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRFRENKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFQQPGALGSTPFLQQHGFNFPPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPPPQPAQLSVQQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTBHGNK
_			SQGQRENPTEIDKVLKGIENSRWGAPKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK FPACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGGGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAMSTGGDTMPYLTS YCQLSNGEPHFLPDAMFGQPGALGSTPFLGYGFNFFPSGIDFS AWGNNSSQGSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQCTQPLPPPPPQPAQLSVQQQAAQPTRWV APRNRGSGFGINGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG
_			SQGQRENPTEIDKVLKGIENSRWGAPKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KFFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGGSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQVG QQANNSPPVAQASVGQQTQPLPPPPPQPAQLSVQQQAAQPTRWV APRNRGSGFGHNGVDGNGVGSOSGSFTSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMRGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG VWSQDKWKGRFDVWIFVKDVPNSQLRHIRLENNENKPVTNSRD
			SQGQRENPTEIDKVLKGIENSRWGAPKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK FPACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGGGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAMSTGGDTMPYLTS YCQLSNGEPHFLPDAMFGQPGALGSTPFLGYGFNFFPSGIDFS AWGNNSSQGSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQCTQPLPPPPPQPAQLSVQQQAAQPTRWV APRNRGSGFGINGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Į	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	1		Codon, /=possible nucleotide deletion,
	amino acid	sequence	\-possible nucleotide insertion)
	sequence	1070	
6228	47	1978	GRRCRRGAVMELAQEARBLGCWAVEEMGVPVAARAPESTLRRL
l			CLGQGADIWAYILQHVHSQRTVKKIRGNLLWYGHQDSPQVRRKL
			ELEAAVTRLRAEIQELDQSLELMERDTEAQDTAMEQARQHTQDT
			QRRALLLRAQAGAMRRQQHTLRDPMQRLQNQLRRLQDMERKAKV
	1		DVTFGSLTSAALGLEPVVLRDVRTACTLRAQFLQNLLLPQAKRG
	1	Ì	SLPTPHDDHFGTSYQQWLSSVETLLTNHPPGHVLAALEHLAAER
l .			EAEIRSLCSGDGLGDTEISRPQAPDQSDSSQTLPSMVHLIQEGW
ļ			RTVGVLVSQRSTLLKERQVLTQRLQGLVEEVERRVLGSSERQVL
l			ILGLRRCCLWTELKALHDQSQELQDAAGHRQLLLRELQAKQQRI
1			LHWRQLVEETQEQVRLI.IKGNSASKTRLCRSPGEVLALVQRKVV
			PTFEAVAPQSRELLRCLEEEVRHLPHILLGTLLRHRPGELKPLP
			TVLPSIHQLHPASPRGSSFIALSHKLGLPPGKASELLLPAAASL
1			RQDLLLLQDQRSLWCWDLLHMKTSLPPGLPTQELLQIQASQBKQ
!			QKENLGQALKRLEKLLKQALERIPELQGIVGDWWEQPGQAALSE
1			ELCQGLSLPQWRLRWVQAQGALQKLCS
6229	1571	560	GPSLLGTRGTPNPARTLQIFFLIIGRRLTGRMAAVDDLQFEEFG
			NAATSLTANPDATTVNIEDPGETPKHQPGSPRGSGREEDDELLG
			NDDSDKTELLAGQKKSSPFWTFEYYQTFFDVDTYQVFDRIKGSL
1			LPIPGKNFVRLYIRSNPDLYGPFWICATLVFAIAISGNLSNFLI
		İ	HLGEKTYHYVPEFRKVSIAATIIYAYAWLVPLALWGFLMWRNSK
			VMNIVSYSFLEIVCVYGYSLFIYIPTAILWIIPHKAVRWILVMI
			ALGISGSLLAMTFWPAVREDNRRVALATIVTIVLLHMLLSVGCL
			AYFFDAPEMDHLPTTTATPNQTVAAAKSS
6230	1723	600	SKMSGRSGKKKMSKLSRSARAGVIFPVGRLMRYLKKGTFKYRIS
			VGAPVYMAAVIEYLAAEILELAGNAARDNKKARIAPRHILLAVA
Ì			NDEELNQLLKGVTIASGGVLPRIHPELLAKKRGTKGKSETILSP
			PPEKRGRKATSGKKGGKKSKAAKPRTSKKSKPKDSDKEGTSNST
			SEDGPGDGFTILSSKSLVLGQKLSLTQSDISHIGSMRVEGIVHP
			TTAEIDLKEDIGKALEKAGGKEFLETVKELRKSQGPLEVAEAAV
ł			SQSSGLAAKFVIHCHIPQWGSDKCEEQLEETIKNCLSAAEDKKL
		-	KSVAFPPFPSGRNCFPKQTAAQVTLKAISAHFDDSSASSLKNVY
			FLLFDSESIGIYVQEMAKLDAK
6231	149	870	LIFSSSTMDRSLRNVLVVSFGFLLLFTAYGGLQSLQSSLYSEEG
			LGVTALSTLYGGMLLSSMFLPPLLIERLGCKGTIILSMCGYVAF
1			SVGNFFASWYTLIPTSILLGLGAAPLWSAOCTYLTITGNTHAEK
ł			AGKRGKDMVNQYFGIFFLIFQSSGVWGNLISSLVFGQTPSQETL
		l l	PEEQLTSCGASDCLMATTTTNSTQRPSQQLVYTLLGIYTGSGVL
	Į		AVLMIAAFLQPIRDVQRESE
6232	3679	1476	FVAGTTMAGFWVGTAPLVAAGRRGRWPPQQLMLSAALRTLKHVL
			YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC
			KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA
1			IMEAIKKTRAQAVHPGYGFLSENKEFARCLAAEDVVFIGPDTHA
			IOAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEEAVRIAREIGY
			PVMIKASAGGGGKGMRIAWDDEETRDGFRLSSQEAASSFGDDRL
			LIEKFIDNPRHIEIQVLGDKHGNALWLNERECSIQRRNQKVVEE
			APSIFLDAETRRAMGEOAVALARAVKYSSAGTVEFLVDSKKNFY
			FLEMNTRLQVEHPVTECITGLDLVQEMIRVAKGYPLRHKQADIR
			INGWAVECRVYAEDPYKSFGLPSIGRLSOYOEPLHLPGVRVDSG
		1	IOPGSDISIYYDPMISKLITYGSDRTEALKRMADALDNYVIRGV
1			THNIALLREVIINSRFVKGDISTKFLSDVYPDGFKGHMLTKSEK
1			1
	1		NQLLAIASSLFVAFQLRAQHFQENSRMPVIKPDIANWELSVKLH
1		1	DKVHTVVASNNGSVFSVEVDGSKLNVTSTWNLASPLLSVSVDGT
			QRTVQCLSREAGGNMSIQFLGTVYKVNILTRLAAELNKFMLEKV
١.	1		TEDTSSVLRSPMPGVVVAVSVKPGDAVAEGQEICVIEAMKMQNS
6222		2654	MTAGKTGTVKSVHCQAGDTVGEGDLLVELE
6233	1	2654	HSTRENLNAGNFNFPSEGHLVRSTGPGGSFAKHMVAQCVSPKGP

ID beginning nucleotide (A-Alanine, C-C	ment containing signal peptide
] ==	
	•
	F=Phenylalanine, G=Glycine,
	=Isoleucine, K=Lysine,
**************************************	ethionine, N=Asparagine,
to first   amino acid   P=Proline, Q=G	lutamine, R=Arginine,
amino acid residue of S=Serine, T=Thr	reonine, V≖Valine,
	Y=Tyrosine, X=Unknown, *=Stop
	ble nucleotide deletion,
	· · · · · · · · · · · · · · · · · · ·
	leotide insertion)
1 1	PYLGGDSKLPKKTEQIRLLSQIYAAVIEAV
LAGIACYAKTSSLTI	KAKEVAEQTLGSGLDSFELIPFKAALRSKM
TFHIHAVNNQGRIV	PLDSEDSLSFVKTACMAVYDIPDLLGGNGC
LGSVVFSESFLTSO	ILVKEKDGTVTTETSSVVLTAAVPRFCSWL
	AVRGDESFLGTYLTGGEGAYLYSSNLQSWP
1 1 -	
	SHCRHGSIIISKDHMNSISFYDGDSTSTVA
	PVHFHGSSNFLMIALFPKSKIYQAFYSBVF
STMKÖÖDNSGISTKA	VIQEDGLSVEQKRLHSSAQKLFSALSQPAG
EKRSSLKLLSAKLPI	ELDWFLQHFAISSISQEPVMRTHLPVLLQQ
AEINTTHRIESDKV	IISIVTGLPGCHASELCAFLVTLHKECGRW
	AAHFORYLSSALEAQONRSARQSAYIRKKT
•	
	VVQALQTHPDSNVKASFTIGAITACVEPMS
•	QCSQGLVSNVVFTSHTTEQRHPLLVQLQSL
IRAANPAAAFILAEN	NGIVTRNEDIELILSENSFSSPEMLRSRYL
MYPGWYEGKLNAGS	VYPLMVQICVWFGRPLEKTRFVAKCKAIQS
SIKPSPFSGNIYHII	LGKVKFSDSERTMEVCYNTLANSLSIMPVL
	DSSGQQECYLVFIGCSLKEDSIKDWLRQSA
1 1	LTOOEIRSIHVKRHLEPLPAGYFYNGTOFV
	OLWNDAARETEKANGETEÖOEAHDTL
ELKP	
6234 1731 404 PRVREDMDHKSPGNI	KGSLVYAGIKSIVKSSLGMVESSRHNWSGL
DKOSDIQNLNEERI	LALQLCGWIKKGTDVDVGPFLNSLVQEGEW
ERAAVALFNLDTRI	RAIQILNEGASSEKGDLNLNVVAMALSGYT
	RLOLNNPYLCVMFAFLTSETGSYDGVLYEN
	-
	LSDTQLNRYIEKLTNEMKEAGNLEGILLTG
	RTGDVQTASYCMLQGSPLDVLKDERVQYWI
ENYRNLLDAWRFWH)	Kraefdihrskldpsskplagvfvscnfcg
KSISYSCSAVPHQG	RGFSQYGVSGSPTKSKVTSCPGCRKPLPRC
ALCLINMGTPVSSCI	PGGTKSDEKVDLSKDKKLAQFNNWFTWCHN
	RDHAECPVSACTCKCMQLDTTGNLVPAETV
OP	ADIABLE VOIGEONEIGEDITOREVITEIV
	LKVPGRGGRVGTTPELAAGGIMATRNPPPQ
DYESDDDSYEVLDLT	TEYARRHQWWNRVFGHSSGPMVEKYSVATQ
IVMGGVTGWCAGFL	FQKVGKLAATAVGGGFLLLQIASHSGYVQI
1 1	QIKKRANKAAPEINNLIEEATEFIKQNIVI
SSGFVGGFLLGLAS	
	LPSLPSARFSAGPPTQRSRPTMSNMEKHLF
	KCDKEEKAEKAKIKKAIQKGNMEVARIHAE
	MSARVDAVAARVQTAVTMGKVTKSMAGVVK
SMDATLKTMNLEKIS	SALMDKFEHQFETLDVQTQQMEDTMSSTTT
LTTPONOVDMLLOE	MADEAGLDLNMELPQGQTGSVGTSVASAEQ
DELSORLARLEDOV	
1 1	MDVNTALQEVLKTALIHDGLARGIREAAKA
-	CDEPMYVKLVEALCABHQINLIKVDDNKKL
GEWVGLCKIDREGKI	PRKVVGCSCVVVKDYGKESQAKDVIEEYFK
CKK	
6238 2 4666 EEVPTQESVKWEIN	VIIKNPEIVFVADMTKNDAPALVITTOCEI
1 1 1 1	IKDLOVRACPFLPVKRKGKITTVLOPCDLF
	MSVKSLTLKVSPVIINTMITITSALYTTKE
, ,	EKKDTKTLKMWFLEESNETEKIAPTTELVP
KGEMIKMNIDSIFI	VLEAGIGHRTVPMLLAKSRFSGEGKNWSSL
INLHCQLELEVHYY	NEMFGVWEPLLEPLEIDQTEDFRPWNLGIK
	EEENYKVPEYKTVISFHSKDQLNITLSKCG
I I I I I I I I I I I I I I I I I I I	ATGSSADFVKDLAPFMILNSLGLTISVSPS
ואסיפים אינו זותוא, זותוא, זותוא די די די די די די די די די די די די די	
1 1	
DSFSVLNIPMAKSY	VLKNGESLSMDYIRTKDNDHFNAMTSLSSK DKIPLTKVGRRLYTVRHRESGVERSIVCQI

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	1	sequence	Codon, /=possible nucleotide deletion,
	sequence		\-possible nucleotide insertion)
i			DTVEGSKKVTIRSPVQIRNHFSVPLSVYEGDTLLGTASPENEFN
			IPLGSYRSFIFLKPEDENYQMCEGIDFEEIIKNDGALLKKKCRS
			KNPSKESFLINIVPBKDNLTSLSVYSEDGWDLPYIMHLWPPILL
		l .	RNLLPYKIAYYIEGIENSVFTLSEGHSAQICTAQLGKARLHLKL
	+		LDYLNHDWKSEYHIKPNQQDISFVSFTCVTEMEKTDLDIAVHMT
1		ĺ	YNTGQTVVAFHSPYWMVNKTGRMLQYKADGIHRKHPPNYKKPVL
İ			FSFQPNHFFNNNKVQLMVTDSELSNQFSIDTVGSHGAVKCKGLK
	1		MDYQVGVTIDLSSFNITRIVTFTPFYMIKNKSKYHISVAEEGND
			KWLSLDLEQCIPFWPEYASSKLLIQVERSEDPPKRIYFNKQENC
			ILLRLDNELGGIIAEVNLAEHSTVITFLDYHDGAATFLLINHTK
			NELVQYNQSSLSEIEDSLPPGKAVFYTWADPVGSRRLKWRCRKS
1			HGEVTQKDDMMMPIDLGEKTIYLVSFFEGLQRIILFTEDPRVFK
1			VTYESEKAELAEQEIAVALQDVGISLVMNYTKQEVAYIGITSSD
1			VVWETKPKKKARWKPMSVKHTEKLEREFKEYTESSPSEDKVIQL
			DTNVPVRLTPTGHNMKILQPHVIALRRNYLPALKVEYNTSAHQS
			SFRIQIYRIQIQNQIHGAVFPFVFYPVKPPKSVTMDSAPKPFTD
ļ			VSIVMRSAGHSQISRIKYFKVLIQEMDLRLDLGFIYALTDLMTE
		1	AEVTENTEVELFHKDIEAFKEEYKTASLVDQSQVSLYEYFHISP
			IKLHLSVSLSSGREEAKDSKONGGLIPVHSLNLLLKSIGATLTD
		[	VQDVVFKLAFFELNYQFHTTSDLQSEVIRHYSKQAIKQMYVLIL
			GLDVLGNPFGLIREFSEGVEAFPYEPYQGAIQGPEEFVEGMALG
			LKALVGGAVGGLAGAASKITGAMAKGVAAMTMDEDYQQKRREAM
			NKQPAGFREGITRGGKGLVSGFVSGITGIVTKPIKGAOKGGAAG
			FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR
		İ	PPRFFNEDGVIRPYRLRDGTGNOMLOKIOFYREWIMTHSSSSDD
1		j	DDDDDDDDDESDLNH
6239	2108	634	KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVERSFNLOA
			THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVYVL
		1	SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM
			FCWVTAMQPHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI
1		1	WLSAFAIIVFRVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG
			ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL
1		1	WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL
			PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI
			GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI
1		1	DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA
		}	PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL
			ERLPRPS
6240	2202	1176	HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF
1	1		DPLSSGSRSSSLKSAOGTGFELGOLOSIRSEGTTSTSYKSLANO
			TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL
			AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLOEREKL
			LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP
			LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS
1			SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS
	1		ASPOPGQPPLSSPTRGGVKKVSGVGGTTYEISV
6241	3	1341	RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT
"271		1341	RVEELTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR
			EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTO
			KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV
			FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP
		-	TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGGCQYKM
		1	WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNNPSALAMHECKC
1		ł	
			LWPDVPLECIVSLGTGRYESDVRNTVTYTSLKTKLSNVINSATD

CEO	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ	l .		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	1	Bequence	\=possible nucleotide insertion)
	sequence	<b></b>	FFSKL
	l	<u> </u>	
6242	198	1310	QHFLPGAETWSPGAAVCTARRFPGRSLAAFPRPAAPRRAVEMGE
		l	SSEDIDQMFSTLLGEMDLLTQSLGVDTLPPPDPNPPRAEFNYSV
			GFKDLNESLNALEDQDLDALMADLVADISEAEQRTIQAQKESLQ
	1	ł	NQHHSASLQASIFSGAASLGYGTNVAATGISQYEDDLPPPPADP
	1		VLDLPLPPPPPEPLSQEEEEAQAKADKIKLALEKLKBAKVKKLV
			VKVHMNDNSTKSLMVDERQLARDVLDNLFEKTHCDCNVDWCLYE
	İ		IYPELOIERFFEDHENVVEVLSDWTRDTENKILFLEKEEKYAVF
		-	KNPONFYLDNRGKKESKETNEKMNAKNKESLLEVRLILQSGRKE
	1		KDVCSIFKSFASENNGKI
6243	1509	614	RSASRFSGCWSRDSTCCCCCPSTCWSRSSASCPRARWPPSSAPAT
ļ			TSRASSRRLACGPQTRAGAETRSTAMIRANSAARDTRRATCRSA
1			AGTPSPTTMTCLTDVPTGCAAVEPTARLPAAAWASTITTGCCPA
	1		MGQAGAGPAGRKGSEAGGGPGRAHHAHPSPLPREPRVRTGPPAH
1	1	· L	SPTPGSIDPSPELSWGSAGVTQESPLLDPVDFLLFRTRAVDPLR
		1	RVFFFFYQHLTFFSIQPQPPPCHAFHPRDPPAGTKRQLILVPLK
ł	1	1	GPPILAPILSLTPILSRWSCYFPRSRIAQGWHLS
6244	2119	1745	FEHAYASQFGTFLGNNESERCKLKLQQKTMSLWSWVNQPSELSK
0244	2113	1 2,45	FTNPLFEANNLVIWPSVAPQSLPLWEGIFLRWNRSSKYLDEAYE
	1		EMVNIIEYNKELQAKVNILRRQLAELETEDGMQESP
6245	81	1148	LSLRNAKYSFPQELISLFSMTDLNDNICKRYIKMITNIVILSLI
1			ICISLAFWIISMTASTYYGNLRPISPWRWLFSVVVPVLIVSNGL
İ			KKKSLDHSGALGGLVVGFILTIANFSFFTSLLMFFLSSSKLTKW
ľ	[		KGEVKKRLDSEYKEGGQRNWVQVFCNGAVPTBLALLYMIENGPG
			EIPVDFSKQYSASWMCLSLLAALACSAGDTWASEVGPVLSKSSP
		1	RLITTWEKVPVGTNGGVTVVGLVSSLLGGTFVGIAYFLTQLIFV
	i		NDLDISAPCWPIIAFGGLAGLLGSIVDSYLGATMQYTGLDESTG
Į.	ļ	į.	MVVNSPTNKARHIAGKPILDNNAVNLFSSVLIALLLPTAAWGFW
			PRG
	4 - 10	<del></del>	SLWPWILMDDSLMQISLQLLCVYTANFPNGCSSLCWSSCGQHPV
6246	1177	359	OATHRGAVSNSLMLCILKLASQMPLENTTVQQMVFMLLSNLALS
	1	Į.	
	į		HDCKGVIQKSNFLQNFLSLALPKGGNKHLSNLTILWLKLLLNIS
		i i	SGEDGQQMILRLDGCLDLLTEMSKYKHKSSPLLPLLIFHNVCFS
	1		PANKPKILANEKVITVLAACLESENQNAQRIGAAALWALIYNYQ
			KAKTALKSPSVKRRVDEAYSLAKKTFPNSEANPLNAYYLKCLEN
	1		LVQLLNSS
6247	3	1678	NSRVWGPWTEPSAGSLRPMARKQNRNSKELGLVPLTDDTSHAGP
1	1	1	PGPGRALLECDHLRSGVPGGRRRKDWSCSLLVASLAGAFGSSFL
			YGYNLSVVNAPTPYIKAFYNESWERRHGRPIDPDTLTLLWSVTV
		1	SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGFAISAALLMACS
			LQAGAFEMLIVGRFIMGIDGGVALSVLPMYLSEISPKEIRGSLG
1			QVTAIFICIGVFTGQLLGLPELLGKESTWPYLFGVIVVPAVVQL
		1	
1			LSLPFLPDSPRYLLLEKHNEARAVKAFQTFLGKAHVSQEVEEVL
1			AESRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGLNA
1			IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL
			GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI
			IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNFAVG
1			LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI
1			SQAFSKRNKAYPPEEKIDSAVTDGKINGRP
6248	56	1773	VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI
0248	30	1 1//3	AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL
1	}		ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP
1			
			SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII
1	1		LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP
1			YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF
-1			LINEQSPRASEETLLGISKKAKQMKINVQNNVDLGQPVKNKRVF
			<u> </u>

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	1	sequence	\=possible nucleotide insertion)
ļ	sequence		KEESSEFDVRAFCNOLKHKATOETSFDFKCSOSRLKTTKYSSOK
ļ			VIGTPHAKSFVQRFREAESFTQLSEEIQMAVVWCRSKKLKAQAI
ł			FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLLRGSGIK
	}		TSKHHLRQRRSQNKFLRRQRKPQRKLQSTLLREIQQFSQGTRKS
ļ			ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPVIQTKEKMI
			HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV
6249	56	1773	VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI
ļ			AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL
1			ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP
			SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII
			LNLVMVGLVSRLWVLYKGVLKRLILLYBPLFGLLQEVARIQPMP
		1	YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF
1	1	1	LINEQSPRASEETLLGISKKAKQMKINVQNNVDLGQPVKNKRVF
			KEESSEFDVRAFCNQLKHKATQETSFDFKCSQSRLKTTKYSSQK
			VIGTPHAKSFVQRFREAESFTQLSEEIQMAVVWCRSKKLKAQAI
1	l	ĺ	FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLLRGSGIK
1			TSKHHLRQRRSQNKFLRRQRKPQRKLQSTLLREIQQFSQGTRKS
1			ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPVIQTKEKMI
			HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV
6250	232	1306	LAALHIMALPFRKDLEKYKDLDEDELLGNLSETELKQLETVLDD
1			LDPENALLPAGFRQKNQTSKSTTGPFDREHLLSYLEKEALEHKD
ı			REDYVPYTGEKKGKIFIPKQKPVQTFTEEKVSLDPELEEALTSA
1	}		SDTELCDLAAILGMHNLITNTKFCNIMGSSNGVDQEHFSNVVKG
1			EKILPVFDEPPNPTNVEESLKRTKENDAHLVEVNLNNIKNIPIP
			TLKDFAKALETNTHVKCFSLAATRSNDPVATAFAEMLKVNKTLK
		Į.	SLNVESNFITGVGILALIDALRDNETLAELKIDNQRQQLGTAVE
1		1	LEMAKMLEENTNILKFGYQFTQQGPRTRAANAITKNNDLVRKRR
		<u> </u>	VEGDHQ
6251	62	972	TPGSGPMSAWAAASLSRAAARCLLARGPGVRAAPPRDPRPSHPE
1			PRGCGAAPGRTLHFTAAVPAGHNKWSKVRHIKGPKDVERSRIFS
			KLCLNIRLAVKEGGPNPEHNSNLANILEVCRSKHMPKSTIETAL
1			KMBKSKDTYLLYEGRGPGGSSLLIEALSNSSHKCQADIRHILNK
			NGGVMAVGARHSFDKKGVIVVEVEDREKKAVNLERALEMAIEAG
	<b>†</b>	1	AEDVKETEDEEERNVFKFICDASSLHQVRKKLDSLGLCSVSCAL
			EFIPNSKVQLAEPDLEQAAHLIQALSNHEDVIHVYDNIE
6252	27	1897	EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE
1		1	ETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPQV
			PKKPREWKNPESQRGLSGAQDPFPGPAPVPVEVVQKFCRIDKSR
1			KLPHSKAKTRSRLEVABAEEEETSIKAARSELLLAEEPGFLEGE
		1	DGEDTAKICQADIVEAVDIASAAKHFDLNLRQFGPYRLNYSRTG
			RHLAFGGRRGHVAALDWVTKKLMCEINVMEAVRDIRFLHSEALL
			AVAQNRWLHIYDNQGIELHCIRRCDRVTRLEFLPFHFLLATASE
		ļ	TGFLTYLDVSVGKIVAALNARAGRLDVMSQNPYNAVIHLGHSNG
			TVSLWSPAMKEPLAKILCHRGGVRAVAVDSTGTYMATSGLDHQL
	1	1	KIFDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVAGMGDVVNIWA
			GQGKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT
			SMLVPGAGEPNFDGLESNPYRSRKQRQEWEVKALLEKVPAELIC
		1	LDPRALAEVDVISLEQGKKEQIERLGYDPQAKAPFQPKPKQKGR
		1	SSTASLVKRKRKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS
			ALDRFVR
6253	27	1897	EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE
			ETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPQV
	(		PKKPREWKNPESQRGLSGAQDPFPGPAPVPVEVVQKFCRIDKSR
			KLPHSKAKTRSRLEVAEABEEETSIKAARSELLLAEEPGFLEGE
			DGEDTAKICQADIVEAVDIASAAKHFDLNLRQFGPYRLNYSRTG
			RHLAFGGRRGHVAALDWVTKKLMCEINVMEAVRDIRFLHSEALL
	.1	<u> </u>	

- 250	1 57 1 2		T
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
}	sequence	•	\=possible nucleotide insertion)
ļ	<del> </del>		AVAQNRWLHIYDNQGIELHCIRRCDRVTRLEFLPFHFLLATASE
			TGFLTYLDVSVGKIVAALNARAGRLDVMSQNPYNAVIHLGHSNG
			TVSLWSPAMKEPLAKILCHRGGVRAVAVDSTGTYMATSGLDHQL
i		Į	KIFDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVAGMGDVVNIWA
1			GQGKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT
			SMLVPGAGEPNFDGLESNPYRSRKQRQEWEVKALLEKVPAELIC
İ	ļ.		LDPRALAEVDVISLEQGKKEQIERLGYDPQAKAPFQPKPKQKGR
			SSTASLVKRKRKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS
			ALDRFVR
6254	155	1139	HALGRRGGSQELSAAACGCFALRLRAPGSGRPALAPGAAAFAGL
		· .	GGAPRFPPRGSAAGRTMLLKBYRICMPLTVDEYKIGQLYMISKH
	1		SHEQSDRGEGVEVVQNEPFEDPHHGNGQFTEKRVYLNSKLPSWA
1	1	İ	RAVVPKIFYVTEKAWNYYPYTITEYTCSFLPKFSIHIBTKYEDN
1			KGSNDTIFDNEAKDVEREVCFIDIACDEIPERYYKESEDPKHFK
1	1	ĺ	SEKTGRGQLREGWRDSHQPIMCSYKLVTVKFEVWGLQTRVEQFV
1			HKVVRDILLIGHRQAFAWVDEWYDMTMDDVREYEKNMHEQTNIK
	}		VCNQHSSPVDDIESHAOTST
6255	1	1444	J., "
6255	1 1	1444	PTRPQQELLVSLATVIFVASQKALSVESKAVIKQQLESVSNGWT
1			VYRIARQASRMGNHDMAKELYQSLLTQVASKHFYFWLNSLKEFS
	ļ		HAEQCLTGLQEENYSSALSCIAESLKFYHKGIASLTAASTPLNP
ļ		i	LSFQCEFVKLRIDLLQAFSQLICTCNSLKTSPPPAIATTIAMTL
1			GNDLQRCGRISNQMKQSMEEFRSLASRYGDLYQASFDADSATLR
1			NVELQQQSCLLISHAIEALILDPESASFQEYGSTGTAHADSEYE
		1	RRMMSVYNHVLEEVESLNGKYTPVSYMHTACLCNAIIALLKVPL
			SFQRYFFQKLQSTSIKLALSPSPRNPAEPIAVQNNQQLALKVEG
	1		VVQHGSKPGLFRKIQSVCLNVSSTLQSKSGQDYKIPIDNMTNEM
			EQRVEPHNDYFSTQFLLNFAILGTHNITVESSVKDANGIVWKTG
}			PRTTIFVKSLEDPYSQQIRLQQQQAQQPLQQQQQRNAYTRF
6256	1	1542	CRGAGAEPAANPRSPRSLVPSLESTSTSVPPAPGTMATDSWALA
Į.			VDEQEAAAESLSNLHLKEEKIKPDTNGAVVKTNANAEKTDEEEK
1		1	EDRAAQSLLNKLIRSNLVDNTNQVEVLQRDPNSPLYSVKSFEEL
l	ļ		RLKPQLLQCVYAMGFNRPSKIQENALPLMLAEPPONLIAOSOSG
1	ł		TGKTAAFVLAMLSQVEPANKYPQCLCLSPTYELALQTGKVIEQM
ł			
			GKFYPELKLAYAVRGNKLERGQKISEQIVIGTPGTVLDWCSKLK
	1		FIDPKKIKVFVLDEADVMIATQGHQDQSIRIQRMLPRNCQMLLF
1	1	]	SATFEDSVWKFAQKVVPDPNVIKLKREEETLDTIKQYYVLCSSR
1		i	DEKFQALCNLYGAITIAQAMIFCHTRKTASWLAAELSKEGHQVA
1			LLSGEMMVEQRAAVIERFREGKEKVLVTTNVCARGIDVEQVSVV
1	1	1	INFDLPVDKDGNPDNETYLHRIGRTGRFGKRGLAVNMVDSKHSM
L	<u></u>		NILNRIQEHFNKKIERLDTDDLDEIEKIAN
6257	210	615	AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE
	1		NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI
1			TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG
	1		KA
6258	210	615	AFIPAMAELIOKKLOGEVEKYOOLOKDLSKSMSGROKLEAOLTE
		1	NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI
			TAEIKRYESQLRDLERQSBOORETLAQLQOEFORAQAAKAGAPG
1			KA
6250		1540	
6259	2	1540	ILEKGFPSQCHPERKWKVDDVLESSQENEDDHFWELLFHNNKTV
1		{	SVENGDRGSKTFNLGTDPVSLRNYPYKICDSCEMNLKNISGLII
1			SKKNCSRKKPDEFNVCEKLLLDIRHEKIPIGEKSYKYDQKRNAI
1			NYHQDLSQPSFGQSFEYSKNGQGFHDEAAFFTNKRSQIGETVCK
	1		YNECGRTFIESLKLNISQRPHLEMEPYGCSICGKSFCMNLRFGH
			QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVSD
			KTWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTQLRRAHT
1			GEKTFECGECGKTFWEKSNLTQHQRTHTGEKPYECTECGKAFCO
·	·	l	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	bequence	\=possible nucleotide insertion)
	bequence	· · · · · · · · · · · · · · · · · · ·	KPHLTNHORTHTGEKPYECKOCGKTFCVKSNLTEHORTHTGEKP
		ļ	YECNACGKSFCHRSALTVHQRTHTGEKPFICNECGKSFCVKSNL
		}	IVHQRTHTGEKPYKCNECGKTFCEKSALTKHQRTHTGBKPYECN
			ACGKTFSORSVLTKHORIHTRVKALSTS
6260	2081	1436	GTGPEIHACAHASARAPGSRAMALRELKVCLLGDTGVGKSSIVW
0200	2001	1430	RFVEDSFDPNINPTIGASFMTKTVQYQNELHKFLIWDTAGQERF
			15 15
			RALAPMYYRGSAAAIIVYDITKEETFSTLKNWVKELRQHGPPNI
			VVAIAGNKCDLIDVREVMERDAKDYADSIHAIFVETSAKNAINI
			NELFIEISRRIPSTDANLPSGGKGFKLRRQPSEPKRSCC
6261	3	1188	FWYRLGPGTRSRWPRRGSWAASLVPRGPSPAALVTSPCPPDPLR
		1	SPACEPCRPDFAPRPALLLRSGPRSAPAVTGKPALKGQPGPWPG
			MAEVSIDQSKLPGVKEVCRDFAVLEDHTLAHSLQEQEIEHHLAS
		1	NVQRNRLVQHDLQVAKQLQEEDLKAQAQLQKRYKDLEQQDCEIA
			QEIQEKLAIEAERRRIQEKKDEDIARLLQEKELQEEKKRKKHFP
		]	EFPATRAYADSYYYEDGGMKPRVMKEAVSTPSRMAHRDQEWYDA
			EIARKLQEEELLATQVDMRAAQVAQDEEIARLLMAEEKKAYKKA
			KEREKSSLDKRKODPEWKPKTAKAANSKSKESDEPHHSKNERPA
			RPPPPIMTDGEDADYTHFTNQQSSTRHFSKSESSHKGFHYKH
6262	2	1759	PECHSQGLCSVHRPGKVPQARMSGLVLGQRDEPAGHRLSQEEIL
			GSTRLVSQGLEALRSBHQAVLQSLSQTIECLQQGGHEEGLVHEK
			ARQLRRSMENIELGLSEAQVMLALASHLSTVESEKQKLRAQVRR
ı	1		LCQENQWLRDELAGTQQRLQRSEQAVAQLEBEKKHLEFLGQLRQ
			YDEDGHTSEEKEGDATKDSLDDLFPNEEEEDPSNGLSRGQGATA
			AQQGGYEIPARLRTLHNLVIQYAAQGRYEVAVPLCKQALEDLER
			TSGRGHPDVATMLNILALVYRDQNKYKEAAHLLNDALSIRESTL
			GPDHPAVAATLNNLAVLYGKRGKYKEAEPLCQRALEIREKVLGT
			NHPDVAKQLNNLALLCQNQGKYEAVERYYQRALAIYEGQLGPDN
			PNVARTKNNLASCYLKQGKYAEAETLYKEILTRAHVQEFGSVDD
Į			DHKPIWMHAEEREEMSKSRHHEGGTPYAEYGGWYKACKVSSPTV
			NTTLRNLGALYRRQGKLEAAETLEECALRSRRQGTDPISQTKVA
1	1		ELLGESDGRRTSQEGPGDSVKFEGGEDASVAVEWSGDGSGTLQR
			SGSLGKIRDVLRR
6263	1	2408	RELDSLADLPERIKPPYANGLSTSHLRSSSVEDVKLIISEGRPT
	_	1	IEVRRCSMPSVICEHTKQFQTISEESNQGSLLTVPGDTSPSPKP
			EVFSNVPERDLSNVSNIHSSFATSPTGASNSKYVSADRNLIKNT
			APVNTVMDSPVHLEPSSQVGVIQNKSWEMPVDRLETLSTRDFIC
	1		PNSNIPDQESSLQSFCNSENKVLKENADFLSLRQTELPGNSCAQ
			DPASFMPPQQPCSFPSQSLSDAESISKHMSLSYVANQEPGILQQ
1			KNAVQIISSALDTDNESTKDTENTFVLGDVQKTDAFVPVYSDST
	1		IQEASPNFEKAYTLPVLPSEKDFNGSDASTQLNTHYAFSKLTYK
			SSSGHEVENSTTDTQVISHEKENKLESLVLTHLSRCDSDLCEMN
1			AGMPKGNLNEQDPKHCPESEKCLLSIEDEESQQSILSSLENHSQ QSTQPEMHKYGQLVKVELEENAEDDKTENQIPQRMTRNKANTMA
1			NOSKQILASCTLLSEKDSESSSPRGRIRLTEDDDPQIHHPRKRK
1	1		
	1		VSRVPQPVQVSPSLLQAKEKTQQSLAAIVDSLKLDEIQPYSSER
			ANPYFEYLHIRKKIEEKRKLLCSVIPQAPQYYDEYVTFNGSYLL
			DGNPLSKICIPTITPPPSLSDPLKELFRQQEVVRMKLRLQHSIE
1			REKLIVSNEQEVLRVHYRAARTLANQTLPFSACTVLLDAEVYNV
			PLDSQSDDSKTSVRDRFNARQFMSWLQDVDDKFDKLKTCLLMRQ
			QHEAAALNAVQRLEWQLKLQELDPATYKSISIYEIQEFYVPLVD
	<u> </u>		VNDDFELTPI
6264	143	1960	KHRQENNALDMAPEIHMTGPMCLIENTNGELVANPEALKILSAI
			TQPVVVVAIVGLYRTGKSYLMNKLAGKNKGFSLGSTVKSHTKGI
		ļ	WMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAVLL
1	1		SSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENENEDS
1			ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT
			SSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENENEDS

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	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
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1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
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	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1 1	sequence		\=possible nucleotide insertion)
<b></b>		<del></del>	SQKDKNFNLPRLCIRKFFPKKKCFVFDLPIHRRKLAQLEKLQDE
			ELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPRLESLVLTY
i			INAISRGDLPCMENAVLALAQIENSAAVQKAIAHYDQQMGQKVQ
			LPAETLQELLDLHRVSEREATEVYMKNSFKDVDHLFQKKLAAQL
			DKKRDDFCKQNQEASSDRCSALLQVIFSPLEEEVKAGIYSKPGG
1			YCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVTDAIL
			QTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQQMMEEK
			EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKER
			CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI
6265	143	1960	KHRQENNALDMAPEIHMTGPMCLIENTNGELVANPEALKILSAI
5255	473	1500	TOPVVVVAIVGLYRTGKSYLMNKLAGKNKGFSLGSTVKSHTKGI
j 1			WMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAVLL
			SSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENENEDS
			ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT
] [			SOKDKNFNLPRLCIRKFFPKKKCFVFDLPIHRRKLAOLEKLODE
1	!		ELDPEFVQOVADFCSYIFSNSKTKTLSGGIKVNGPRLESLVLTY
			INAISRGDLPCMENAVLALAQIENSAAVQKAIAHYDQQMGQKVQ
1			LPAETLOELLDLHRVSEREATEVYMKNSFKDVDHLFOKKLAAOL
1			DKKRDDFCKONOEASSDRCSALLOVIFSPLEEEVKAGIYSKPGG
l i			YCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVTDAIL
			QTDQILTEKEKEIEVECVKABSAQASAKMVEEMQIKYQQMMEEK
			EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKER
	•		COGESTOLONEIOKLOKTLKKKTKRYMSHKLKI
6266	276	1421	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE
0200	2,0		GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD
l'			ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF
!!			PSGLVVLSGGMDAOLKIWSAEDASCVVTFKGHKGGILDTAIVDR
1 !			GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN
1			SINLGSPEOMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF
i i			LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH
, ,			RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD
1 !			PVYKVATWEKQIYTCCRDGLVRRYQLSDL
6267	3	622	LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK
			NRYVVLKGDOLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS
			RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA
]			ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA
			VASTSTSDGMLTLDLIQEEDPSPEEPTSLC
6268	160	1368	HRELCONLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV
			DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA
1 1			PNSDIPEEBPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV
			LKQMESAQBKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE
[			SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ
]			KSCEROKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK
			IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS
1 1		1	GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ
1			SSHLIRHORTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR
			KKKQPTS
6269		1449	HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL
	2886	1	TOYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT
1217	2886		
	2886		
	2886		GSSVKLDKELDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN
	2886		GSSVKLDKELDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN FPKACELWEQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR
	2886		GSSVKLDKELDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN FPKACELWEQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR IYPFWTPDIPLSSYVKGIYSFGLMETNFYDQAEKLAKBALSINP
	2886		GSSVKLDKELDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN FPKACELWEQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR IYPFWTPDIPLSSYVKGIYSFGLMETNFYDQAEKLAKEALSINP TDAWSVHTVAHIHEMKAEIKDGLEFMQHSETLWKDSDMLACHNY
	2886		GSSVKLDKELDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN FPKACELWEQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR IYPFWTPDIPLSSYVKGIYSFGLMETNFYDQAEKLAKEALSINP TDAWSVHTVAHIHEMKAEIKDGLEFMQHSETLWKDSDMLACHNY WHWALYLIEKGEYEAALTIYDTHILPSLQANDAMLDVVDSCSML
	2886		GSSVKLDKELDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN FPKACELWEQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR IYPFWTPDIPLSSYVKGIYSFGLMETNFYDQAEKLAKEALSINP TDAWSVHTVAHIHEMKAEIKDGLEFMQHSETLWKDSDMLACHNY

SEQ Predicted Predicted end Amino acid segment co	ntaining signal peptide
	e, D=Aspartic Acid, E=
	ylalanine, G=Glycine,
location corresponding H=Histidine, I=Isoleu	
corresponding to first L=Leucine, M=Methioni	
1 dozzaspanienia	
	ine, X=Unknown, *=Stop
amino acid sequence Codon, /=possible nuc	
sequence \=possible nucleotide	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GGSNAQRDVFNQLLIHAALNCTS
SVHKNVARSLLMERDALKPNS	
6270 23 2086 SVTVTLGSEGDGRPPTYHLEE	MEQEPONGEPAEIKIIREAYKKA
FLFVNKGLNTDELGQKEEAKN	YYKQGIGHLLRGISISSKESEHT
GPGWESARQMQQKMKETLQNV	RTRLEILEKGLATSLQNDLQEVP
KLYPEFPPKDMCEKLPEPQSF	'SSAPQHAEVNGNTSTPSAGAVAA
PASLSLPSQSCPAEAPPAYTP	QAAEGHYTVSYGTDSGEFSSVGE
EFYRNHSOPPPLETLGLDADE	LILIPNGVQIFFVNPAGEVSAPS
	PPGFLQVCDWLYPLVPDRSPVLK
	VVLSSELPEDDRELFEDLLRQMS
	RTRPSSDQLKEASGTDVKQLDQG
	VNLSHIVPCEPVPEEKPKELPEW
1 1	GAEITGKAIQKGASKLRERIQPE
	GGAAKVSQFLVDGVCTVANCVGK
	KDGKSPLDGAMVVAASSVQGFST
	OTVRYKYGYNAGEATHHAVDSAV
	ATQTGHTLLEDYQIVDNSQRENQ
EGAANVNVRGEKDEQTKEVKE	
	PGSCRLVEEEVNIPNRRVLVTGA
	CGFRRARPKFEQVNLLDSNAVHH
	venopdaasolnvdasgnlakea
	PPYREEDIPAPLNLYGKTKLDGEK
	/EKLEESAVTVMFDKVQFSNKSAN
	LAEKRMLDPSIKGTFHWSGNEQM
TKYEMACAIADAFNLPSSHLR	RPITDSPVLGAQRPRNAQLDCSKL
ETLGIGQRTPFRIGIKESLWF	PFLIDKRWRQTVFH
6272 1136 528 GAVMEDAAAPGRTEGVLERQG	APPAAGQGGALVELTPTPGGLAL
	VQKADEFIRANATNKLTVIAEQI
QHLQEQARKVLEDAHRDANLH	HVACNIVKKPGNIYYLYKRESGQ
OYFSIISPKEWGTSCPHDFLG	AYKLQHDLSWTPYEDIEKQDAKI
SMMDTLLSQSVALPPCTEPNE	
	LNCSPDHIRRGSCWGRPQDLKIA
02.5	ARTLWYDRPRYVFMEFCVEDSTDV
1 1	YNEIEFYAKVNSKDSQDKRSSRS
	DIKPVWLSVDFDNWRDWEGDEEME
LAHVEHYAEVRDNTYCVLPT	JIM VILLOVDI DIMIKDILLODDILI.B
	EDGGI ACALI CDOUGCEVEAUDT
	FRGCLAGALLGDCVGSFYEAHDT
	SERTEALYYTDDTAMARALVQSL
	CDPDRGYGAGVVTVFKKLLNPKCR
	MRVAGISLAYSSVQDVQKFARLS
	/HLALQGESSSKHFLKQLLGHMED
	SSRLKKIGELLDQASVTREEVVS
1	RCMEPDPEIPSAFNSLQRTLIYSI
SLGGDTDTIATMAGAIAGAY	GMDQVPESWQQSCEGYEETDILA
QSLHRVFQKS	
6275 20 565 SRRGRARCLARGSRRPVPRPA	AKTMAFMVKTMVGGQLKNLTGSLG
	EEYEEYQKQLVEEKMERDAQFTQR
KAERATLRSHFRDKYRLPKNF	ETDESQIQMAGGDVELPRELAKMI
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GLNLGSLKDKAQATLGDLKQSAE
KCHVM	
	LEGTVAENPYPIVHTPSGNILTLE
1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	PAALRPSLALLARLSSLGLLHWP
	RELLTAVAEVFPHVTVAPGWPBEV
1 1	
	QPVSFQMQAMLLGHSTAGAIGRL
LASSPRATVIVEHNPAGGDYA	ASVRTALLAARAVDRTRVYYRLPQ
GYHKDLLAHVGRN	

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
_			
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E≈
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1			
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6277	4600	2744	MAFRTEMGLYYSYFKTIVEAPSFLNGVWMIMNDKLTEYPLVINT
			LKRFNLYPBVILASWYRIYTKIMDLIGIOTKICWTVTIGEGLSP
			TESCEGLGDPACFYVAVIFILNGLMMALFFIYGTYLSGSRLGGL
	1		=
Į.	į.	]	VTVLCFFFNHGECTRVMWTPPLRESFSYPFLVLQMLLVTHILRA
t			TKLYRGSLIALCISNVFFMLPWQFAQFVLLTQIASLFAVYVVGY
			IDICKLRKIIYIHMISLALCFVLMFGNSMLLTSYYASSLVIIWG
			ILAMKPHFLKINVSELSLWVIQGCFWLFGTVILKYLTSKIFGIA
1			NDAHIGNLLTSKFFSYKDFDTLLYTCAAEFDFMEKETPLRYTKT
1		!	LLLPVVLVGFVAIVRKIISDMWGVLAKQQTHVRKHQFDHGELVY
i		l	
		1	HALQLLAYTALGILIMRLKLFLTPHMCVMASLICSRQLFGWLFC
	ł	1	KVHPGAIVFAILAAMSIQGSANLQTQWNIVGEFSNLPQEELIEW
			IKYSTKPDAVFAGAMPTMASVKLSALRPIVNHPHYEDAGLRART
			KIVYSMYSRKAAEEVKRELIKLKVNYYILEESWCVRRSKPGCSM
			PEIWDVEDPANAGKTPLCNLLVKDSKPHFTTVFONSVYKVLEVV
1			KE
6330	<del></del>	000	
6278	3	823	ILFRLVLLSLVYLLNSVATEERKPAEVLIVEGQQYAVVGTVLLL
			IRIILEYCQGVDNIPSVTTDMLTRLSDLLKYFNSRSCQLVLGAG
			ALQVVGLKTITTKNLALSSRCLQLIVHYIPVIRAHFEARLPPKQ
		Í	YSMLRHFDHITKDYHDHIAEISAKLVAIMDSLFDKLLSKYEVKA
1			PVPSACFRNICKOMTKMHEAIFDLLPEEQTOMLFLRINASYKLH
1		1	LKKQLSHLNVINDGGPQNGLVTADVAFYTGNLQALKGLKDLDLN
			MAEIWEOKR
6279	127	1687	GGAMASDGARKQFWKRSNSKLPGSIQHVYGAQHPPFDPLLHGTL
}	ſ		LRSTAKMPTTPVKAKRVSTFQEFESNTSDAWDAGEDDDELLAMA
			AESLNSEVVMETANRVLRNHSQRQGRPTLQEGPGLQQKPRPEAE
		1	PPSPPSGDLRLVKSVSESHTSCPAESASDAAPLQRSQSLPHSAT
			VTLGGTSDPSTLSSSALSEREASRLDKFKQLLAGPNTDLEELRR
!		ļ	LSWSGIPKPVRPMTWKLLSGYLPANVDRRPATLQRKQKEYFAFI
1		Ī	
1	l		EHYYDSRNDEVHQDTYRQIHIDIPRMSPEALILQPKVTEIFERI
1			LFIWAIRHPASGYVQGINDLVTPFFVVFICEYIEAEEVDTVDVS
1		ĺ	GVPAEVLCNIEADTYWCMSKLLDGIQDNYTFAQPGIQMKVKMLE
			ELVSRIDEQVHRHLDQHEVRYLQFAFRWMNNLLMREVPLRCTIR
			LWDTYQSEPDGFSHFHLYVCAAFLVRWRKEILEEKDFQELLLFL
1		1	QNLPTAHWDDEDISLLLAEAYRLKFAFADAPNHYKK
6390	857	2575	
6280	03/	2515	ECCDQKMGSRNSSSAGSGSDPSEGLPRRGAGLRRSEEEEEEDE
		l	DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA
		1	WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA
			QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS
1			YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA
		[	RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD
1			LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREONRRTLO
1			
1		]	IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK
			PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR
1			BGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH
	1		GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK
1	1	i	LTNHKACVRDVSWHPPEEKIVSSSWDGNLRLWQYRQAEYFQDDM
			PESEECASAPAPVPOSSTPFSSPO
	ļ		
6281	857	2515	ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEBEEEDE
			DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA
1			WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA
		1	QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS
			YSQKAFCGIYSKDGQIPMSACQDQTIRLYDCRYGRFRKFKSIKA
1	J		· · · · · · · · · · · · · · · · · · ·
	1	1	RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD
			LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ
			IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK
			PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR
	<del></del>		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanina C. Combaining signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH
			GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK
1			LTNHKACVRDVSWHPFEEKIVSSSWDGNLRLWQYRQAEYFQDDM
			PESEECASAPAPVPQSSTPFSSPQ
6282	125	906	
0202	125	306	RMAACRALKAVLVDLSGTLHIEDAAVPGAQEALKRLRGASVIIR
ĺ		1	FVTNTTKESKQDLLERLRKLEFDISEDEIFTSLTAARSLLERKQ
		]	VRPMLLVDDRALPDFKGIQTSDPNAVVMGLAPEHFHYQILNQAF
1			RLLLDGAPLIAIHKARYYKRKDGLALGPGPFVTALEYATDTKAT
}			VVGKPEKTFFLEALRGTGCEPEEAVMIGDDCRDDVGGAQDVGML
			GILVKTGKYRASDEEKINPPPYLTCESFPHAVDHILQHLL
6283	140	1043	LSLFGIHVMNPFWSMSTSSVRKRSEGEEKTLTGDVKTSPPRTAP
1			KKQLPSIPKNALPITKPTSPAPAAQSTNGTHASYGPFYLEYSLL
]			AEFTLVVKQKLPGVYVQPSYRSALMWFGVIFIRHGLYQDGVFKF
1			TVYIPDNYPDGDCPRLVFDIPVFHPLVDPTSGELDVKRAFAKWR
1			RNHNHIWQVLMYARRVFYKIDTASPLNPEAAVLYEKDIQLFKSK
	,		VVDSVKVCTARLFDQPKIEDPYAISFSPWNPSVHDEAREKMLTQ
			KKKPEEQHNKSVHVAGLSWVKPGSVQPFSKEEKTVAT
6284	1	2879	RSVIPGSTISSRWPGLSRPRFMAAHEWDWFQREELIGQISDIRV
	_		QNLQVERENVQKRTFTRWINLHLEKCNPPLEVKDLFVDIQDGKI
			LMALLEVLSGRNLLHEYKSSSHRIFRLNNIAKALKFLEDSNVKL
			VEIDAREADONDOLUI GI INVIII DECIMAL RELEDINVAL
			VSIDAAEIADGNPSLVLGLIWNIILFFQIKELTGNLSRNSPSSS
1			LAPGSGGTDSDSSFPPTPTAERSVAISVKDQRKAIKALLAWVQR
-			KTRKYGVAVQDFAGSWRSGLAFLAVIKAIDPSLVDMKQALENST
1			RENLEKAFSIAQDALHIPRLLEPEDIMVDTPDEQSIMTYVAQFL
}			ERFPELEAEDIFDSDKEVPIESTFVRIKETPSEQESKVFVLTEN
			GERTYTVNHETSHPPPSKVFVCDKPESMKEFRLDGVSSHALSDS
			STEFMHQIIDQVLQGGPGKTSDISEPSPESSILSSRKENGRSNS
			LPIKKTVHFEADTYKDPFCSKNLSLCFEGSPRVAKESLRQDGHV
1			LAVEVAEEKEQKQESSKIPESSSDKVAGDIFLVEGTNNNSQSSS
1			CNGALESTARHDEESHSLSPPGENTVMADSFQIKVNLMTVEALE
			EGDYFEAIPLKASKFNSDLIDFASTSQAFNKVPSPHETKPDEDA
			EAFENHAEKLGKRSIKSAHKKKDSPEPQVKMDKHEPHQDSGEEA
			EGCPSAPEETPVDKKPEVHEKAKRKSTRPHYEEEGEDDDLQGVG
			EELSSSPPSSCVSLETLGSHSEEGLDFKPSPPLSKVSVIPHDLF
			YFPHYEVPLAAVLEAYVEDPEDLKNEEMDLEEPEGYMPDLDSRE
			EEADGSQ9SSSSSVPGESLPSASDQVLYLSRGGVGTTPASEPAP
j			LAPHEDHQQRETKENDPMDSHQSQESPNLENIANPLEENVTKES
	!		ISSKKKEKRKHVDHVESSLFVAPGSVQSSDDLEEDSSDYSIPSR
j	1		TCHCDCCTVI.DDUTUDCCDCDUECY.COVERDOC
6285	2157	1331	TSHSDSSIYLRRHTHRSSESDHFSLCSVEERSRSG
"2"	2431	1231	SCKTENLLEMWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHH
] [			
1	l		ALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVS
1			GAVLTFGMGSLYMFVQTILSYQMQPKIHGKQVFWIRLLLVIWCG
1			
	i		EWSMSFSFFGFFLTYIRDFQKISLRVEANLHGLTLYDTAPCPIN
			NERTRLLSRDI
6286	1619	276	KAGASCCGSANPYVSVGKSCVLLAMAOLOTRFYTDNKKYAVDDV
			PFSIPAASEIADLSNIINKLLKDKNEFHKHVEFDFLIKGOFI.RM
			PLDKHMEMENISSREVVEIEYVEKYTAPODEOCMEHDDWTCCTF
1		•	
1 1			
j			
1			
[		ſ	
ļ [			VESGSLKSTLTGNKVFNCISYSPLCKRLASGSTDRHIRLWDPRT
}			
	1		RSCKAPLYDLAAHEDKVLSVDWTDTGLLLSGGADNKLYSYRYSP
6286	1619	. 276	GAVLTFGMGSLYMFVQTILSYQMQPKIHGKQVFWIRLLLVIWCG VSALSMLTCSSVLHSGNFGTDLEQKLHWNPEDKGYVLHMITTAA EWSMSFSFFGFFLTYIRDFQKISLRVEANLHGLTLYDTAPCPIN NERTRLLSRDI KAGASCCGSANPYVSVGKSCVLLAMAQLQTRFYTDNKKYAVDDV PFSIPAASEIADLSNIINKLLKDKNEFHKHVEFDFLIKGQFLRM PLDKHMEMENISSEEVVEIEYVEKYTAPQPEQCMFHDDWISSIK GAEWILTGSYDKTSRIWSLEGKSIMTIVGHTDVVKDVAWVKKD SLSCLLLSASMDQTILLWEWNVERNKVKALHCCRGHAGSVDSIA VDGSGTKFCSGSWDKMLKIWSTVPTDEEDEMEESTNRPRKKQKT EQUGLTRTPIVTLSGHMEAVSSVLWSDAEEICSASWDHTIRVWD VESGSLKSTLTGNKVFNCISYSPLCKRLASGSTDRHIRLWDPRT KDGSLVSLSLTSHTGWVTSVKWSPTHEQQLISGSLDNIVKLWDT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	
NO.	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /-possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
			TTSHVGA
6287	270	1402	
0207	278	1482	MOFFFNFQIGLRSTSGKEKYSGDAGFLGDALQLFLQCLALDEDF
1	Ì		APAKLQVQKILCDLLLPENLKEGLKESSWSSLPCTKNRPFDFHS
1			VMEESQSLNEPSPKQSEEIPEVTSEPVKGSLNRAQSAQSINSTE
Ì	Į		MPAREDCLKRVSSEPVLSVQEKGVLLKRKLSLLEQDVIVNEDGR
ł	1		NKLKKQGETPNEVCMFSLAYGDIPEELIDVSDFECSLCMRLFFE
1			PVTTPCGHSFCKNCLERCLDHAPYCPLCKESLKEYLADRRYCVT
İ			QLLEELIVKYLPDELSERKKIYDEETAELSHLTKNVPIFVCTMA
ľ			YPTVPCPLHVFEPRYRLMIRRSIQTGTKQFGMCVSDTONSFADY
1			GCMLQIRNVHFLPDGRSVVDTVGGKRFRVLKRGMKDGYCTADIE
1			YLEDV
6288	1	743	
0200	1	743	VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECLR
1			MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDM
			HMMVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRENGM
			KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMM
1			PKVHWLRTQFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM
			RSEDPRSVINLLRNVCSEAAQKRSLDR
6289	1	743	VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECLR
i			MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDM
			HMMVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRENGM
1			KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMM
1			PKVHWLRTQFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM
1			RSEDPRSVINLLRNVCSEAAQKRSLDR
6290	3	1056	
6290	٥	1856	TLGRWLLGVYETVAPTLACLPRPRLRRRRRRRRRRRRRRMISRYTRKA
			VPQSLELKGITKHALNHHPPPBKLEEISPTSDSHEKDTSSQSKS
1		1	DITRESSFTSADTGNSLSAFPSYTGAGISTEGSSDFSWGYGELD
			QNATEKVQTMFTAIDELLYEQKLSVHTKSLQEECQQWTASFPHL
1	•		RILGRQIITPSEGYRLYPRSPSAVSASYETTLSQERDSTIFGIR
			GKKLHFSSSYAHKASSIAKSSSFCSMERDEEDSIIVSEGIIEEY
			LAFDHIDIEEGFHGKKSEAATEKQKLGYPPIAPFYCMKEDVLAY
			VFDSVWCKVVSCMEQLTRSHWEGFASDDESNVAVTRPDSESSCV
			LSELHPLVLPRVPQSKVLYITSNPMSLCQASRHQPNVNDLLVHG
1			MPLQPRNLSLMDKLLDLDDKLLMRPGSSTILSTRNWPNRAVEFS
			TSSLSYTVQSTRRRNPPPRTLHPISTSHSCAETPRSVEEILRGA
			RVPVAPDSLSSPSPTPLSRNNLLPPIGTAEVEHVSTVGPQRQMK
1			
1			PHGDSSRAQSAVVDEPNYQQPQERLLLPDFFPRPNTTQSFLLDT
			QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGGRPVSRTRQG
	1555		P
6291	1732	602	LVAKMASSASARTPAGKRVINQEELRRLMKEKORLSTSRKRIES
l	'		PFAKYNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG
			AKEASQGSSASSAPQSVKRKAPDADDQDVKRAKATLVPQVQPST
		1	SAWTTNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEEEGD
ļ			GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPPK
			APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV
			RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRO
			IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN
1			ADSDDEGELQDLLSQDWRVKGALL
6292	1835	1142	
1 2232	1035	1142	TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV
			LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI
			LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN
1		,	SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY
1			LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA
1			AKEPPPPYVSA
6293	2382	1035	FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL
1			VGSRTLPVDFHIKMVESMKYPFRQGMRLEVVDKSQVSRTRMAVV
1			DTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIK
L			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Clutaria Baid E Phanel I haspartic Acid, E=
1.0.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first		L=Leucine, M=Methionine, N=Asparagine,
}	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
[	1	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			MSERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMK
1	ļ	[	LEAIDPLNLGNICVATVCKVLLDGYLMICVDGGPSTDGLDWFCY
1	``		HASSHAIFPATFCQKNDIELTPPKGYEAQTFNWENYLEKTKSKA
1			APSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRL
1		-	LSIHFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVAAEP
Į.			ATPLKAKEATKKKKKQFGKKRKRIPPTKTRPLRQGSKKPLLEDD
į .	ł	1	PQGARKISSEPVPGEIIAVRVKEEHLDVASPDKASSPELPVSVE
ļ		Ì	NIKQETDD
6294	354	1814	AQLTTRGRTVAGGVRWIPSPFPDLELYSCCLGTDRGFPELSHHC
			KNVIATASDYDMAEITNIRPSFDVSPVVAGLIGASVLVVCVSVT
			VFVWSCCHQQAEKKHKNPPYKFIHMLKGISIYPETLSNKKKIIK
	1	1	VRRDKDGPGREGGRRNLLVDAAEAGLLSRDKDPRGPSSGSCIDQ
		1	LPIKMDYGEELRSPITSLTPGESKTTSPSSPEEDVMLGSLTFSV
			DYNFPKKALVVTIQEAHGLPVMDDQTQGSDPYIKMTILPDKRHR
			UMTERIADO VII QUANGEPVINDO QUAGGOPPI I KMTI LPDKRAR
			VKTRVLRKTLDPVFDETFTFYGIPYSQLQDLVLHFLVLSFDRFS
-			RDDVIGEVMVPLAGVDPSTGKVQLTRDIIKRNIQKCISRGELQV
[	[		SLSYQPVAQRMTVVVLKARHLQKMDIAGLSGNPYVKVNVYYGRK
	1		RIAKKKTHVKKCTLNPIFNESFIYDIPTDLLPDISIEFLVIDFD
Ì	l		RTTKNEVVGRLILGAHSVTASGAEHWREVCESPRKPVAKWHSLS
6205	0.505		EY
6295	2795	617	VSSALLTGATSGSDAAKSEGASASPLSCTNAVAMDRPDEGPPAK
ļ			TRRLSSSESPQRDPPPPPPPPPPLLRLPLPPPQQRPRLQEETEAA
j			QVLADMRGVGLGPALPPPPPYVILEEGGIRAYFTLGAECPGWDS
			TIESGYGEAPPPTESLEALPTPEASGGSLEIDFQVVQSSSFGGE
			GALETCSAVGWAPQRLVDPKSKEEAIIIVEDEDEDERESMRSSR
			RRRRRRRKQRKVKRESRERNAERMESILQALEDIQLDLEAVNI
l			KAGKAFLRLKRKFIQMRRPFLERRDLIIQHIPGFWVKAFLNHPR
Ì	· .		ISILINRRDEDIFRYLTNLQVQDLRHISMGYKMKLYFQTNPYFT
			NMVIVKEFQRNRSGRLVSHSTPIRWHRGQEPQARRHGNQDASHS
l	•		FFSWFSNHSLPEADRIAEIIKNDLWVNPLRYYLRERGSRIKRKK
	1		QEMKKRKTRGRCEVVIMEDAPDYYAVEDIFSEISDIDETIHDIK
			ISDFMETTDYFETTDNEITDINENICDSENPDHNEVPNNETTDN
ŀ	i		NESADDHETTDNNESADDNNENPEDNNKNTDDNEENPNNNENTY
ł	l i		GNNFFKGGFWGSHGNNQDSSDSDNEADEASDDEDNDGNEGDNEG
ł			SDDDGNEGDNEGSDDDDRDIEYYEKVIEDFDKDQADYEDVIEII
	1		SDESVEEEGIEEGIQQDEDIYEEGNYEEEGSEDVWEEGEDSDDS
			DLEDVLQVPNGWANPGKRGKTG
6296	727	1199	RHCGCDAQGACDSLPPTGTSSPVTARNAIPEARCCVWLLDGTTV
			EAVRPARERLARKELROKRMOOFSRDSAYSSNKDSTCLLTBRDT
}			LGTSLQFPSPFSGTISFGSFSDSGIFPLGSQCCLGFQQFSISGK
			KWALIHKRVRLSVFGARWGRIYFGK
6297	1	922	QRAAAASPSSCGPRGAEYGALMAMEGYWRFLALLGSALLVGFLS
	]		VIFALVWVLHYREGLGWDGSALEFNWHPVLMVTGFVFIQGIAII
1			VYRLPWTWKCSKLLMKSIHAGLNAVAAILAIISVVAVFENHNVN
1			
			NIANMYSLHSWVGLIAVICYLLQLLSGFSVFLLPWAPLSLRAFL
	į i		MPIHVYSGIVIFGTVIATALMGLTEKLIFSLRDPAYSTFPPEGV
			FVNTLGLLILVFGALIFWIVTRPQWKRPKEPNSTILHPNGGTEQ
6298	ļ		GARGSMPAYSGNNMDKSDSELNNEVAARKRNLALDEAGQRSTM
0278	3	985	SVPLRRLSLSGTLQGAGTTTKMAVARLAAVAAWVPCRSWGWAAV
			PFGPHRGLSVLLARIPQRAPRWLPACRQKTSLSFLNRPDLPNLA
			YKKLKGKSPGIIFIPGYLSYMNGTKALAIEEFCKSLGHACIRFD
			YSGVGSSDGNSEESTLGKWRKDVLSIIDDLADGPQILVGSSLGG
			WLMLHAAIARPEKVVALIGVATAADTLVTKFNQLPVELKKEVEM
			KGVWSMPSKYSEEGVYNVQYSFIKEAEHHCLLHSPIPVNCPIRL
			LHGMKDDIVPWHTSMQVADRVLSTDVDVILRKHSDHRMREKADI
			QLLVYTIDDLIDKLSTIVN
	L		

SEQ Predicted predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence Predicted end nucleotide location (A=Alanine, C=Cysteine, D=Aspartic Acid, E Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Sto Codon, /=possible nucleotide deletion, _possible nucleotide insertion)
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence corresponder and sequence location corresponding to first amino acid residue of amino acid sequence location corresponding to first amino acid residue of amino acid residue of amino acid sequence location location location location location location location location location location location labeled location labeled labeled labeled location labeled labeled labeled location labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labeled labele
location corresponding to first amino acid residue of amino acid sequence sequence corresponding to first amino acid residue of amino acid sequence sequence sequence corresponding to first amino acid residue of amino acid sequence sequence sequence sequence corresponding to first Lateucine, Mamemethionine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagine, Nasparagi
corresponding to first to first amino acid residue of amino acid sequence  sequence  corresponding to first amino acid residue of amino acid sequence sequence  corresponding to first
to first amino acid residue of sequence Sequence P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Sto Codon, /=possible nucleotide deletion, sequence                                                                                                                                                                                                                                                                                                                   \
amino acid residue of residue of amino acid sequence S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Sto Codon, /=possible nucleotide deletion, \
residue of amino acid w=Tryptophan, Y=Tyrosine, X=Unknown, *=Sto Codon, /=possible nucleotide deletion, sequence \text{\text{ = possible nucleotide insertion}} \text{6299} \text{512} \text{814} \text{\text{BCDLEGIMPNVTISLSLPTNGSPLQDILVHPCVTSLDSAILT}}
amino acid sequence Codon, /=possible nucleotide deletion,  sequence \text{\possible nucleotide insertion} \text{ \text{\possible nucleotide insertion}} \text{ \text{\possible nucleotide insertion}} \text{ \text{\possible DLEGIMPNVTISLSLPTNGSPLQDILVHPCVTSLDSAILT}} \text{\text{\possible nucleotide deletion,}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide deletion,}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\possible nucleotide insertion}} \text{\text{\text{\possible nucleotide insertion}}} \text{\text{\text{\possible nucleotide insertion}}} \text{\text{\text{\possible nucleotide insertion}}} \text{\text{\text{\possible nucleotide insertion}}} \text{\text{\text{\possible nucleotide insertion}}} \text{\text{\text{\possible nu
sequence   \=possible nucleotide insertion)   6299   512   814   BCDLEGIMPNVTISLSLPTNGSPLQDILVHPCVTSLDSAILT
6299 512 814 BCDLEGIMPNVTISLSLPTNGSPLQDILVHPCVTSLDSAILT
SIDAMDDSAFSGPYKFPFTPPLESFNLCFYTSQVPVPPILGF MKEEEVOLRNNH
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AQSPFSIPNSSSVPYGSQDSVHSSPEDGGGGRDRPVGGSPGG
LVIGSLPAHLSPHMFGGFKCPVCSKFVSSDEMDLHLVMCLTK
ITYNEDVLSKDAGECAICLEELQQGDTIARLPCLCIYHKGCI
WPEVNRSCPEHPSD 6301 616 284 GKPVPVNWEPPOPLPERKYLPCYPCLLETKPLCCLLCEDICL
on vivillative Representation
AGSSCITLHKKNSSGSDVMVSDCRSKEQMSDCSNTRTSPVSG
IFSQYCFLDFCNDPQNRGLYTP 6302 490 745 IFGFLHLFHMEHSFLLVCALFAHVERSSCGSSVALUSDDCC
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PVLLNCLPGDLRPLDELYAQKLKYKAISEELDHALNDMTSL 6303 2 1961 YWNEYGGGLLWOSWOEKHPGOALSSEDWNEDDTKEDWDDUVG
- Improcedence were the transfer of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the part
YWYYLEQFQYWEAQGWTFDASQSCDTDTYTSKTEADDKNDEK
KVDLVSFLSSPIMGDNDSSGTSDKDHSEILDGISNIKLNSEE
QSQLDSCTSHDGHQQLSEVSSKRECPASGQSEPRNGGTNEES
SGNTNTDPPAEDSQKSSGANTSKDRPHASGTDGDESEEDPPE
PSKLKRSHELDIDENPASDFDDSGSLLGFKYGSGQKYGGIPN
HRQVRYLEKNVKLKSKYLDMRRQIKMKNKHIFFTKESEKPFF
SKILSKVEKFLTWVNKPMDEEASQESSSHDNGHDASTSCDSEI
DMSVKKGDDLLETNNPEPEKCQSVSSAGELETENYERDSLLA
PDEQDCVTQEVPDSRQAETEAEVKKKNKKKNKKKNGLPPEI
VPELAKYWAQRYRLFSRFDDGIKLDREGWFSVTPEKIAEHIA
VSQSFKCDVVVDAFCGVGGNTIQFALTGMRVIAIDIDPVKIA
RNNAEVYGIADKIEFICGDFLLLASFLKADVVFLSPPWGGPD
TAETFDIRTMMSPDGFEIFRLSKKITNNIVYFLPRNADIDQVI
LAGPGGQVEIEQNFLNNKLKTITAYFGDLIRRPASET  6304 1 1438 HRARVDRSRESPGGDLRHPGRVRRDITISGHPRISTOHVALLI
DEVGDPGTKDLGHPQHGSPIQETQSEVVTLVSPLPGSDMAALI
WRATSGLTLWPHTAEGROLLGAENRALTGGQQAEDPTLASGAY
WPGSVEKLQGSVWCDAETLLSSSRTGGQAPPWLTDHDVQMLRI
AQGEVVDKARVPAHGQVLQVGFSTEAALQDLSSPRLSQLCSQC
CGLIKRPGDLPEVLSFHVDRVLGLRRSLPAVARRFHSPLLPYI
TDGGARPVIWWAPDVQHLSDPDEDQNSLALGWLQYQALLAHS(
WPGQAPCPGIHHTEWARLALFDFLLQVHDRLDRYCCGFEPEPS
PCVEERLREKCRNPAELRLVHILVRSSDPSHLVYIDNAGNLQH
EDKLNFRLLEGIDGFPESAVKVLASGCLQNMLLKSLQMDPVFV
SQGGAQGLKQVLQTLEQRGQVLLGHIQKHNLTLFRDEDP 6305 99 420 NMIWRGRSTYRPRPRRSVPPPELIGPMLRPGDEEPDOEEPDTE
International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contract   International Contr
RDPAPGQEREEDQGAAETQVPDLEADLQELSQSKTGDECGDGF
VQGKILTKSEQFKMPEGR 6306 1 1874 PTRPSKVKVPHTFI.IHSYTRPTVCOACKKI.IKGI.EPOGLOCKI
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KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSRADKSALM
ESEDSGVIPGSHSENALHASEEEEGGGKAQSSLGYIPLMRVV
SVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRLDCKCITLF
NNTTNRYYKEIPLSEILTVESAQNFSLVPPGTNPHCFEIVTAN
TYFVGEMPGGTPGGPSGQGARAARGWETAIRQALMPVILQDAF
APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDBVLGSGQ
GVVYGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSL
HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPER
TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKL
DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSV
VIMYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAI
LINNLLQVKMRKRYSVDKSLSHPWLQEYQTWLDLRELEGKMGE
YITHESDDARWEQFAAEHPLPGSGLPTDRDLGGACPPQDHDMQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
J	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	sequence	\=possible nucleotide insertion)
	bequence		LAERISVL
6307	2136	589	CFLLPRGRDPEPPEAGAAAPCAPGAPDMSFRKVVRQSKFRHVFG
""	1 2230	303	QPVKNDQCYEDIRVSRVTWDSTFCAVNPKFLAVIVEASGGAFL
1			VLPLSKTGRIDKAYPTVCGHTGPVLDIDWCPHNDEVIASGSEDC
į.			TVMVWQIPENGLTSPLTEPVVVLEGHTKRVGIIAWHPTARNVLL
Į.			SAGCDNVVLIWNVGTAEELYRLDSLHPDLIYNVSWNHNGSLFCS
1			ACKDKSVRIIDPRRGTLVAEREKAHEGARPMRAIFLADGKVFTT
1			CREEMEEROLAL WERENALEGARPMRAIFLADGRVFTT
			GFSRMSERQLALWDPENLEEPMALQELDSSNGALLPFYDPDTSV
			VYVCGKGDSSIRYFEITEEPPYIHFLNTFTSKEPQRGMGSMPKR
1			GLEVSKCEIARFYKLHERKCEPIVMTVPRKSDLFQDDLYPDTAG
	1	}	PEAALEAEEWVSGRDADPILISLREAYVPSKQRDLKISRRNVLS
}	1	İ	DSRPAMAPGSSHLGAPASTTTAADATPSGSLARAGEAGKLEEVM QELRALRALVKEQGDRICRLEEQLGRMENGDA
6308	<del> </del>	1110	
0300	2	1118	GRPTRPEKMLLSLVLHTYSMRYLLPSVVLLGTAPTYVLAWGVWR
1			LLSAFLPARFYQALDDRLYCVYQSMVLFFFENYTGVQILLYGDL
Ì			PKNKENIIYLANHQSTVDWIVADILAIRQNALGHVRYVLKEGLK
			WLPLYGWYFAQHGGIYVKRSAKFNEKEMRNKLQSYVDAGTPMYL
{			VIFPEGTRYNPEQTKVLSASQAFAAQRGLAVLKHVLTPRIKATH
	1		VAFDCMKNYLDAIYDVTVVYEGKDDGGQRRESPTMTEFLCKECP
			KIHIHIDRIDKKDVPEEQEHMRRWLHERFEIKDKMLIEFYESPD PERRKRFPGKSVNSKLSIKKTLPSMLILSGLTAGMLMTDAGRKL
ļ.			YVNTWIYGTLLGCLWVTIKA
6309	220	563	
1 0303	220	363	LVAEVKEPCSLPMLSVDMENKENGSVGVKNSMENGRPPDPADWA
			VMDVVNYFRTVGFEEQASAFQEQEIDGKSLLLMTRNDVLTGLQL KLGPALKIYEYHVKPLQTKHLKNNSS
6310	36	979	
0310	36	313	GPRCWKFLILSSVNCETLRIGKAWPQSSGQERYWTPRTHSSASE AQRGSLAELNVAAAGLWADCDQPLYDCPMCGLICTNYHILOEHV
			DLHLEENSFQQGMDRVQCSGDLQLAHQLQQEEDRKRRSEESRQE
			IEEFQKLQRQYGLDNSGGYKQQQLRNMEIEVNRGRMPPSEFHRR
			KADMMESLALGFDDGKTKTSGI I EALHRYYONAATDVRRVWLSS
į			VVDHFHSSLGDKGWGCGYRNFQMLLSSLLQNDAYNDCLKGMLIP
			CIPKIQSMIEDAWKEGFDPQGASQLIIRLQGTKAWIGACEVYIL
1			LTSLRV
6311	1	675	PVWWNSCEGPRLAAAARTGHGVGRRARLACLGEPRVKAAVMLTL
	•	5,5	ASKLKRDDGLKGSRTAATASDSTRRVSVRDKLLVKEVAELEANL
	[		PCTCKVHFPDPNKLHCFQLTVTPDEGYYQGGKFQFETEVPDAYN
			MVPPKVKCLTKIWHPNITETGEICLSLLREHSIDGTGWAPTRTL
	j		KDVVWGLNSLFTDLLNFDDPLNIEAABHHLRDKEDFRNKVDDYI
i	(		KRYAR
6312	213	1400	GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW
			GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT
			RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN
			VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC
			DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRONAA
			IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV
			GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEOGPOD
	]		VPLLYLKGMVYMVQALRQSFQGQGDRRTWDRTPVSMAASFEDGL
1			YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL
6313	2	2071	QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL
			FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD
[			RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF
1			TQEPLVEIBGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE
1	·		FLOMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI
			TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK
1	1	i	YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK
		i	QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE
	l		T TDE MONTHON TO THE THE RESERVORS IE

SEQ   Predicted   Predicted end nucleotide   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation   Incation
No: nucleotide location corresponding to first amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence
location corresponding to first amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence (Codon, /=possible nucleotide deletion, /=Stop SKCEICKKRYLRESAWKOHLNCYHLEEGUSKKORTIGKKIHVC (CYCEKOFDHFGHFKEHLKHTGEKPFECNGKEFARNSTLKCH LTACQTGVGAKKGRKKLYECQUCNSVFNSWDQFKDHLVHTGDK PHOLCOLDWFWQONELRHLSDAHNISERLVTEEVLSVETRVQ (PURCEAUCHSTEAUCHSTEVLS) (PURCEAUCHSTEAUCHSTEVLS) (PURCEAUCHSTEAUCHSTEVLS) (PURCEAUCHSTEAUCHSTEVLS) (PURCEAUCHSTEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHSTEVLS) (PURCEAUCHS
corresponding to first amino acid amino acid residue of amino acid residue of amino acid sequence Secrine, T-Threonine, N-Asparagine, P-Proline, Q-Glutamine, R-Arginine, Secrine, T-Threonine, V-Valine, W-Tryptophan, Y-Tyrosine, X-Unknown, *-Stop Codon, /-possible nucleotide deletion, \-possible nucleotide insertion)  SFKCEICNRYLRESAWKOHLNCYHLEBGGVSKKQRTGKKIHVC QYCEKQFDHFGHFKEHLRKHTGEKFFECNCHERFARNSTLKCH LTACQTGVGAKKGRKLYKCQVCNSVFNSWDGFKDHLVHTGDK PMHCTLCDLWFMQGMELRRHLSDAHNISERLVTEEVLSVETRVQ QVHDSHMSELPRQVQSVJEVQRUPSQVVTEQVHPDLLQDS QVHDSHMSELPRQVQVSVLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEINNQEERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE  6314 2 2071 QRSGAARLAFLESPFSPACVHRSPLSFHGGWFFFVVVFMPLGVL FHRRRAHGCTLSCSSFVEQDTAMEAETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEGUSHWASHLALBVRNKENSAPLEENTTGKNEAKKKIABTSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYRGGDRKGQIKEDGCPSDFTSK QVEGIEIVELQLSHVXDLFHCEKCNRSFKLFYHFKEHMKSHSTE SFKCEICNKRYLRESAWKOHKCYHLEGGVSKKQBTKKKHVC QYCEKQFDHFGHFKEHLKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVGAKKGRKKLYECQVCNSYFNSWDGFKDHLVIHTGDK PMHCTLCDLWFMQGMELFRHLSDAHNISERLYTEEVLSVETRVQ QVESTSMTILEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHSHMSELFEQVGVSVLEVGRIGTEEGTEVHVEELHVBRVNQ QVESTSMTILEQUSHVVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHSHMSELFEQVGVSVLEVGRIGTEEGTEVHVEELHVBRVNQ AEDLETKFPTVDSEAEKARNEDRTALPVLE  6315 1 1015 LGLAVNVVTLVLISYCPTATEESTSVTYMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPLEIKKKLIPVLGFLGVSNYF HVILHGGVGKNOSTIAGTSVLSPGLHIGLIILLAIMIYKKSATD
to first amino acid residue of amino acid residue of amino acid sequence  ##Typtophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, _possible nucleotide insertion)  ##SKCEICINKYRJERSAMKOHYHLEEGGVSKKQRTGKKIHVC QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH LTACOTGVGAKKGRKKLYRCQVCNSYFNSWDQFKDHLV1HTGDK PHACTLCDLWFMQGMELRHLSDAHNISERLVTEEVLSVETRVQ QVHDSHMSELPEQVQVSYLEVGRIGOTEEGTEVHVEELHVERVNO MPVEVQTELLEADLDHVTPEIMNQBERESSQADAAEAAREDHED AEDLETKPTVDSEAAKARNEDRTALPVE  ###SGARLAFLESDAHNISERLVTVFVVFMPLGVL  ###SGARLAFLESDAHNISERLVTVFVVFMPLGVL  ###SGARLAFLESDAHNISERLVTEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIGOTEEGTEVHVEELHVERVNO MPVEVQTELLEADLDHVTPEIMNQBERESSQADAAEAAREDHED AEDLETKPTVDSEAAKANEDRTALPVE  ####SGARLAFLESDAHNISERLYTVVFMPLGVL FHRRAHGCTLSCSSFVEQPTAMEAETMECLQEFPEHHKMILD RINNEGREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLJEIEGVSKMAPRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSABSEPVEIEVEILBEGTIEVEDEGIETLEEVASAKOSVK YIQSTGSSDDSALALLADITSKYRQGDRGGIKEDGCPSDPTSK QVEGIEIVELQLSHVKDLFHCEKCRNSFKLFYHFKEHMKSHSTE SFKCEICNKRYLRESAWKOHLNCYHLEEGGVSKKQRTGKKHIVC QVCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK PHHCTLCDLWFMQGMELRRHLSDAHNISERLVTEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNO MFVEVQTELLEADLDHVTPEIMNGERESSQADAAEAARREDHED AEDLETKPTVDSEAKKARNEDRTALPVLE  ###################################
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \
residue of amino acid sequence    Sequence
amino acid sequence  Codon, /~possible nucleotide deletion,
A-possible nucleotide insertion
SPKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC QYCEKQFDHFGHFKEHLRKHTGEKRFFECPNCHERFARNSTLKCH LTACQTGVGAKKGRKKLYECQVCNSVFNSWQFKDHLVIHTGDK PNHCTLCDLWFMQGMELRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSBLPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPBIMNQBERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE 6314 2 2071 QRSGARRLAFLPSPFSPACVHRSPLSFHSCWFYFVVVFMPLGVL FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESFPVEISHAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDFTSK QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKHVC QYCEKQFDHFGHFKEHLRKHTGEKPFFECDNCHERFARNSTLKCH LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK PNHCTLCDLWFMQONELRHLSDAHNISERLVTEEVLSVETRVQ QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQBERESSQADAAEAAREDHED AEDLETKFTVDSEAEKAENEDRTALFVLE 6315 1 1015 LGLAVNVTTLVLISYCPTATEERPYWTYLLCALGLFIYQSLDA IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVYCAHWQTVSGMLRFGKVDVTEIQIALVI VPVLSAFGGATWWDYTIPLIEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGRNGSTIAGTSVLSFGLHIGLIIILAIMIYKKSATD
SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC QYCEKQFDHFGHFKEHLRKHTGKRPFECPNCHERFARNSTLKCH LTACQTGVGAKKGRKKLYECQVCNSVFNSWQFKDHLVIHTGDK PNHCTLCDLWFMQGMELRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSBLPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPBIMNQBERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE  6314 2 2071 QRSGARRLAFLPSPFSPACVHRSPLSFHSCWFYFVVVFMPLGVL FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESFPVEISVBIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDFTSK QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKHVC QYCEKQFDHFGHFKEHLRKHTGEKPFECDNCHERFARNSTLKCH LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK PNHCTLCDLWFMQONELRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED AEDLETKFTVDSEAEKAENEDRTALPVLE 6315 1 1015 LGLAVNVVTTLVLISYCPTATEERPYWTYLLCALGLFIYQSLDA IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVYCAHWQTVVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPLIEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVGAKKGRKLYECQVCNSVFNSWDQFKDHLVIHTGDK PNHCTLCDLWFMQGNEKRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVVDSAQVTVEQVHPDLLQDS QVHDSHMSBLPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE  6314 2 2071 QRSGAARLAFLPSPFSPACVHRSFLSFHSCWFYFVVVVFMPLGVL FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQSF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLERIKALEVRNKENSAPLEENTTGKNEAKKRKTAETSNVI TESLPSAESEPVEIEVBIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE SFKCEICNKRYLRESAWKOHLNCYHLEEGGVSKKQRTGKKTHVC QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MFVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED AEDLETKPTVDSEABKAEMEDRTALPVLE  6315 1 1015 LGLAVNVVTTLVLISYCPTATEERPYWTYLCALGLFIYQSLDA FDWFFSCSFIGMFVFYCAHWQTVVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDVTIPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHTGLIILAIMIYKKSATD
LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK PNHCTLCDLWFMQGNBLIRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSBLPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE  6314 2 2071 QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RINEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFYKFFQEF TQEPLVEIEGVSKMAPRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVBIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYRQGDRKGGIKEDGCPSDPTSK QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE SFKCEICNKRYLRESAAKQHLNCYHLEEGGYSKKQRTGKKHVC QYCEKQFTGHFKHFLKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK PNHCTLCDLWFMQGNBLRRHLSDAHNISERLVTEEVLSVETRVQ QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVBEVNQ MPVEVQTELLEADLDHVTPEIMNQBERESSQADAAEAARBDHED AEDLETKFTVDSEAEKAENEDRTALFVLE AEDLETKFTVDSEAEKAENEDRTALFVLE 1015 LGLAVNVTTLVLISYCPTATEEAPYWTYLCALGLFIYQSLDA LDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDTYTIPILEIKLKILPVLGFLGGVFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILAIMIYKKSATD
PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTI I EQUGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSBLPEQVQVSYLEVGRIQTEEGTEVHVEEVHVERVNQ MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE 6314 2 2071 QRSGAARLAFLPSPFSPACVHRSPLSFHGCMFYPVVVFMPLGVL FHRRAHGCTLSCSSFVEQPTAMEAETMECLQEFPEHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFPYKKFPQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVBIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSAALALLADITSKYRQGDRKGQIKEDGCPSDPTSK QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC QYCEKOFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVGAKKGRKLYECQVCNSVFNSWDQFKDHLVIHTGDK PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVBRVNQ MPVEVQTELLEADLDHVTPEIMNQBERESSQADAAEAAREDHED AEDLETKFTVDSEAEKAENEDRTALPVLE 6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA LDGKQARRINSCSPLGELFPDGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDTYTPILEIKLKILPVLGFLGGVTFSCNNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILAIMIYKKSATD
TEPVTSMTIIEQUGKVHVLPLLQUQVDSAQVTVEQVHPDLLQDS QVHDSHMSBLPEQUQVSYLEVGRIQTEEGTEVHVEELHVERNNQ MPVEVVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE  6314 2 2071 QRSGAARLAFLESPFSPACVHRSFLSFHGCWFYFVVVFMPLGVL FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREGDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIABTSNVI TESLPSAESEPVEIEVELAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKHLVC QYCEKQFFHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE  6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA IDGKQARRTNSCSPLGELFPHGCDSLSTVFMAVGASIAARLGTV VFVLSAFGGATMWDYTTPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILAIMIYKKSATD
QVHDSHMSBLPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE 6314 2 2071 QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIRGVSKMAFRHLIEFTYTAKLMIQGEBEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKKKIAETSNVI TESLPSAAESEPVEIEVBIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH LTACQTGGGAKKGRKKLYECQVCNSVFNSWDGFKDHLVIHTGDK PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVELHVERVNQ MPVEVQTELLEADLDHVTPBIMNQBERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE 6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFTYQSLDA IDGKQARRTNSCSPLGELFPHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE  6314 2 2071 QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIBGVSKMAPRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVBIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK PMHCTLCDLWFMQCNELRRHLSDAHNISERLVTEEVLSVETRVQ QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE  6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLCALGLFIYQSLDA IDGKQARRINSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
AEDLETKPTVDSEAEKAENEDRTALPVLE  6314  2 2071 QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAPRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAI KALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVBIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE SFKCEICNRRYLRESAMKQHLNCYHLEEGGVSKKQRTGKKIHVC QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQBERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDBRTALPVLE  6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFTYQSLDA IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTVVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
6314 2 2071 QRSGARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSABESEPVEIEVBIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYRQGDRKGGIKEDGCPSDPTSK QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC QYCEKQFDHFGHFKEHLIKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQBERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDBRTALPVLE  6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLCALGLFIYQSLDA IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYVCAHWQTVVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPILEIKIKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAPRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVBIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVGAKKGRKLYECQVCRSVFNSMDQFKDHLVIHTGDK PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE 6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPILEIKIKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAPRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIABTSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVCAKKGRKKLYECQVCRSVFNSMDQFKDHLVIHTGDK PNHCTLCDLWFMQDELRRHLSDAHNISERLVTEEVLSVETRVQ TEPYTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE  6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTVVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPLLEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILAIMIYKKSATD
RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAPRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIABTSNVI TESLPSAESEPVEIEVBIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVCAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE  6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTVVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPLIEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILAIMIYKKSATD
TQEPLVEIEGVSKMAPRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVBIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK QVEGIEIVBLQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVCAKKGRKKLYECQVCRSVFNSMDQFKDHLVIHTGDK PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVBRVNQ MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE  6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTVVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDTTIPLEIKIKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEGCEPSDPTSK QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVCAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVBRVNQ MPVEVQTELLEADLDHVTPEIMNQERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE  6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTTVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPLEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILAIMIYKKSATD
TESLPSAESEPVEIEVBIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE SFKCEICNRRYLRESAWKQHLNCYHLEEGGYSKKQRTGKKIHVC QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK PNHCTLCOLWFMQGNBLRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQBERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDBTALPVLE  6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA PDWFFSCSFIGMFVFYCAHWQTTVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE SFKCEICNRRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVGAKKGRKKLYYECQVCNSVFNSWDQFKDHLVIHTGDK PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQBERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDBRTALPVLE  6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTTVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC QYCEKQFDHFGHFKEHLIKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDBRTALPVLE  6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLCALGLFIYQSLDA PDWFFSCSFIGMFVFYVCAHWQTYVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPLEIKIKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILAIMIYKKSATD
SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVGAKKGRKLYECQVCNSVFNSMDQFKDHLVIHTGDK PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE  6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPLIEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILAIMIYKKSATD
QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVGAKKGRKLYECQVCNSVFNSWDQFKDHLVIHTGDK PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVBRVNQ MPVEVQTELLEADLDHVTPEIMNQBERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE  6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPLEIKLKILPVLGFLGGVLFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILAIMIYKKSATD
LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE  1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTVVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQBERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE  1015 LIGHAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA ILDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTTVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVBRVNQ MPVEVQTELLEADLDHVTPEIMNQBERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE  6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTTVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDBRTALPVLE  6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYVCAHWQTTVVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE 6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
AEDLETKPTVDSEAEKAENEDRTALPVLE  6315  1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
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GLLFLDQYFNNFIDEYVVLWMAMVISSFDMVIYFSALCLQISRH
LHLNIFKTACHQAPEQVQVLSSKSHQNNMD
6316 1503 792 VSAGAGTGIMGGTTSTRRVTFEADENENITVVKGIRLSENVIDR
MKESSPSGSKSQRYSGAYGASVSDEELKRRVAEBLALEQAKKES
EDQKRLKQAKELDRERAANEQLTRAILRERICSEEERAKAKHL
ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTEQYQKAA
EEVEAKFKRYESHPVCADLQAKILQCYRENTHQTLKCSALATQY
MHCVNHAKQSMLEKGG
6317 102 839 PEAQTSAVLAREKGHLPTMRHEAPMQMASAQDARYGQKDSSDQN
FDYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDPKVK
TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN
EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG
QHLGEQLGFEFFETSAKDNINVKQTFERLVDIICDKMSESLETD
PAITAAKONTRLKETPPPPQPNCAC
6318 1765 733 PWHPLRTLPLHHPHPRPPRAEGREGADSMSHLPGLELRREAPPL
LGPLLSPFPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI
LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT
VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFEM
ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVFNLN
DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM
EKDALQVAQEMKAEYWAVSSLTGENVREFFFRVAALTFEANVLA
ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP
6319 88 717 AATMRLNQNTLLLGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT
ASEPLTLEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES
CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTEAVLAML
SYGVTTLGLTKFEAKIGQGNEPSIRMFQKLHFEQVATSSVFQEV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
[	residue of	amino acid	
		1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sedneuce	Codon, /-possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			TLRLTVSESEHQWLLEQTSHVEEKPYRDGSAEPC
6320	90	1111	RPRTGREKVAMAAVDSFYLLYREIARSCNCYMEALALVGAWYTA
1			RKSITVICDFYSLIRLHFIPRLGSRADLIKQYGRWAVVSGATDG
			IGKAYAEELASRGLNIILISRNEEKLQVVAKDIADTYKVETDII
			VADFSSGREIYLPIREALKDKDVGILVNNVGVFYPYPQYFTQLS
			EDKLWDIINVNIAAASLMVHVVLPGMVERKKGAIVTISSGSCCK
1			PTPQLAAFSASKAYLDHFSRALQYEYASKGIFVQSLIPFYVATS
1	ļ		MTAPSNFLHRCSWLVPSPKVYAHHAVSTLGISKRTTGYWSHSIO
			FLFAQYMPEWLWVWGANILNRSLRKEALSCTA
6321	1418	341	HRKAALGALMAGRLLGKALAAVSLSLALASVTIRSSRCRGIQAF
5521	7370		RNSFSSSWFHLNTNVMSGSNGSKENSHNKARTSPYPGSKVERSO
1			_
1			VPNEKVGWLVEWQDYKPVEYTAVSVLAGPRWADPQISESNFSPK
F	1		FNEKDGHVERKSKNGLYEIENGRPRNPAGRTGLVGRGLLGRWGP
			NHAADPIITRWKRDSSGNKIMHPVSGKHILQFVAIKRKDCGEWA
			IPGGMVDPGEKISATLKREFGERALNSLQKTSAEKREIEEKLHK
			LFSQDHLVIYKGYVDDPRNTDNAWMETEAVNYHDETGEIMDNLM
			LEAGDDAGKVKWVDINDKLKLYASHSQFIKLVAEKRDAHWSEDS
			EADCHAL
6322	2047	1083	NQEILKNVESSRTVQPHFLEFLLSLGWSVDVGRHPGWTGHVSTS
}		]	WSINCCDDGEGSQQBEVISSEDIGASIFNGQKKVLYYADALTEI
			AFVVPSPVESLTDSLESNISDQDSDSNMDLMPGILKQPSLTLEL
			FPNHTDNLNSSQRLSPSSRMRKLPQGRPVPPLGPETRVSVVWVE
		ľ	RYDDIENFPLSELMTBISTGVETTANSSTSLRSTTLEKEVPVIF
ļ			IHPLNTGLFRIKIQGATGKFNMVIPLVDGMIVSRRALGFLVROT
1			VINICRRKRLESDSYSPPHVRRKQKITDIVNKYRNKQLEPEFYT
1			SLFQEVGLKNCSS
6323	1	656	PASTTDGAQEARVPLDGAFWIPRPPAGSPKGCFACVSKPPALQA
***	•	020	PAAPAPEPSASPPMAPTLFPMESKSSKTDSVRAAGAPPACKHLA
			EKKTMTNPTTVIEVYPDTTEVNDYYLWSIFNFVYLNFCCLGFIA
1			LAYSLKVRDKKLLNDLNGAVEDAKTDRLINITRSGLAASCIMLW
6324		2061	MALSVIATHRGLRSSASILVAEPHDWNTERPQVTFRERCPAL
6324	1	2061	EGAGMRRCPCRGSLNEAEAGALPAAARMGLEAPRGGRRRQPGQQ
1		i	RPGPGAGAPAGRPEGGGPWARTEGSSLHSEPBRAGLGPAPGTES
1			PQAEFWTDGQTEPAAAGLGVETERPKQKTEPDRSSLRTHLEWSW
			SELGTTCLWTETGTDGLWTDPHRSDLQFQPEBASPWTQPGVHGP
			WTELETHGSQTQPERVKSWADNLWTHQNSSSLQTHPEGACPSKE
1	l	}	PSADGSWKELYTDGSRTQQDIEGPWTEPYTDGSQKKQDTEAARK
1	Į.		QPGTGGFQIQQDTDGSWTQPSTDGSQTAPGTDCLLGEPEDGPLE
1	1		EPEPGELLTHLYSHLKCSPLCPVPRLIITPETPEPEAQPVGPPS
			RVEGGSGGFSSASSFDESEDDVVAGGGGASDPEDRSGSKPWKKL
			KTVLKYSPFVVSFRKHYPWVQLSGHAGNFQAGEDGRILKRFCQC
	<u> </u>		EQRSLEQLMKDPLRPFVPAYYGMVLQDGQTFNQMEDLLADFEGP
	1		SIMDCKMGSRTYLEEELVKARERPRPRKDMYEKMVAVDPGAPTP
ſ	1		EEHAQGAVTKPRYMQWRBTMSSTSTLGFRIEGIKKADGTCNTNF
	[		KKTQALEQVTKVLEDFVDGDHVILQKYVACLEELREALEISPFF
	l		KTHEVVGSSLLFVHDHTGLAKVWMIDFGKTVALPDHQTLSHRLP
	i		WAEGNREDGYLWGLDNMICLLOGLAQS
6325	165	944	GLRDPFRRKRRLKPQVKMSNYVNDMWPGSPQEKDSPSTSRSGGS
7525	1 203	344	_
1			SRLSSRSRSRSFSRSSRSHSRVSSRFSSRSRRSKSRSRRRHQ
			RKYRRYSRSYSRSRSRSRSRRYRERRYGFTRRYYRSPSRYRSRS
			RSRSRSRGRSYCGRAYALARGQRYYGFGRTVYPEEHSRWRDRSR
	1		TRSRSRTPFRLSEKDRMELLEIAKTNAAKALGTTNIDLPASLRT
			VPSAKETSRGIGVSSNGAKPEVSILGLSEQNFQKANCQI
6326	238	680	GEPSPATQQKPSATGAGVLHQHFSSGHIYVLMGLLPPPWTISFT
			VQTTLQPPGGLPAAPVSGRMAFEPVGRDLARRMVPRAGKRTQTL
		l	GARRVAAQGARPLPEDRRPKSGERLHVTVAPCWEFVLPSVSLTA
			<u>-</u>

	Predicted	Dundinted and	
SEQ		Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	<del></del>		QAWGGVGORASSGVP
6327	1	1337	SLARLAPAGGSVVMPTQQPAAPSTRAPKPSRSLSGSLCALFSDA
""		1 233.	DSGSGMKAELPPGPGAVGREMTKEEKLQLRKEKKQQKKKRKEEK
1		ļ	
			GAEPETGSAVSAAQCQGPTRELPESGIQLGTPREKVPAGRSKAE
			LRAERRAKQEAERALKQARKGEQGGPPPKASPSTAGETPSGVKR
ļ	ļ		LPEYPQVDDLLLRRLVKKPERQQVPTRKDYGSKVSLFSHLPQYS
}	1		RQNSLTQFMSIPSSVIHPAMVRLGLQYSQGLVRGSNARCIALLR
j			ALQQVIQDYTTPPNEELSRDLVNKLKPYMSFLTQCRPLSASMHN
			AIKFLNKEITSVGSSKREEEAKSELRAAIDRYVQEKIVLAAQAI
}	1		SRFAYQKISNGDVILVYGCSSLVSRILQEAWTEGRRFRVVVVDS
}	1		RPWLEGRHTLRSLVHAGVPASYLLIPAASYVLPEVSTEEKDSKV
			GGEKV
6328	1030	276	HASAEVTTAAARGLGAMEEEMHTDAKIRAENGTGSSPRGPGCSL
			RHFACEQNLLSRPDGSASFLOGDTSVLAGVYGPAEVKVSKEIFN
	1		KATLEVILRPKIGLPGVAEKSRERLIRNTCEAVVLGTLHPRTSI
1	1		TVVLQVVSDAGSLLACCLNAACMALVDAGVPMRALFCGVACALD
ł			SDGTLVLDPTSKQEKEARAVLTFALDSVERKLLMSSTKGLYSDT
	ļ <u>.</u>		ELQQCLAAAQAASQHVFRFYRESLQRRYSKS
6329	3	2016	SSEVAAGGGTRSAMAEGSGEVVTVSATGAANGLINGAGGTSATT
			SNPLSRKLHKILETRLDNDKEMLEALKALSTFFVENSLRTRRNL
			RGDIERKSLAINEBFVSIFKEVKEELESISEDVQAMSNCCQDMT
l .			SRLQAAKEQTQDLIVKTTKLQSESQKLEIRAQVADAFLSKFQLT
1	J	J	SDEMSLLRGTREGPITEDFFKALGRVKQIHNDVKVLLRTNQQTA
l			GLEIMEQMALLQETAYERLYRWAQSECRTLTQESCDVSPVLTQA
[	1		MEALQDRPVLYKYTLDEFGTARRSTVVRGFIDALTRGGPGGTPR
[			PIEMHSHDPLRYVGDMLAWLHQATASEKEHLEALLKHVTTOGVE
}			ENIQEVVGHITEGVCRPLKVRIEQVIVAEPGAVLLYKISNLLKF
1	1	ļ	YHHTISGIVGNSATALLTTIEBMHLLSKKIFFNSLSLHASKLMD
			KVELPPPDLGPSSALNQTLMLLREVLASHDSSVVPLDARQADFV
Ì			QVLSCVLDPLLQMCTVSASNLGTADMATFMVNSLYMMKTTLALF
ļ	Į		EFTDRRLBMLQFQIBAHLDTLINEQASYVLTRVGLSYIYNTVOO
İ			HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL
			LSATVKEQIVKQSTELVCRAYGEVYAAVMNPINEYKDPENILHR
			SPQQVQTLLS
6330	1151	333	FFYYTFYBNKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL
			PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR
			KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC
	1		EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN
			RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV
			NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP
			TYESCLLN
6331	3	495	QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL
	1	]	LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY
			RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA
		,	
6333	<del> </del>		IFGFMATFLCMASIWLSYKISCVTQSTDAAV
6332	1	878	VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI
			NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLGEFLKEIKKNPS
1			SVKFAEMANILVIHCQTTDDLIQLTAMCWMREFIQLAGRVMLPY
1			SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD
	1		ELRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD
			VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG
	1		KLSTMATHSQLVKTGTGLEPRQAVSSSH
6333	3	1467	TRTPSEAEAGGESPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG
	1		QPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSPTMRPGTGAERG
	1		GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP
1	1		MGQMPGMMSSVMPGMMMSHMSQASMQPALPPGVNSMDVAAGTAS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning		
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L-Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
į.	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid		Codon, /=possible nucleotide deletion,
1		sequence	
	sequence		\=possible nucleotide insertion)
			PALRKVYDQMPEPRYVVSMGSCANGGGYYHYSYSVVRGCDRIVP
i			VDIYIPGCPPTAEALLYGILQLQRKIKRERRLQIWYRR
6342	2	1191	DPRVRAMLATLARVAALRKTCLFSGRGGGRGLWTGRPQSDMNNI
	_		KPLEGVKILDLTRVLAGPFATMNLGDLGAEVIKVERPGAGDDTR
1		1	TWGPPFVGTESTYYLSVNRNKKSIAVNIKDPKGVKIIKELAAVC
	}		DVFVENYVPGKLSAMGLGYEDIDEIAPHIIYCSITGYGQTGPIS
ļ			-
}	į.	1	QRAGYDAVASAVSGLMHITGPEVACLSHIAANYLIGQKEAKRWG
1		1	TAHGSIVPYQAFKTKDGYIVVGAGNNQQPATVCKILDLPELIDN
İ		1	SKYKTNHLRVHNRKELIKILSERFEEELTSKWLYLFEGSGVPYG
			PINNMKNVFAEPQVLHNGLVMEMEHPTVGKISVPGPAVRYSKFK
1			MSEARPPPLLGQHTTHILKEVLRYDDRAIGELLSAGVVDQHETH
6343	<del> </del>	936	GTAMVSDEDELNLLVIVVDANFIWWGKQALKESQFTLSKCIDAV
0343	2	930	
1			MVLGNSHLFMNRSNKLAVIASHIQESRFLYPGKNGRLGDFFGDP
1	1		GNPPEFNPSGSKDGKYELLTSANEVIVEEIKDLMTKSDIKGQHT
			ETLLAGSLAKALCYIHRMNKEVKDNQEMKSRILVIKAAEDSALQ
1			YMNFMNVIPAAQKQNILIDACVLDSDSGLLQQACDITGGLYLKV
			POMPSLLQYLLWVFLPDQDQRSQLILPPPVHVDYRAACFCHRNL
		}	IBIGYVCSVCLSIFCNFSPICTTCETAFKISLPPVLKAKKKLK
1		1	VSA
	2500	147	TMPTATLGNLRGYGMASPGLAAPSLTPPQLATPNLQQFFPQATR
6344	2508	14'	
			QSLLGPPPVGVPMNPSQFNLSGRNPQKQARTSSSTTPNRKDSSS
		ļ	QTMPVEDKSDPPEGSEEAAEPRMDTPEDQDLPPCPEDIAKEKRT
		ŀ	PAPEPEPCEASELPAKRLRSSEEPTEKEPPGQLQVKAQPQARMT
1		1	VPKQTQTPDLLPEALEAQVLPRFQPRVLQVQAQVQSQTQPRIPS
			TDTQVQPKLQKQAQTQTSPEHLVLQQKQVQPQLQQEAEPQKQVQ
			POVOPOAHSOGPROVOLOGEAEPLKOVOPOVOPOAHSOPPROVO
			LQLQKQVQTQTYPQVHTQAQPSVQPQEHPPAQVSVQPPEQTHEQ
	)	}	
1		ļ	PHTQPQVSLLAPEQTPVVVHVCGLEMPPDAVEAGGGMEKTLPEP
			VGTQVSMEEIQNESACGLDVGECENRAREMPGVWGAGGSLKVTI
i		J.	LOSSDSRAFSTVPLTPVPRPSDSVSSTPAATSTPSKQALQFFCY
		i	ICKASCSSQQEFQDHMSEPQHQQRLGEIQHMSQACLLSLLPVPR
			DVLETEDEEPPPRRWCNTCQLYYMGDLIQHRRTQDHKIAKQSLR
			PFCTVCNRYFKTPRKFVEHVKSQGHKDKAKELKSLEKEIAGQDE
		1	DHFITVDAVGCFEGDEEEBEDDEDEEEIEVEEBLCKQVRSRDIS
			REEWKGSETYSPNTAYGVDFLVPVMGYICRICHKFYHSNSGAQL
			· ·
i			SHCKSLGHFENLQKYKAAKNPSPTTRPVSRRCAINARNALTALF
	<u> </u>	<u> </u>	TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT
6345	2	3483	PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV
1			HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK
			ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE
		1	IRNLENVIQSQRGQIEELEHLAEILKTQLRRKENEIELSLLQLR
			EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK
1			QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER
1			RIEELODRINDLEKERELLKENYDKLYDSAFSAAHEEOWKLKEO
1			
1		i	QLKVQIAQLETALKSDLTDKTEILDRLKTERDQNEKLVQENREL
1	1		QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE
1	1		QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM
1	1		LIMQHKINKDYQMBVEAVTRKMENLQQDYELKVEQYVHLLDIRA
i			ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG
1	1		ENLFEIHINKVTFSSEVLOASGDKEPVTFCTYAFYDFELOTTPV
1			VRGLHPEYNFTSQYLVHVNDLFLQYIQKNTITLEVHQAYSTEYE
1	1		
1	1		TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEYWFRL
1			RVPMDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL
1	I		SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA
1	]		DHDTAIIPSSNDPOFDDHMYFPVPMNMDLDRYLKSESLSFYVFD
1	1		DSDTQENIYIGKVNVPLISLAHDRCISGIFELTDHQKHPAGTIH
•	1	1	

SEQ	Predicted	Predicted end	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
,	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first		L=Leucine, M=Methionine, N=Asparagine,
	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		residue of	S=Serine, T=Threonine, V=Valine,
	residue of amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1		sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			VILKWKFAYLPPSGSITTEDLGNFIRSEEPEVVQRLPPASSVST
1	İ		LVLAPRPKPRQRLTPVDKKVSFVDIMPHQSDVSQEGSVDEVKEN
	ł		TEKMQQGKDDVSLLSEGQLAEQSLASSEDETEITEDLEPEVEED
			MSASDSDDCIIPGPISKNIKQPSEKIRIEIIALSLNDSOVTMDD
		,	TIQRLFVECRFYSLPAEETPVSLPKPKSGOWVYYNYSNVIYVDK
1	İ		ENNKAKRDILKAILQKQEMPNRSLRFTVVSDPPEDEQDLECEDI
-	ļ		GVAHVDLADMFQEGRDLIEQNIDVFDARADGEGIGKLRVTVEAL
			HALQSVYKQYRDDLEA
6346	2921	533	QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL
			AKYTQKEESAEQPEFYYDEFGFRVYKEEGDEPGSSLLANSPLME
			DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA
			GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK
			QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC
1	1		QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ
			TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV
			DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI
1	1		FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL
1			IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL
	}		KAKNIKQTELVADLREAILRVARHPQCTDPKNCSVVSRQLPGLL
			PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH
1			RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL
1			RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK
1			ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL
	l i		CYTERI DEDCENI TREE I VERNOGERIE DE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE LE CONTRE
			CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL
ĺ			ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC
			ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG
6347	2921	533	1
		333	QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEFYYDBFGFRVYKEEGDEPGSSLLANSPLME
			DADORI DWOALL PETUALDUCCH TUDY TALLS DAGGER
			DAPORLRWOAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA
			GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK
			QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC
			QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ
1		i	TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV
			DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI
	[		FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL
			IADOGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL
1			KAKNI KQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL
]		[	PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH
]			RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL
			RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK
			ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL
			CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL
		1	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC
			ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW
6348			DVDG
0348	3	3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE
		1	KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN
1 1			EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAOHLVOKLSPENDN
1 1			DDDEDVQVEVAEKVQKSSSPRBMQKAEEKEVPEDSLEECAITCS
	,	Į	NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECODALN
			ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA
			EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN
1 1			ERQFKEEKLAEQLKQAEELRQYKVLVHSQBRELTQLREKLREGR
			DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK
L			LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE

PCT/US00/34263

SEQ Predicted Predicted end nucleotide (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid forcesponding corresponding to first amino acid p=Proline, Q=Glutamine, N=Asparagine, amino acid residue of amino acid w=Tryptophan, Y=Tyrosine, X=Unknown, acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal segment containing signal segment containing signal segment containing signal segment containing signal segment contai	cid, E=
NO: nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid w=Tryptophan, Y=Tyrosine, X=Unknown,	-
location corresponding to first L=Leucine, M=Methionine, N=Asparagine to first amino acid residue of residue of amino acid w=Tryptophan, Y=Tyrosine, X=Unknown,	
corresponding to first L=Leucine, M=Methionine, N=Asparagine to first amino acid P=Proline, Q=Glutamine, R=Arginine, amino acid residue of S=Serine, T=Threonine, V=Valine, residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unknown,	yeine,
to first amino acid P=Proline, Q=Glutamine, R=Arginine, amino acid residue of S=Serine, T=Threonine, V=Valine, residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unknown,	
amino acid residue of S=Serine, T=Threonine, V=Valine, residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unknown,	<b>2</b> ,
residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unknown,	
amino acid sequence Codon, /=possible nucleotide deletion	n,
sequence \=possible nucleotide insertion)	
BCAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIC	SSSHVEW
EDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEV	PQESWDEG
YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIG	RHRWDQVK
KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPS	CLELTDS
CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQD	PSCPRLSR
ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYS:	SAVYSLEE
QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEV	
SLDRCYSTPSSCLEOPDSCOPYGSSFYALKEKHVGF	-
KKGKGKKRRGRRSKKERRGRKEGEEDONPPCPRLS	
PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILE	
DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQ	
TPSGCLELTDSCOPYRSAFYILEQQRVGLAVDMDEI	
DODPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGY	_
PYSSAVYSLEEQYLGLALDVDRIKKDQEEERDQGPP	
LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSS	
VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGE:	
RINSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSF	
SFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFP	·
6349 3 3679 AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLR	_
KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREG	
EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQ	
DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSL	
NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSH	
ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEIN	eklrpqla
EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKD	LIKFMLRN
ERQFKEEKLAEQLKQAEBLRQYKVLVHSQERELTQL	
DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCR	LAQHLVQK
LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEK	EVPEDSLE
ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIG	SSSSHVEW
EDAVHI I PENESDDEEEEEKGPVSPRNLQESEEEEV	PQESWDEG
YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIG	RHRWDQVK
KEDHBATGPRLSRELLDEKGPEVLQDSLDRCYSTPS	CLELTDS
CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQD	PSCPRLSR
ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYS	SAVYSLEE
QYLGLALDVDRIKKDQEEBEDQGPPCPRLSRELLEV	VEPEVLQD
SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGF	BLDVGEIE
KKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCPRLS	RELLDEKG
PEVLQDSLDRCYSTPSGCLBLTDSCQPYRSAFYILE	QRVGLAV
DMDEIEKYQEVERDQDPSCPRLSGELLDEKEPEVLQ	
TPSGCLELTDSCQPYRSAFYI LEQQRVGLAVDMDE I	
DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGY	
PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPP	
LEVVEPEVLODSLDRCYSTPSSCLEQPDSCQPYGSS:	
VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGE	
RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSPO	
SFEERHISFALYVDNRFFTLTVTSLHLVFQMGVIFP(	
6350 3 3679 AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRI	
KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGI	
EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQ	
DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLI	
NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHI	
ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINI TWYCOGRAW WRANGEN TOLLAGEL ANGONYWYWEEGKROL	
EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDI	
ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQL	
DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRI	
LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEK	EVPEDSLE

ID beginning nucleotide location corresponding to first amino acid residue of amino acid sequence sequence corresponding to first lamino acid residue of amino acid sequence sequence codon, lepose codon, lepose codon sequence codon sequence codon sequence codon sequence codon sequence codon sequence codon sequence codon sequence codo codon sequence codo codon sequence codo codon sequence codo codo codo codo codo codo codo co	acid segment containing signal peptide nine, C=Cysteine, D=Aspartic Acid, E= nic Acid, F=Phenylalanine, G=Glycine, idine, I=Isoleucine, K=Lysine, nine, M=Methionine, N=Asparagine, nine, Q=Glutamine, R=Arginine, ne, T=Threonine, V=Valine, tophan, Y=Tyrosine, X=Unknown, *=Stop /=possible nucleotide deletion, ible nucleotide insertion)  SNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW	
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence codon, sequence location corresponding to first L=Leuc amino acid residue of sequence codon, \mathbb{\pi} possession problem (corresponding to first L=Leuc amino acid residue of sequence codon, \mathbb{\pi} possession problem (codon, \mathbb{\pi} possession problem (corresponding to first L=Leuc amino acid residue of sequence codon, \mathbb{\pi} possession problem (corresponding to first L=Leuc amino acid residue of sequence codon corresponding to first L=Leuc amino acid residue of sequence codon corresponding to first L=Leuc amino acid residue of sequence codon codon codon codon codon codon codon codon codon codon codon codon codon codon codon codon codon codon codo codo	cic Acid, F=Phenylalanine, G=Glycine, idine, I=Isoleucine, K=Lysine, ine, M=Methionine, N=Asparagine, ine, Q=Glutamine, R=Arginine, ne, T=Threonine, V=Valine, tophan, Y=Tyrosine, X=Unknown, *=Stop /=possible nucleotide deletion, ible nucleotide insertion)	
location corresponding H=Hist corresponding to first L=Leuc amino acid residue of S=Seri residue of amino acid sequence Codon, sequence ECAITC EDAVHI YSTLSI	idine, I=Isoleucine, K=Lysine, ine, M=Methionine, N=Asparagine, ine, Q=Glutamine, R=Arginine, ne, T=Threonine, V=Valine, tophan, Y=Tyrosine, X=Unknown, *=Stop /=possible nucleotide deletion, ible nucleotide insertion)	
corresponding to first L=Leuc to first amino acid P=Prol amino acid residue of S=Seri residue of amino acid W=Tryr amino acid sequence Codon, sequence ECAITC EDAVHI YSTLSI	ine, M=Methionine, N=Asparagine, ine, Q=Glutamine, R=Arginine, ne, T=Threonine, V=Valine, tophan, Y=Tyrosine, X=Unknown, *=Stop /=possible nucleotide deletion, ible nucleotide insertion)	
to first amino acid P=Prol amino acid residue of S=Seri residue of amino acid W=Try Codon, sequence CAITC EDAVHI YSTLSI	ine, Q=Glutamine, R=Arginine, ne, T=Threonine, V=Valine, tophan, Y=Tyrosine, X=Unknown, *=Stop /=possible nucleotide deletion, ible nucleotide insertion)	
amino acid residue of S=Seri residue of amino acid W=Trym amino acid sequence Codon, sequence ECAITO EDAVHI YSTLSI	ne, T=Threonine, V=Valine, tophan, Y=Tyrosine, X=Unknown, *=Stop /=possible nucleotide deletion, ible nucleotide insertion)	
residue of amino acid W=TryF amino acid sequence Codon, sequence ECAITC EDAVHI YSTLSI	tophan, Y=Tyrosine, X=Unknown, *=Stop /=possible nucleotide deletion, ible nucleotide insertion)	
amino acid sequence Codon, \=poss ECAITO EDAVHI YSTLSI	/=possible nucleotide deletion, ible nucleotide insertion)	
sequence \\=poss	ible nucleotide insertion)	
sequence \\=poss	ible nucleotide insertion)	
ECAITO EDAVHI YSTLSI	G. C.	SNSHGPYDSNOPHRKTKITFEEDKVDSTLIGSSSHVEW
YSTLSI	IPENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEG	
1 1	PPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDOVK	
, I Rabinar	TGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS	
I I CORVES	AFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR	
	EPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE	
	LDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD	
1 1	STPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE	
	KRRGRRSKKERRRGRKEGEEDONPPCPRLSRELLDEKG	
	SLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV	
	KYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCYS	
	ELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE	
DQDPSC	PRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ	
	YSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL	
	EVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH	
	VGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP	
	MEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY	
	ISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ	
	TERSQLGRMLVVEVANGRSLVWGAEAVQALRERLGVGG	
1	PRGPRQNSRLGLPLLLMPEEARLLAEIGAVTLVSAPRP	
1 1	LALTSFKRQQEESFQEQSALAAEARETRRQELLEKITE	
	QKLEQASGASSSQEAGSSQAAKEDETSDGQASGEQEEA	
, , ,	AGPSNGVAPLPRSALLVQLATARPRPVKARPLDWRVQS	
	GRPAHELRYSIYRDLWERGFFLSAAGKFGGDFLVYPGD	
	HYIAQCWAPEDTIPLQDLVAAGRLGTSVRKTLLLCSPQ	
	YTSLQWASLQ	
6352 235 923 WSRWLS	PCHAAKCKGLSMLRITMKTRAISLAADATEFVQGRSAP	
AMARSI	VHDTVFYCLSVYQVKISPTPQLGAASSAEGHVGQGAPG	
LMGNMN	PEGGVNHENGMNRDGGMIPEGGGGNQEPRQQPQPPPEE	
PAQAAM	EGPQPENMQPRTRRTKFTLLQVEELESVFRHTQYPDVP	
	ENLGVTEDKVRVWFKNKRARCRRHORELMLANELRADP	
DDCVYI	- · · · · · · · · · · · · · · · · · · ·	
	ATPEARARPPDVQAAEEEKEMDLPDSASRVFCGRILSM	
1 1 1	NAIILAQKNMLDRFEKTNEMLLNFNNLSSARLQOMSER	
	TLVEMKRDLDSIFRRIRTLKGKLARQHPEAFSHIPEAS	
	EDPIPPSTTTTIATSEQSTGSCDTSPDTVSPSLSPGFE	
	PGSPAINGRSQTDDEEMTGE	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	EPTRDCPLFGGAFSAILPMGAIDVSDLRPVPDNQEVFC	
	SLIVELLELQAHVRGEAAARYHFEDVGGVQGARAVHVE	
	LENLALRGRCQEAWVLSGKQQIAKENQQVAKDVTLHQA	
	YQTDLLLTFNQPP	
	FRGSGLRGAMIRRVLPHGMGRGLLTRRPGTRRGGFSLD	
WDGKVS	EIKKKIKSILPGRSCDLLQDTSHLPPBHSDVVIVGGGV	
	YWLKKLESRRGAIRVLVVERDHTYSQASTGLSVGGICO	
1 1	NIQLSLFSASFLRNINEYLAVVDAPPLDLRFNPSGYLL	
	AAAMESNVKVQRQEGAKVSLMSPDQLRNKFPWINTEGV	
	MEDEGWFDPWCLLQGLRRKVQSLGVLFCQGEVTRFVSS	
	TDDKAVVLKRIHEVHVKMDRSLEYQPVECAIVINAAGA	
	ALAGVGEGPPGTLQGTKLPVEPRKRYVYVWHCPQGPGL	
	DTSGAYFRREGLGSNYLGGRSPTEQEEPDPANLEVDHD	
I I I I I I I I I I I I I I I I I I I	WPHLALRVPAFETLKVQSAWAGYYDYNTFDQNGVVGPH	
	YFATGFSGHGLQQAPGIGRAVAEMVLKGRFQTIDLSPF	
	LGEKIQENNII	
6356 354 633 TGLTSS	CLPLQVMMTKRTKDMGKFSSVTVSTIDEBEEEIEAREV	
ADSYAQ	NAKVIEKQLERKGMSKRRLQELABLEAKKAKMKGTLID	
NQFK		

<u> </u>	I Decedion a	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:			
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
6357	2	915	GLLRNMALLVRVLRNQTSISQWVPVCSRLIPVSPTQGQGDRALS
ŀ			RTSQWPQMSQSQACGGSEQIPGIDIQLNRKYHTTRKLSTTKDSP
			QPVEEKVGAFTKIIBAMGFTGPLKYSKWKIKIAALRMYTSCVEK
			TDFEEFFLRCQMPDTFNSWFLITLLHVWMCLVRMKQEGRSGKYM
1	1		CRIIVHFMWEDVQQRGRVMGVNPYILKKNMILMTNHFYAAILGY
l	1		DEGILSDDHGLAAALWRTFFNRKCEDPRHLELLVEYVRKQIQYL
			DSMNGEDLLLTGEVSWRPLVEKNPQSILKPHSPTYNDEGL
6358	2009	1040	ASDALHSLSAPVLRLSSRSAARPATMTEQAISFAKDFLAGGIAA
0330	2003	1040	AISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPK
			EQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHT
1			OFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGKSGTE
		1	REFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYRAAYFGVY
			DTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
1	,		1-
1			MQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMG
		1.00	GAFVLVLYDELKKVI
6359	98	1086	VCRQEEEKMKEDCLPSSHVPISDSKSIQKSELLGLLKTYNCYHE
1			GKSFQLRHREEEGTLIIEGLLNIAWGLRRPIRLQMQDDREQVHL
l .	1 '		PSTSWMPRRPSCPLKEPSPQNGNITAQGPSIQPVHKAESSTDSS
1			GPLEEAEEAPQLMRTKSDASCMSQRRPKCRAPGEAQRIRRHRFS
	1		INGHFYNHKTSVFTPAYGSVTNVRVNSTMTTLQVLTLLLNKFRV
	į		EDGPSEFALYIVHESGERTKLKDCEYPLISRILHGPCEKIARIF
	ł		LMEADLGVEVPHEVAQYIKFEMPVLDSFVEKLKEEEEREIIKLT
İ	1	İ	MKFQALRLTMLQRLEQLVEAK
6360	1	345	GTRGAVPSTLEEVVLPPRSCRVFWIHSGTTMSKVSFKITLTSDP
		ļ	RLPYKVLSVPESTPFTAVLKFAAEEFKVPAATSAIITNDGIGIN
i	1	1	PAQTAGNVFLKHGSELRI I PRDRVGSC
6361	615	158	RPGLGQLQHCALAPQAGNRRCRFHGRLHALTRSTHRGKPMSIMQ
			FKDTLNTPLPDSSPVAVPLGAPIAVASTLSVEHNDGVETGIWAC
			APGRWRRQITSQEFCHFIQGRCTFTPDDGETLHIQAGDALMLPA
			NSTGIWDIQETVRKTYVLIL
6362	350	1576	TTMDGSHSAALKLQQLPPTSSSSAVSEASFSYKENLIGALLAIF
	1		GHLVVSIALNLOKYCHIRLAGSKDPRAYFKTKTWWLGLFLMLLG
1			ELGVFASYAFAPLSLIVPLSAVSVIASAIIGIIFIKEKWKPKDF
	1		LRRYVLSFVGCGLAVVGTYLLVTFAPNSHEKMTGENVTRHLVSW
			PFLLYMLVEIILFCLLLYFYKEKNANNIVVILLLVALLGSMTVV
			TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAAFLSQ
	1		ASOMYDSSLIASVGYILSTTIAITAGAIFYLDFIGEDVLHICMF
			ALGCLIAFLGVFLITRNRKKPIPFEPYISMDAMPGMONMHDKGM
	1	}	TVOPBLKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG
			VPYRVLEHTKKB
	<del> </del>	1201	RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG
6363	21	1201	
1			DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI
}	1		RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL
			NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD
	1	1	SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY
			DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS
	1		TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR
		1 '	RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE
		1	RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF
6364	21	1201	RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG
			DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI
1		İ	RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL
	i	1	NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD
			SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY
			SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPBLLFRPDLIGEESEGIHEVLVPAIQKSDMDLR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	sequence	sequence	
	sequence	ļ	\=possible nucleotide insertion)
1		i	RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE
6365			RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF
6365	234	1989	KHKSRASCAARAQAFGPSREREVHSRFRSGLRRLGESNSGCCTM
			ASMGTLAFDEYGRPFLIIKDQDRKSRLMGLEALKSHIMAAKAVA
			NTMRTSLGPNGLDKMMVDKDGDVTVTNDGATILSMMDVDHQIAK
			LMVELSKSQDDEIGDGTTGVVVLAGALLEEAEQLLDRGIHPIRI
			ADGYEQAARVAIEHLDKISDSVLVDIKDTEPLIQTAKTTLGSKV
i			VNSCHRQMAEIAVNAVLTVADMERRDVDFELIKVEGKVGGRLED
			TKLIKGVIVDKDFSHPQMPKKVEDAKIAILTCPFEPPKPKTKHK
			LDVTSVEDYKALQKYEKEKFEEMIQQIKETGANLAICQWGFDDE
			ANHLLLQNNLPAVRWVGGPEIELIAIATGGRIVPRFSELTAEKL
			GFAGLVQEISFGTTKDKMLVIEQCKNSRAVTIFIRGGNKMIIEE
			AKRSLHDALCVIRNLIRDNRVVYGGGAAEISCALAVSQEADKCP
			TLEQYAMRAFADALEVIPMALSENSGMNPIQTMTEVRARQVKEM
	]		NPALGIDCLHKGTNDMKQQHVIETLIGKKQQISLATQMVRMILK
			IDDIRKPGESEE
6366	257	1898	GNKEGAHSSTFWVLLSIFLGAVAMLCKEQGITVLGLNAVFDILV
			IGKFNVLEIVQKVLHKDKSLENLGMLRNGGLLFRMTLLTSGGAG
	1		MLYVRWRIMGTGPPAFTEVDNPASFADSMLVRAVNYNYYYSLNA
}	Ì		WLLLCPWWLCFDWSMGCIPLIKSISDWRVIALAALWFCLIGLIC
1			QALCSEDGHKRRILTLGLGFLVIPFLPASNLFFRVGFVVAERVL
	1		YLPSVGYCVLLTFGFGALSKHTKKKKLIAAVVLGILFINTLRCV
ļ	1		LRSGEWRSEEQLFRSALSVCPLNAKVHYNIGKNLADKGNQTAAI
	1		RYYREAVRLNPKYVHAMNNLGNILKERNELQEAEELLSLAVQIQ
			PDFAAAWMNLGIVQNSLKRFEAAEQSYRTAIKHRRKYPDCYYNL
İ			GRLYADLNRHVDALNAWRNATVLKPEHSLAWNNMIILLDNTGNL
			AQAEAVGREALELIPNDHSLMFSLANVLGKSQKYKESEALFLKA
1	}		IKANPNAASYHGNLAVLYHRWGHLDLAKKHYEISLQLDPTASGT
			KENYGLLRRKLELMQKKAV
6367	287	1934	SIGFPVMLVLSILLYTCEMFQDSVAFEDVAVSFTQEEWALLDPS
l			QKNLYRDVMQETFKNLTSVGKTWKVQNIEDEYKNPRRNLSLMRE
			KLCESKESHHCGESFNQIADDMLNRKTLPGITPCESSVCGEVGT
			GHSSLNTHIRADTGHKSSEYQEYGENPYRNKECKKAFSYLDSFQ
			SHDKACTKEKPYDGKECTETFISHSCIQRHRVMHSGDGPYKCKF
1	]		CGKAFYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER
	]		THTGVNADECKECGNAFSFPSEIRRHKRSHTGEKPYECKQCGKV
-			FISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG
1			EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA
			SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH
}			ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR
	}		YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC
			GKAFIRASSCREHERTHTINR
6368	1	327	RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE
			DSETYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK
			DQFVCGETVPAPSANKELVKC
6369	1	1745	AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT
]			PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET
}			FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG
			ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD
			TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY
			DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL
			IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE
			CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM
	<b> </b>		THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA
			FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG
			EKPHECKECGKVFKYFSSLRIHERTHTGEKPHECKQCGKAFRYF

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Predicted	- ATO	1 5 - 37 - 5 - 3	Dundleted and	Amino agid comment containing cignal mentide
NO: location corresponding to first maino acid residue of maino acid residue of maino acid residue of maino acid sequence solution (and the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the c	ŠEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Cocresponding   to first		, , ,		
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VGKNYKLYDMVLQFLRTLPLRTRNVHYCTLRABLLMSLHDLDUG EICTVDPCHKFTMCLDACTRERFVDSKRARELQGFLDGVKKQQE QVLGDLSMILCDPFAINTLALSTVRHLQELVGQETLPRDSPDLL LLIRLLALGQSAMDMIDSQVFKEPKMEVELITTPFLPMLMSPLVD DYTFNVDQKLPAEEKAPVSYPNTLPESTFKFLQEQRMACEVGLY YVLHITKQRNKNALLRLIPGLVETFGDLAFGDIFLHLLTGNLAL LADEFALEDFCSSLFDGFFLTASFRENVRRHALRLLIHHHPRV AFSKLEALQKALEPTGQSGEAVKLYSQLGEKLEQLDHRKYSPA QAAETPALELDPLSVPRAPAL  6373 67 711 PSRAARASPARLPAMVSWIISRLVVLIFGTLYPAYYSYKAVKS DIKEYVKMMMYWIIFALFTTAETFTDIFLCMPPFYYELKIAFVA WILSPYTKGSSLLYKFVHFTLSSKEKEIDDCLVQAKDRSYDAL VHFGKRGLNVAATAAVMAASKQQALSERLRSFSMQDLTIRGD GAPAPSGPPPFGSGRASGKGPVMSRSASEASSSTAD HKLFCSYISTSEFPSSTRHSCPTHTFCNYTSSTIFLSSTRDHS CPHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDH CPHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDH SCPHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRD SCHTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDH SCCPABLQTEGSNGKKEVLSGPQVVLEDTVLPFEGGGQPDDRGTIN DISVLRVTRRGEQADHFTQTPLDPESGVLVRVDWERRFDHMQQH SCGHLITAVADHJFKLKTTSWELGBFRSALELDTFSMTAEQVAA IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTERGKKNRINLIFL GKNNLNLERLAVHIAHSLENSPDWGGVVILHRKEGDSEFMNII ANEIGSSETLLFITTVTVGDEKGGLIFLLAGPPASVETLGPRVAEVL EGKGAGKKGRPQGKATKMSRRMEAQALLQDYISTGSAKE  6375 1 1535 AIMAAATRPVRLPEAGCGGERECKNPSRSRSHGGGGLAAWSHT CPGFRFRPQQOVVRGPTMLVTAYLALFVGLLASCLIGLELSRCRAK PPGRACNFSFILRFQLDFYQVYFLALAADMLQAFYLYKLYQHYY FLEGGIALLYVCGLASTVLFGLVASSLVDMLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFFAWYHHEHVER HDPPAENIPATFARAAFWNIVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLLAGLALLRNMGENYDRGRAFSRTCAGGIRCLLSDR RVLLLGTIQALFESVIFIFVFLMTPVLDPHGAPLGIFISFSFMAA SLLGSSLYRIATSKRYHLQPMLLSLAVLIVVSELFMLTFSTSP	1			
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SGQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKLQNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSEETLLFLTVGDEKGGGLFLLAGPPASVETLGFRVAEVL EGKGACKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE  6375 1 1535 AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAFYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYHHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP				-
IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIBGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKLQNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSEETLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE  6375 1 1535 AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGGIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP				
VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKLQNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSEETLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE AIMAAATRPVRLPEAGCEGREECWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAFYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP		i		
SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKLQNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSEETLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE 6375 1 1535 AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAFYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYHHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP			,	
QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSEETLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE 6375 1 1535 AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLPSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP				VIII 25 V 25 III 1 C C C III 1 C C C C C C C C C C C
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CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP		<u> </u>	<u></u>	
PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAFYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP	6375	1	1535	,
FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP	1	1	1	
FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP				PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAFYLYKLYQHYY
SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP				
HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP				1 · · · · · ·
FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP		i		
RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP				
SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP				
	1			
GQESPVESFIAFILIELACGLIFFSMSFLRRRVIPETEQAGVEN			1	
	L		<u> </u>	GGESPVESFIAFLLIELACGLIFPSMSFLRKKVIPETEQAGVLN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID			
!	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
]	amino acid	sequence	Codon, /=possible nucleotide deletion,
	1	sequence	codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		!	WFRVPLHSLACLGLLVLHDSDRKTGTRNMFSICSAVMVMALLAV
			VGLFTVVRHDAELRVPSPTEEPYAPEL
6376	380	1437	ISSTDIDHYRFSFLVNSKMPSKESWSGRKTNRAAVHKSKQEGRQ
1 1	j		QDLLIAALGMKLGSPKSSVTIWQPLKLFAYSQLTSLVRRATLKE
1 1	1		
	1		NEQIPKYEKIHNFKVHTFRGPHWCEYCANFMWGLIAQGVKCADC
		i	GLNVHKQCSKMVPNDCKPDLKHVKKVYSCDLTTLVKAHTTKRPM
1			VVDMCIREIESRGLNSEGLYRVSGFSDLIEDVKMAFDRDGEKAD
1	}		ISVNMYEDINIITGALKLYFRDLPIPLITYDAYPKFIESAKIMD
l i			PDEQLETLHEALKLLPPAHCETLRYLMAHLKRVTLHEKENLMNA
		1	ENLGIVFGPTLMRSPELDAMAALNDIRYQRLVVELLIKNEDILF
6377	2311	1845	SRIRRRSSRRPREPPGPSRRRRRRRPDPRTMPSEKTFKQRRTFE
		-3.5	QRVEDVRLIREQHPTKIPVIIERYKGBKQLPVLDKTKFLVPDHV
1 1			
]	1		NMSELIKIIRRRLQLNANQAFFLLVNGHSMVSVSTPISEVYESE
			KDEDGFLYMVYASQETFGMKLSV
6378	686	191	GAGPWEAFPDGIGRRSRRARLPQYKRPPGRVGGGDSGRRNMAVA
1	ľ		DLALIPDVDIDSDGVFKYVLIRVHSAPRSGAPAAESKEIVRGYK
i i		1	WAEYHADIYDKVSGDMQKQGCDCECLGGGRISHQSQDKKIHVYG
		1	YSMAYGPAQHAISTEKIKAKYPDYEVTWANDGY
6379	35	378	ERAGSPSPSRAALRRCAPORSQAPRWPDRAACRRSFOGSOGRAY
1 03/3	""	] 3,0	
	Į		LFNSVVNVGCGPAEERVLLTGLHAVADIYCENCKTTLGWKYEHA
			FESSQKYKEGKYIIELAHMIKDNGWD
6380	1414	462	PAVQGQRGAGPPTGRGSGNMARFALTVVRHGETRFNKEKIIQGQ
		)	GVDEPLSETGFKQAAAAGIFLNNVKFTHAFSSDLMRTKQTMHGI
1			LERSKFCKDMTVKYDSRLRERKYGVVEGKALSELRAMAKAAREE
		ĺ	CPVFTPPGGETLDQVKMRGIDFFEFLCQLILKEADQKEQFSOGS
		1	PSNCLETSLAEIFPLGKNHSSKVNSDSGIPGLAASVLVVSHGAY
1			MRSLFDYFLTDLKCSLPATLSRSELMSVTPNTGMSLFIINFEEG
1		1	
			REVKPTVQCICMNLQDHLNGLTENSLGLNLPSKSNHFEPLKGVP
			LALFTSLLC
6381	1668	218	AVVRAQGSRGFSGAGWRPRQAAAMNFSEVFKLSSLLCKFSPDGK
1 1	1	(	YLASCVQYRLVVRDVNTLQILQLYTCLDQIQHIEWSADSLFILC
	i	1	AMYKRGLVQVWSLEQPBWHCKIDEGSAGLVASCWSPDGRHILNT
1			TEFHLRITVWSLCTKSVSYIKYPKACLQGITFTRDGRYMALAER
			RDCKDYVSIFVCSDWQLLRHFDTDTQDLTGIEWAPNGCVLAVWD
1			TCLBYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSOFLAVG
( I			
			SYDGKVRILNHVTWKMITEFGHPAAINDPKIVVYKEAEKSPQLG
			LGCLSFPPPRAGAGPLPSSESKYEIASVPVSLQTLKPVTDRANP
]			KIGIGMLAFSPDSYFLATRNDNIPNAVWVWDIQKLRLFAVLEQL
1			SPVRAFQWDPQQPRLAICTGGSRLYLWSPAGCMSVQVPGBGDFA
			VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT
6382	2	1062	FEEDEDRNLCLIAYPLKGDHGIVDIVDNSDCEPKSKLLRWTTNK
I			KHHVLETEKTPKDWVRQHRKEEKMKSHKLEEEFEWLKKSEVLYY
\			TVEKKGNISSQLKHYNPWSMKCHOOOLORMKENAKHRNOYKFIL
		}	
1	)		LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS
j l			AVIGVRVCGMQVYQAGSGQLMFMNKYHGRKLSVQGFKEALFQFF
1			HNGRYLRRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG
1			KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM
1 1			IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG
]			E
6383	3159	1061	SPAPGRPSPHGSOPAARAAAAPAMPSAKORGSKGGHGAASPSEK
		2002	
1			GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP
1	i		AARAAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKK
			PPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGKS
1 1	l		SSSSSASAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFS
1 1			
			GWCVHHVLEEVQQVRRSHQDFSRQREELGQGLQGVEQKVQSLQA
			GWCVHHVLEEVQQVRRSHQDFSRQREELGQGLQGVBQKVQSLQA TFGTFESILRSSQHKQDLTEKAVKQGESEVSRISEVLQKLQNEI

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LKDLSDGIHVVKDARERDFTSLENTVEERLTELTKSINDNIAIF
			TEVQKRSQKEINDMKAKVASLEESEGNKQDLKALKEAVKEIOTS
			AKSREWDMEALRSTLQTMESDIYTEVRELVSLKQEQQAFKEAAD
		[	TERLALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGP
			KEDGGFRHSEAFEALQQKSQGLDSRLQHVEDGVLSMQVASARQT
	,		ESLESLISKSQEHEQRLAALQGRLEGIGSSEADQDGLASTVRSL
			GETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLLSQDQA
			QAARLPPQDFLDRLSSLDNLKASVSQVEADLKMLRTAVDSLVAY
			SVKIETNENNLESAKGLLDDLRNDLDRLFVKVEKIHEKV
6384	738	1904	IWEVPVCLTHLLHLQQANQPLPPPSSSINEEDADEANRAIGEKR
	, , , ,	1,04	AAPDSGKKPKTPKTKQQKDPNEPQKPVSAYALFFRDTQAAIKGQ
		1	NPNATFGEVSQIVASMWDSLGEEQKQVYKRKTEAAKKEYLKALA
			AYRASLVSKAAAESAEAQTIRSVQQTLASTNLTSSLLLNTPLSQ
			HGTVSASPQTLQQSLPRSIAPKPLTMRLPMNQIVTSVTIAANMP
			SNIGAPLISSMGTTMVGSAPSTQVSPSVQTQQHQMQLQQQQQQQ
			QQQMQQMQQQQLQQHQMHQQIQQQMQQQHFQHHMQQHLQQQQQQQQ
			LQQQINQQQLQQQLQQQLQQLQQLQHMQHQSQPSPRQHSPVASQI
			TSPIPAIGSPQPASQQHQSQIQSQTQTQVLSQVSIF
6385	2	1584	PRVRAADVAAGAQAVVSAGMAKSNGENGPRAPAAGESLSGTRES
•••	_	1304	LAQGPDAATTDELSSLGSDSEANGFAERRIDKFGFIVGSQGAEG
			ALEEVPLEVLRQRESKWLDMLNNWDKWMAKKHKKIRLRCQKGIP
			PSLRGRAWQYLSGGKVKLQQNPGKFDELDMSPGDPKWLDVIERD
			LHRQFPFHEMFVSRGGHGQQDLFRVLKAYTLYRPEEGYCQAQAP
			IAAVLLMHMPAEQAFWCLVQICEKYLPGYYSEKLEAIQLDGEIL
			FSLLQKVSPVAHKHLSRQKIDPLLYMTEWPMCAFSRTLPWSSVL
			RVWDMFFCEGVKIIFRVGLVLLKHALGSPEKVKACQGQYETIER
			LRSLSPKIMQEAFLVQEVVELPVTERQIEREHLIQLRRWQETRG
			ELQCRSPFRLHGAKAILDAEPGPRPALQPSPSIRLPLDAPLPGS
			KAKPKPPKQAQKEQRKQMKGRGQLEKPPAPNQAMVVAAAGDACP
	•		PQHVPPKDSAPKDSAPQDLAPQVSAHHRSQESLTSQESEDTYL
6386	819	195	TVCGSFYLGIMQRASRLKRELHMLATEPPPGITCWQDKDQMDDL
	023	173	RAQILGGANTPYEKGVFKLEVIIPERYPFEPPQIRFLTPIYHPN
			IDSAGRICLDVLKLPPKGAWRPSLNIATVLTSIQLLMSEPNPDD
	'		PLMADISSEFKYNKPAFLKNARQWTEKHARQKQKADEEEMLDNL
			PEAGDSRVHNSTQKRKASQLVGIEKKFHPDV
6387	1	662	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAELVKR
		002	FGFTHASADAWADAWAQPNMAMHNKAAPPQTPDTRRELAELVKR   KQELAETLANLERQIYAFEGSYLEDTQMYGNIIRGWDRYLTNOK
j			NSNSKNDRRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK
			REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQKAAS STSSGSHHSSHKKRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY
6388	1	662	DCDTUACADAWADAWADAWADAWADAWAWAWAAAAAAAAAAAAA
~ > 0 0	*	002	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAELVKR
			KQELAETLANLERQIYAFEGSYLEDTQMYGNIIRGWDRYLTNQK
			NSNSKNDRRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK
			REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQKAAS
6389	1074	407	STSSGSHHSSHKKRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY
0000	10/4	497	AEPGDRMAGHRLVLVLGDLHIPHRCNSLPAKFKKLLVPGKIQHI
			LCTGNLCTKESYDYLKTLAGDVHIVRGDFDENLNYPEQKVVTVG
			QFKIGLIHGHQVIPWGDMASLALLQRQFDVDILISGHTHKFEAF
			EHENKFYINPGSATGAYNALETNIIPSFVLMDIQASTVVTYVYQ
6390			LIGDDVKVERIEYKKP
0990	158	535	GEERKEGRAPGKAFAPERNPAKMEKEETTRELLLPNWQGSGSHG
			LTIAQRDDGVFVQEVTQNSPAARTGVVKEGDQIVGATIYFDNLQ
			SGEVTQLLNTMGHHTVGLKLHRKGDRFFPSLGQTWDP
6391	5386	2897	VRWNSKTECYLSIQTQENFPANLNELVNCIVISSLVTTQRKLKA
6391	5386	2897	

Section   Designing   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declarion   Declar	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Note   docation   corresponding to first anino acid residue of since anino acid residue of anino acid sequence   https://docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com/docation.com				(A=Alanine, C=Cysteine, D=Assartic Acid F=
corresponding   to first   amino acid   amino acid   residue of   amino acid   ence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequen	1			Glutamic Acid. Faphenvialanine G-Glucine
to first amino acid residue of seidue of seidue of seidue of amino acid residue of amino acid sequence    Peptoline_Geolutamine_Navaline,   Seserine_Tathreomine_Vavaline,   Seserine_Tathreomine_Vavaline,   Seserine_Tathreomine_Vavaline,   Seserine_Tathreomine_Vavaline,   Seserine_Tathreomine_Vavaline,   Seserine_Tathreomine_Vavaline,   Seserine_Tathreomine_Vavaline,   Seserine_Tathreomine_Vavaline,   Seserine_Tathreomine_Vavaline,   Seserine_Tathreomine_Vavaline,   Seserine_Tathreomine_Vavaline_Vavaline,   Seserine_Tathreomine_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_Vavaline_V	140:			
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mino acid residue of amino acid sequence whytophan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-Typoshan, Y-				
residue of amino acid sequence				
### Sequence   Codon, /-possible nucleotide deletion,    -possible nucleotide insertion				
Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence				Codon /-nossible nucleotide deletion
LTENGEKOHSDENSNAKIGORVLVCAJSKAADELMIKITI ILE KEKCKOKKNILOROINUVKLOBES INSSULKSENDSQUVHE MKKELPSIVOAMHKREFEJDYGLDELSIGGRALCHGGEEIGGUL DENISKYSKERGELASKIRVEVGEPKYTGSIILIESHITOCTLE TSGGLLLESAFROOGGVPSSCVIVDERGGSEEIEFLFPLIHERCY KLILVODPKOLPFVISMKAQEYGYDOSMARPCRLLEENVEHN MISRAPIIQLIVQIRMHPDICLPPSNYVYRRUKATNAGTEAIRC SSUMFFOPTLVFDVGDSSRRDNDSYINVOBERGARPEVDTVDA KREVSYFRINGIITHYTAGKYTHIQKOLDEKSFORKAPAEVDTVDA FOGROKOCVIVTCVRANSIGSIGFLASLGRIAVYTITRAKYSLE LICHLERTIMENGHMONGLIQDARGGAIKTCONSPARVIK LKVVLQRSIHHPPTIAPEGSFPCOGLISSKLDSGFARTSVARSI YHTPSDSEETLITVISSDEERPFVHOOLOGPRLUKERGIEVKOG IFJWDPOPSSPQHBOATPTGEFGFPVVHOOLOSHVOQPAAVVA LSHKPPVRGEPPAASSEASTOGSCOGLISSKLDSGFARTSVARSI YHTPSDSEETLITVISSDEERPFVHOOLOGPRLUKERGIEVKOG IFJWDPOPSSPQHBOATPTGEFGFPVVHOOLSHVOQPAAVVA LSHKPPVRGEPPAASSEASTOGSCOGLISSKKRKLL GROWDLASSMAHRIGIRLITWOVENTLLEKHPILGEGATATKRA ALGEVEPSALEGGFRQAYRAGSRSFPHVGLSGLITSROMMLDV VLOTPHLAGVODAOVAPIARGUIKTJELARHPILGEAVATKRA AHGLEVEPSALEGGFRQAYRAGSRSFPHVGLSGLITSROMMLDV VLOTPHLAGVODAOVAPIARGUIKTJELARHPILGEAVATKRA AHGLEVEPSALEGGFRQAYRAGSRSFPHVGLSGLITSROMMLDV VLOTPHLAGVODAOVAPIARGUIKTJELARHPIVTSEAAGHP KPDPRIFFGEALRAHREPVVAAHRONILCDVGGRADFUTE ECTRIGLELAVISNFDBRILGGILGGGLRHFDFVUTSEAAGHP KPDPRIFFGEALRAHREPVVAAHRONILCDVGGRADFUTE ECTRIGLELAVISNFDBRILGGILGGGLRHFDFVUTSEAAGHP KPDPRIFFGEALRAHREPVVAAHRONILCDVGGRADFUTE ECTRIGLELAVISNFDBRILGGILGGGLRAVGTV VLOGPALDPVVRDSVPREHILPSLAHLIPALDCLEGSTFGL LLIEBCKNITYSFILDFRYFLAGGIUKGNILLGGGLAVGTV VLSGPALLSVSTAGTRSSVANSTGSAVATASSKSNTSFFREGERAFAVI DESCRIPTYVALLDPIONITYESGPADOVATKSSPLANTESSTLKV BPCSLTPGVYKLLDPIONITYESGPADOVATKSSPLANTESSTLKV BPCSLTPGVYKLLDPIONITYESGPAGNILLGGGLAVGTV LLIEBCKNITYSFILDFRYFLAGGIUKGNILLGGGLAVGTV LLIEBCKNITYSFILDFRYFLAGGIUKGNILLGGGLAVGTV LLIEBCKNITYSFILDFRYFLAGGIUKGNILLGGGLAVGTV LLIEBCKNITYSFILDFRYFLAGGIUKGNILLGGGLAVGTV LLIEBCKNITYSFILDFRYFLAGGIUKGNILLGGGLAVGTV LLIEBCKNITYSFILDFRYFLAGGIUKGNILLGGGLAVGTV LLIEBCKNITYSFILDFRYFLAGGIUKGNILLGGGGRAVGT GROWAANTATGGGGGRANGARGGGRAGGRAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	Ì		sequence	
KEKCHOKNIPLONCODINIVALOPEKSINSPALKENSDOOVHAN MKKELDSHOOMHAKKERFIJOVLOBLISUGRALORGEIORGEL DENISKYS KERQELASKILEVAGROOKTSGUTOUDAGOGGEI TILESHITOCTA TSGGILLESAFROGGOVPSCUTUDAGOGGEI TILESHITOCTA KLILVGDPKQLPPTVISMKAQEYGTOGMARAFCHLESNVEHM MISRAPILGITVQTRHERDICLPSSVYTYRRALKTINGOTEAHC SSDWPFOPTLVEVENDOGSERRDNSVINVOEIKLMESIKHIKO KRADYSFRIGIITHYKAGKTMIQNDLOKSFORKOPAEVUTVO PKORQCCVIVTOVARNSIQGSIEGHASLGRIKUVTITRAKVSLE ILGHURTUMENOHMOQLIQDAQKKGAIIKTCOKNYRHDAVKLI LKAVUVGRIHTPPTTABGGSRPGGIPSSKLOSGPARTSVAASI. YHTTSDSSEITITVTSKDERPPVHODLOPPALLKRNGIEVAGI. LKAVUVGRIHTPPTTABGGSRPGGIPSSKLOSGPARTSVAASI. YHTTSDSSEITITVTSKDERPPVHODLOPPALLKRNGIEVAGI. SSHKPPVRGEPPAASPERSTCQSKCDDPEELCHREARAFSS GEGEKCGSETHITRINSROMRIKTEGDESSKKRAT. SSHKPPVRGEPPAASPERSTCQSKCDDPEELCHREARAFSS GEGEKCGSETHITRINSROMRIKTEGDESSKKRAT. SSHKPPVRGEPPAASPERSTCQSKCDDPEELCHREARAFSS GEGEKCGSETHITRINSROMRIKTEGDESSKRATGERVADAV LSHKPPVRGEPPAASPERSTCQSKCDDPEELCHREARAFSS GEGEKCGSETHITRINSROMRIKTEGDESSKRATGERVADAV LUTPHLAGVORAQAVAPIRGQIVKOFSHPCTIVOULOGAEDTE ECRTRCLLALVISHOPPAASPERSTPVIGHOLISTBOMILDV VLOTPHLAGVORAQAVAPIRGQIVKOFSHPCTIVOULOGAEDTE ECRTRCLLALVISHOPPAASPERSTPVIGHOLISTBOMILDV VLOTPHLAGVORAQAVAPIRGQIVKOFSHPCTIVSGLAGHER KPDPRIPGEALILLAMBEVVAAHVONIULOCXGPRAVCHHSFL VUGPQALIDPVVRDSVYREHILIPSAHILIPSAHOCLISTBOMILDV LLIEBDKYNIYSPINDERLIGGILGGIJERHENPUTISEAGHER KPDRRIPGSEALRAMBYNAATHVORNIULOCXGPRAVCHHSFL VUGPQALIDPVVRDSVYREHILIPSAHILIPSAHOCLISTBOMILDV LLIEBDKYNIYSPILKYRLAGGIGGINGHALIVAKSSVTSTEPKRGFRASVY NDSSPRLUSYSTATTRSSVRRGQLINSTGLIAGGILAVGTV LLIEBDKYNIYSPILKYRLAGGIGGINGHALIVAKSSVTSTEPKRGFRASVY NDSSPRLUSYSTATTRSSVRRGQLINSTGLIAGGILAVGTV LLIEBDKYNIYSPILKYRLAGGIGGINGHALIVAKSSVTSTEPKRGFRASVY DESSTFOTYTKLLOPICNI IYEBGPOSNOKKORNILLBIOLD LGSPJUMGDICCAGARGGINSHILKFYLVILKGLIKHSISTIKV BPCSLTTOYTYKLLOPICNI IYEBGPOSNOKKORNILLBIOLD LGSPJUMGDICCAGARGGINSHILKFYLVILKGLIKHSISTIKU BPCSLTTOYTYKLLOPICNI IYEBGPOSNOKKORNILLBIOLD LGSPJUMGDICCAGARGGINSHILKFYLVILKGLIKHSISTIKUSTAV BPCSLTTOYTYKLLOPICNI LYGGSTEGDAKQGRNILLBIOLD LIGHTALPOKARGGARGAGGGRSHILLBARRINDAYNININKICLIVTY LIGHQADANATUALIHFAPEROKOR	-	sequence		
MKKELPSKVOAMHRKEFELDYGLDELSKOEALCRGGEEIGREI  DENISKVSKERGELASKIEKEVGERGYGYGGI II LESIITCCTLE TSGGLLLESAFRGOGGVPSGVTGGITALESIITCCTLE TSGGLLLESAFRGOGGVPSGVTGGMARGFCLLESTVENH KLIVODPKGLDPYTIGMKAGEVYDGGMARGFCLLESTVENH MISRLPILOLTVOYEMSPDICLPSMYYTHRIKKTNROTEAIRC SSDMPPGPYLLVPDVOGSKERDNSVINVOSIKLUMEIKLIKU KRKDVSFRNIGIITHYKAQKTMIQKDLDKSFDKRAREVDTVDA PGGRGACVAVTCVRANSIGGSIGHASIGRIAVTITRAKYSIL LIGHLETIMSNOHMIQLIQDAKGATIKKTOKYRDDAVTILA LIGHLETIMSNOHMIQLIQDAKGATIKKTOKYRDDAVTILA LKEVLQRSILTHPPTIABESSPGGGLPSSKLDSGFAKTSVASAL LKEVLQRSILTHPPTIABESSPGGGLPSSKLDSGFAKTSVASAL LKEVLQRSILTHPTIABESSPGGGLPSSKLDSGFAKTSVASAL LKEVLQRSILTHPTIABESSPGGGLPSSKLDSGFAKTSVASAL LKEVLQRSILTHPTIABESSPGGGLPSSKLDSGFAKTSVASAL LKEVLQRSILTHPTIABESSPGGGLPSSKLDSGFAKTSVASAL LKEVLQRSILTHPTIABESSPGGGLPSSKLDSGFAKTSVASAL LKEVLQRSILTHPTIABESSPGGGLPSSKLDSGFAKTSVASAL LKEVLQRSILTHPTIABESSPGGGLPSSKLDSGFAKTSVASAL LKEVLQRSILTHPTIABESSPGGGLPSSKLDSGFAKTSVASAL LKEVLQRSILTHPTIABESSPGGLESSFOKTAGENAGE GEGKKGGSTHHTTRNSRROURTLEQEDSSKKAKLL  GRTGVULLASVANGTGALAGENGALAGENGALAGENIAGENGAKTSGALAGENGG FFANGLIALVISNFDRALEGGLSGENDESELLGSGTAKTSAN KAPPORGEPAASSPASTAGGAVADGTALLEGGIAVGTAKARA AHGLEVEBSALBQGFQAYRAQSKSFENYGLSGLITSROMMLDV VLOTPHLAGVQDAQAVADJARGU, MEDSHACHAVANGTSEL ECTTRICLALAVISNFDRALEGGILGGGLRRFFDFVUTSERAGMP KAPDPET FGEALRAHMEPVVAAHVADNILTLEKERFDFAUTSERAGMP KAPDPET FGEALRAHMEPVVAAHVADNILTLEKERFDFVUTSERAGMP KAPDPET FGEALRAHMEPVVAAHVANTSKSNVTSFGRRGPFASVY NDSGFRLUSTAGTAVANGTALAKSVANTSGALAGETTAR TORSSSRFCHLASVANSTGSAVATASKSNVTSFGRRGPFASVY LLEEGKYNTYSFLYKPALLAGELSSTICKY BEGSJTPGVYKLLDPIONITYSEGGLEAGNAGGKRALDF GSSPRLUSTAGTAVANGTALAKSPACLLOGGLAVATOKAT LLEEGKYNTYSFLYKPALLAGELSSTICKY BPCSJTPGVYKLLDPIONITYSEGGRAGGKRALDFG GSRAMAAVATOLTSGARAGATATSKANTYTESSACLITM PTHLIQUNALIANTTISDVVALLBSFTYGGRAGATHIGSCGTAVATOKATAR ULKQLGOLLEAGSSRGALAGGRAGGAMAGGKRALDF THATTITLEETASGTTHMSARALFTYALTRALTHPSSACLITM PTHLIQUNALIANTTISDVVALLBSFTYGGRAGATHIGSCGTAVATOKATAR VLKQLGOLLEAGSSRDMAGGRAGATHGAGGANFBAGGARHATTISGSGV THATATTITLEETASGGTMAGGARHAGGARHENGGARHATHATAR THATTITLEETASGGTMAGGARHAGGARHENGGARHATHATARGE T	1			
DENISKYSKEROKLASKIKEVOGROGIVOSIIILESHIICTILCTLS TSGGLLLESARGOGGUPPTUSTOVIDEAGOSCISTITTPILIRCY KLILVODPKOLPPTUSMKAGEVOTOOSMAARPCKLLEENUSHM MISKLPILOLTVOYRMHOPICLIPSNYVYNRNIKTNOTEAIRC SSDWPPOPTUVFUVOODSSERDNDSYINVOSIKLAWEIIKLIKU KRKUVSFRNIGIITHYKAGATMIOODLOEFTRAGRASUTIVOA POGROKOCUTVUTOVARNIGSIGFLASIQRINVITTRAKYSLI LICHLERTIMENOHMAQIIQDAQKRGAIIKTCOKNYHHDAVILK LKEVULGRSLITHPTITAPGSERPOGGLESKLOSPARTSVASSI, YHTESDSKETTLTVTSKOPERPPVHOOLOOPRILKRAMGIEVKOG IFFUNDOPOSSOPOHOATPTOTGEPOPVVHOOLOOPRILKRAMGIEVKOG IFFUNDOPOSSOPOHOATPTOTGEPOPVVHOOLOOPRILKRAMGIEVKOG IFFUNDOPOSSOPOHOATPTOTGEPOPVVHOOLOOPRILKRAMGIEVKOG IFFUNDOPOSSOPOHOATPTOTGEPOPVVHOOLOOPRILKRAMGIEVKOG IFFUNDOPOSSOPOHOATPTOTGEPOPVVHOOLOOPRILKRAMGIEVKOG IFFUNDOPOSSOPOHOATPTOTGEPOPVVHOOLOOPRILKRAMGIEVKOG IFFUNDOPOSSOPOHOATPTOTGEPOPVVHOOLOOPRILKRAMGIEVKOG IFFUNDOPOSSOPOHOATPTOTGEPOPVVHOOLOOPRILKRAMGIEVKOG IFFUNDOPOSSOPOHOATPTOTGEPOPVVHOOLOOPRILKRAMGIEVKOG IFFUNDOPOSSOPOHOATPTOTGEPOPVVHOOLOOPRILKRAMGIE SHEEPPINGOPOHOATPTOTGEPOPVHOOLOOPRILKRAMGIE GRONGOPOHOATPTOTGEPOPVHOOLOOPRILKRAMGIEVE LESHKUNDONOANATAGEOROATRAKA KAPOPATATAA HARDEVESALAGEOROATRAGHIEVAGUATAVARA KAPOPATATAATAATAATAATAATAATAATAATAATAATAATAA				
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PCKPSCVSQLGQRAEPKATERGILRATGVAWESQLKPEELPSMQ DLLEEASSRDMQMGPGLFLRMQLVPSIEERETPLTREDRPALQE PPWSLGCTGLKAAMQIQRVVIPVPTLGHRNPWVARDSGE  6396  1 1221 ANILSSPSKRGGKGTLIGYSPEGTPLYNFMGDAFQHSSQSIPRF IKESLKQILEESDSRQIFYFLCLNLLFTFVELFYGVLTNSLGLI SDGFHMLFDCSALVMGLFAALMSRWKATRIFSYGYGRIEILSGF INGLFLIVIAFFVFMESVARLIDPPELDTHMLTPVSVGGLIVNL IGICAFSHAHSHAHGASQGSCHSDHSHSHHMHGHSDHGHSH GSAGGGMNANMRGVFLHVLADTLGSIGVIVSTVLIEQFGWFIAD PLCSLFIAILIFLSVVPLIKDACQVLLRLPPEYEKELHIALEK IQKIEGLISYRDPHFWRHSASIVAGTIHIQVTSDVLEQRIVQQV TGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES MKYCKDGTYIM  6397  391  122 GAGGVGRFEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK	6395	13	658	
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PPWSLGCTGLKAAMQIQRVVIPVPTLGHRNPWVARDSGE  6396  1 1221 ANILSSPSKRGQKGTLIGYSPEGTPLYNFMGDAFQHSSQSIPRF IKESLKQILEESDSRQIFYFLCLNLLFTFVELFYGVLTNSLGLI SDGFHMLFDCSALVMGLFAALMSRWKATRIFSYGYGRIEILSGF INGLFLIVIAFFVFMESVARLIDPPELDTHMLTPVSVGGLIVNL IGICAFSHAHSHAHGASQGSCHSSDHSHSHHMGHSHHGHSHH GSAGGGMNANMRGVFLHVLADTLGSIGVIVSTVLIEQFGWFIAD PLCSLFIALLIFLSVVPLIKDACQVLLLRLPPEYEKELHIALEK IQKIEGLISYRDPHFWRHSASIVAGTIHIQVTSDVLEQRIVQQV TGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES MKYCKDGTYIM  6397 391 122 GAGGVGRFEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK			1 .	= =
6396 1 1221 ANILSSPSKRGQKGTLIGYSPEGTPLYNFMGDAFQHSSQSIPRF IKESLKQILEESDSRQIFYFLCLNLLFTFVELFYGVLTNSLGLI SDGFHMLFDCSALVMGLFAALMSRWKATRIFSYGYGRIEILSGF INGLFLIVIAFFVFMESVARLIDPPELDTHMLTPVSVGGLIVNL IGICAFSHAHSHAHGASQGSCHSSDHSHSHHMHGHSDHGHSH GSAGGGMNANMRGVFLHVLADTLGSIGVIVSTVLIEQFGWFIAD PLCSLFIAILIFLSVVPLIKDACQVLLLRLPPEYEKELHIALEK IQKIEGLISYRDPHFWRHSASIVAGTIHIQVTSDVLEQRIVQQV TGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES MKYCKDGTYIM 6397 391 122 GAGGVGRFEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK			1	
IKESLKQILEESDSRQIFYFLCLNLLFTFVELFYGVLTNSLGLI SDGFHMLFDCSALVMGLFAALMSRWKATRIFSYGYGRIEILSGF INGLFLIVIAFFVFMESVARLIDPPELDTHMLTPVSVGGLIVNL IGICAFSHAHSHAHGASQGSCHSSDHSHSHHMHGHSDHGHSHH GSAGGGMNANMRGVFLHVLADTLGSIGVIVSTVLIEQFGWFIAD PLCSLFIAILIFLSVVPLIKDACQVLLLRLPPEYEKELHIALEK IQKIEGLISYRDPHFWRHSASIVAGTHHIQVTSDVLEQRIVQQV TGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES MKYCKDGTYIM  6397 391 122 GAGGVGRFEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK				
SDGFHMLFDCSALVMGLFAALMSRWKATRIFSYGYGRIEILSGF INGLFLIVIAFFVFMESVARLIDPPELDTHMLTPVSVGGLIVNL IGICAFSHAHSHAHGASQGSCHSSDHSHSHHMHGHSDHGHSHH GSAGGGMNANMRGVFLHVLADTLGSIGVIVSTVLIEQFGWFIAD PLCSLFIAILIFLSVVPLIKDACQVLLLRLPPEYEKELHIALEK IQKIEGLISYRDPHFWRHSASIVAGTIHIQVTSDVLEQRIVQQV TGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES MKYCKDGTYIM 6397 391 122 GAGGVGRFEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK	6396	1	1221	
INGLFLIVIAFFVFMESVARLIDPPELDTHMLTPVSVGGLIVNL IGICAFSHAHSHAHGASQGSCHSSDHSHSHHMHGHSDHGHSHH GSAGGGMNANMRGVFLHVLADTLGSIGVIVSTVLIEQFGWFIAD PLCSLFIAILIFLSVVPLIKDACQVLLLRLPPEYEKELHIALEK IQKIEGLISYRDPHFWRHSASIVAGTIHIQVTSDVLEQRIVQQV TGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES MKYCKDGTYIM 6397 391 122 GAGGVGRFEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK		I	1	
IGICAFSHAHSHAHGASQGSCHSSDHSHSHHMHGHSDHGHGHSH GSAGGGMNANMRGVFLHVLADTLGSIGVIVSTVLIEQFGWFIAD PLCSLFIAILIFLSVVPLIKDACQVLLLRLPPEYEKELHIALEK IQKIEGLISYRDPHFWRHSASIVAGTIHIQVTSDVLEQRIVQQV TGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES MKYCKDGTYIM 6397 391 122 GAGGVGRFEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK		1		
GSAGGGMNANMRGVFLHVLADTLGSIGVIVSTVLIEQFGWFIAD PLCSLFIAILIFLSVVPLIKDACQVLLLRLPPEYEKELHIALEK IQKIEGLISYRDPHFWRHSASIVAGTIHIQVTSDVLEQRIVQQV TGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES MKYCKDGTYIM 6397 391 122 GAGGVGRFEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK				
PLCSLFIAILIFLSVVPLIKDACQVLLLRLPPEYEKELHIALEK IQKIEGLISYRDPHFWRHSASIVAGTIHIQVTSDVLEQRIVQQV TGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES MKYCKDGTYIM 6397 391 122 GAGGVGRFEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK			1	IGICAFSHAHSHAHGASQGSCHSSDHSHSHHMHGHSDHGHGHSH
IQKIEGLISYRDPHFWRHSASIVAGTIHIQVTSDVLEQRIVQQV TGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES MKYCKDGTYIM 6397 391 122 GAGGVGRFEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK				GSAGGGMNANMRGVFLHVLADTLGSIGVIVSTVLIEQFGWFIAD
TGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES MKYCKDGTYIM 6397 391 122 GAGGVGRFEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK		1	}	PLCSLFIAILIFLSVVPLIKDACQVLLLRLPPEYEKELHIALEK
MKYCKDGTYIM 6397 391 122 GAGGVGRFEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK			1	IQKIEGLISYRDPHFWRHSASIVAGTIHIQVTSDVLEQRIVQQV
6397 391 122 GAGGVGRFEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK			1	TGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES
	L		ļ	MKYCKDGTYIM
KLIAAQTGTRWNKIVLKKWYTIFKDHVSLGDYEIHDGMNLELYY	6397	391	122	GAGGVGRFEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK
				KLIAAQTGTRWNKIVLKKWYTIFKDHVSLGDYEIHDGMNLELYY

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Character Acid, E-
I NO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	bequence	\=possible nucleotide insertion)
<b>—</b>	bequeince		
6398	353	1702	Q
6398	353	1306	HKQMGPLINRCKKILLPTTVPPATMRIWLLGGLLPFLLLLSGLQ
			RPTEGSEVAIKIDFDFAPGSFDDQYQGCSKQVMEKLTQGDYFTK
1		Į.	DIEAQKNYFRMWQKAHLAWLNQGKVLPQNMTTTHAVAILFYTLN
1		i	SNVHSDFTRAMASVARTPQQYERSFHFKYLHYYLTSAIQLLRKD
1	4		SIMENGTLCYEVHYRTKDVHFNAYTGATIRFGQFLSTSLLKEEA
	1	1	QEFGNQTLFTIFTCLGAPVQYFSLKKEVLIPPYELFKVINMSYH
ı	1		PRGDWLQLRSTGNLSTYNCQLLKASSKKCIPDPIAIASLSFLTS
		]	
6300			VIIFSKSRV
6399	75	1245	PNLETYFGRRCEKDSMNFTPTHTPVCRKRTVVSKRGVAVSGPTK
1		1	RRGMADSLESTPLPSPEDRLAKLHPSKELLEYYQKKMAECEAEN
1			EDLLKKLELYKEACEGQHKLECDLQQREEEIAELQKALSDMQVC
1		1	LFQEREHVLRLYSENDRLRIRELEDKKKIQNLLALVGTDAGEVT
			YFCKEPPHKVTILQKTIQAVGECEQSESSAFKADPKISKRRPSR
1	1		ERKESSEHYQRDIQTLILQVEALQAQLGEQTKLSREQIEGLIED
	1		RRIHLEEIQVQHQRNQNKIKELTKNLHHTQELLYESTKDFLQLR
1			SENQNKEKSWMLEKDNLMSKIKQYRVQCKKKEDKIGKVLPVMHE
1			
	0500		SHHAQSEYIKVMSLCRNEVVYFSGRVEGIPKNLQFVM
6400	2520	1053	KTMKCDEVVYEVQSAILRHNCGYAMKTGKFFHNLMERKDFETWL
			DNISVTFLSLTDLQKNETLDHLISLSGAVQLRHLSNNLETLLKR
1			DFLKLLPLELSFYLLKWLDPQTLLTCCLVSKQWNKVISACTEVW
1			QTACKNLGWQIDDSVQDALHWKKVYLKAILRMKQLEDHEAFETS
			SLIGHSARVYALYYKDGLLCTGSDDLSAKLWDVSTGQCVYGIOT
ł		ı	HTCAAVKFDEQKLVTGSFDNTVACWEWSSGARTQHFRGHTGAVF
1			CUDANDEL DIT MOCCA DEMINATIVA CA CHICA STRIP TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICAL TO CHEROLOGICA TO CHEROLOGICA TO CHEROLOGICA TO CHEROLOGICA TO CHEROLOGICA TO CHEROLOGICA TO CHER
	l i		SVDYNDELDILVSGSADFTVKVWALSAGTCLNTLTGHTEWVTKV
1			VLQKCKVKSLLHSPGDYILLSADKYEIKIWPIGREINCKCLKTL
			SVSEDRSICLQPRLHFDGKYIVCSSALGLYQWDFASYDILRVIK
	l .		TPEIANLALLGFGDIFALLFDNRYLYIMDLRTESLISRWPLPEY
			RKSKRGSSFLAGEASWLNGLDGHNDTGLVFATSMPDHSIHLVLW
			KEHG
6401	109	766	PGAAWSRPDLRGCCTGPQPALRMLVLPSPCPQPLAFSSVETMEG
			PPRRTCRSPEPGPSSSIGSPQASSPPRPNHYLLIDTQGVPYTVL
1			VDEESQREPGASGAPGQKKCYSCPVCSRVFEYMSYLQRHSITHS
	i		
			EVKPFECDICGKAFKRASHLARHHSIHLAGGGRPHGCPLCPRRF
			RDAGELAQHSRVHSGERPFQCPHCPRRFMEQNTLQKHTRWKHP
6402	1196	279	TTSQCGGIRQSSAIPVASMEFAAICLRNALLLLPEEQQDPKQEN
			GAKNSNQLGGNTESSESSETCSSKSHDGDKFIPAPPSSPLRKQE
1			LENLKCSILACSAYVALALGDNLMALNHADKLLQQPKLSGSLKF
			LGHLYAAEALISLDRISDAITHLNPENVTDVSLGISSNEQDQGS
1			DKGENEAMESSGKRAPQCYPSSVNSARTVMLFNLGSAYCLRSEY
1			
1	]		DKARKCLHQAASMIHPKEVPPEAILLAVYLELQNGNTQLALQII
C400			KRNQLLPAVKTHSEVRKKPVFQPVHPIQPIQMPAFTTVQRK
6403	2	1690	RGIHTSVLQGNLQNQMYSHNVVIMNLNNLNLTQVQQRNLITNLQ
i			RSVDDTSQAIQRIKNDFQNLQQVFLQAKKDTDWLKEKVQSLQTL
			AANNSALAKANNDTLEDMNSQLNSFTGQMENITTISQANEONLK
1			DLQDLHKDAENRTAIKFNQLEERFQLFETDIVNIISNISYTAHH
1			LRTLTSNLNEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSVSLR
1			MQQDLMRSRLDTEVANLSVIMEEMKLVDSKHGQLIKNPTILOGP
1			PGPRGPRGDRGSQGPPGPTGNKGQKGEKGEPGPPGPAGERGPIG
1			PAGPPGERGGKGSKGSQGPKGSRGSPGKPGPQGPSGDPGPPGPP
1			GKEGLPGPQGPPGFQGLQGTVGEPGVPGPRGLPGLPGVPGMPGP
			KGPPGPPGPSGAVVPLALQNEPTPAPEDNSCPPHWKNFTDKCYY
1			FSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVGRESH
			WIGLTDSERBNEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDC
1			AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAL
6404	1012	222	AAALAMAAPAPGLISVFSSSQELGAALAQLVAQRAACCLAGARA

CEO	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ			Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ			
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ı	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
<b></b>	sequence		
1	ł		RFALGLSGGSLVSMLARELPAAVAPAGPASLARWTLGFCDERLV
	1		PFDHAESTYGLYRTHLLSRLPIPESQVITINPELPVEEAAEDYA
j	1		KKLRQAFQGDSIPVFDLLILGVGPDGHTCSLFPDHPLLQEREKI
1	ì		VAPISDSPKPPPORVTLTLPVLNAARTVIFVATGBGKAAVLKRI
i			
	ļ <u>.</u>		LEDQEENPLPAALVQPHTGKLCWFLDBAAARLLTVPFEKHSPL
6405	1	1456	AALPRPTPRAPLGREGTGSDSEMAASMFYGRLVAVATLRNHRPR
i	t		TAQRAAAQVLGSSGLFNNHGLQVQQQQQRNLSLHEYMSMELLQE
1	1	ĺ	AGVSVPKGYVAKSPDEAYAIAKKLGSKDVVIKAQVLAGGRGKGT
l	į.		FESGLKGGVKIVFSPEEAKAVSSQMIGKKLFTKQTGEKGRICNO
	İ		
I			VLVCERKYPRREYYFAITMERSFQGPVLIGSSHGGVNIEDVAAE
I			TPEAIIKEPIDIEBGIKKEQALQLAQKMGFPPNIVESAAENMVK
1			LYSLFLKYDATMIBINPMVEDSDGAVLCMDAKINFDSNSAYRQK
i			KIFDLQDWTQEDERDKDAAKANLNYIGLDGNIGCLVNGAGLAMA
I			TMDIIKLHGGTPANFLDVGGGATVHQVTEAFKLITSDKKVLAIL
	}		1
I			VNIFGGIMRCDVIAQGIVMAVKDLEIKIPVVVRLQGTRVDDAKA
l			LIADSGLKILACDDLDEAARMVVKLSEIVTLAKQAHVDVKFQLP
			I
6406	1036	167	HPROMRGEDTPEAPPYSSGRYDSIKTEVSGCPEDLTVGRAPTAD
1			DDDDDDDDDDDDKMNDSEGMDPERLKAFNMFVRLFVDENLDRM
i		ľ	
	1		VPISKQPKEKIQAIIESCSRQFPEFQERARKRIRTYLKSCRRMK
	1		KNGMEMTRPTPPHLTSAMAENILAAACESETRKAAKRMRLEIYQ
	1	1	SSQDEPIALDKQHSRDSAAITHSTYSLPASSYSQDPVYANGGLN
		1	YSYRGYGALSSNLQPPASLQTGNHSNGESGEARALASRPAPSWV
ł	1		CRAALGSGMGRGKQRPVMERGCLTA
	ļ		
6407	492	150	VGLCLAVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGV
	1		SWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNAC
	l		VLTISPVQPEDDADYYCSVGYGFSP
6408	1458	903	RGCITSSQAWRLFGGVTRGFNMRIEKCYFCSGPIYPGHGMMFVR
1 4 -			NDCKVFRFCKSKCHKNFKKKRNPRKVRWTKAFRKAAGKELTVDN
	1		1
	i		SFEFEKRRNEPIKYQRELWNKTIDAMKRVEBIKQKRQAKFIMNR
]		Į.	LKKNKELOKVODIKEVKONIHLIRAPLAGKGKOLEEKMVOOLQE
	ľ	i e	DVDMEDAP
6409	150	446	NTALANLLRCFTCDRLCGGCTAPAPPAHOGIVLOPVMPSCDPGP
			GPACLPTKTFRSYLPRCHRTYSCVHCRAHLAKHDELISKSFOGS
I		;	<b>-</b>
			HGRAYLFNSV
6410	85	607	RGGTAGCVACLGCWGQSSSPKAAFPAGSACLPADSCPCLLFQAC
			AISGLFNCITIHPLNIAAGVWMIMNAFILLLCEAPFCCQFIEFA
ŀ	1		NTVAEKVDRLRSWQKAVFYCGMAVVPIVISLTLTTLLGNAIAFA
I			TGVLYGLSALGKKGDAISYARIQQQRQQADEEKLAETLEGEL
	200	750	I
6411	302	772	RLSIMASSLNEDPEGSRITYVKGDLFACPKTDSLAHCISEDCRM
			GAGIAVLFKKKFGGVQELLNQQKKSGEVAVLKRDGRYIYYLITK
			KRASHKPTYENLQKSLEAMKSHCLKNGVTDLSMPRIGCGLDRLQ
			WENVSAMIEEVFEATDIKITVYTL
6412	61	1709	RPVTSFSPLPGSCGGRLGTRTMLGRSLREVSAALKOGOITPTEL
0412	0.1	1,03	1 1
			CQKCLSLIKKTKFLNAYITVSEEVALKQAEESEKRYKNGQSLGD
	1		LDGIPIAVKDNFSTSGIBTTCASNMLKGYIPPYNATVVQKLLDQ
1			GALLMGKTNLDEFAMGSGSTDGVFGPVKNPWSYSKQYREKRKON
1			PHSENEDSDWLITGGSSGGSAAAVSAFTCYAALGSDTGGSTRNP
ŀ		•	1
		•	AAHCGLVGFKPSYGLVSRHGLIPLVNSMDVPGILTRCVDDAAIV
ł	1		IGALAGPDPRDSTTVHEPINKPFMLPSLADVSKLCIGIPKEYLV
			PELSSEVQSLWSKAADLFESEGAKVIEVSLPHTSYSIVCYHVLC
			TSEVASNMARFDGLQYGHRCDIDVSTEAMYAATRREGFNDVVRG
			1
1			RILSGNFFLLKENYENYFVKAQKVRRLIANDFVNAFNSGVDVLL
			TPTTLSEAVPYLEFIKEDNRTRSAQDDIFTQAVNMAGLPAVSIP
I		)	VALSNQGLPIGLQFIGRAFCDQQLLTVAKWFEKQVQFPVIQLQE
1			LMDDCSAVLENEKLASVSLKQ
1			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6413	2	885	HEPRCAGMAASLWMGDLEPYMDENFISRAFATMGETVMSVKIIR
			NRLTGIPAGYCFVEFADLATAEKCLHKINGKPLPGATPAKRFKL
			NYATYGKQPDNSPEYSLFVGDLTPDVDDGMLYEFFVKVYPSCRG
			GKVVLDQTGVSKGYGFVKFTDELEQKRALTECQGAVGLGSKPVR
1	1	ļ	LSVAIPKASRVKPVEYSQMYSYSYNQYYQQYQNYYAQWGYDQNT
			GSYSYSYPQYGYTQSTMQTYEEVGDDALEDPMPQLDVTEANKEF
6414	1	538	MEQSEBLYDALMDCHWQPLDTVSSEIPAMM RGGRAALLPWRRFPCCRPRPQPARPSSRATPGPRSPGMATSIGV
0414	1 *	536	SFSVGDGVPEAEKNAGEPENTYILRPVFQQRFRPSVVKDCIHAV
		-	LKEELANAEYSPEEMPQLTKHLSENIKDKLKEMGPDRYKMVVQV
ĺ			VIGEORGEGVFMASRCFWDADTDNYTHDVFMNDSLFCVVAAFGC
			FYY
6415	2	1168	FVRQWQSSHRRACGLGCEARAGGGEEPRGRASSVAGWVGAFRAP
	_		FIEAAVAGLGAGSGKRRRGWKMPVHSRGDKKETNHHDEMEVDYA
1			ENEGSSSEDEDTESSSVSEDGDSSEMDDEDCERRRMECLDEMSN
			LEKQFTDLKDQLYKERLSQVDAKLQEVIAGKAPEYLEPLATLQE
			NMQIRTKVAGIYRELCLESVKNKYECEIQASRQHCESEKLLLYD
			TVQSELBEKIRRLBEDRHSIDITSELWNDELQSRKKRKDPFWPD
			KKKPGVVSGPYIVYMLQDLDILEDWTTIRKAMATLGPHRVKTEP
			PVKLEKHLHSARSEEGRLYYDGEWYIRGQTICIDKKDECPTSAV
			ITTINHDEVWFKRPDGSKSKLYISQLQKGKYSIKHS
6416	410	1519	EIAPADLEIPACAPVLLSRATSSTMSVTGGKMAPSLTQEILSHL
	}		GLASKTAAWGTLGTLRTFLNFSVDKDAQRLLRAITGQGVDRSAI
			VDVLTNRSREQRQLISRNFQERTQQDLMKSLQAALSGNLERIVM
1			ALLQPTAQFDAQELRTALKASDSAVDVAIBILATRTPPQLQECL
			AVYKHNFQVEAVDGITSETSGILQDLLLALAKGGRDSYSGIIDY
			NLAEQDVQALQRAEGPSREETWVPVFTQRNPEHLIRVFDQYQRS TGQELEEAVQNRFHGDAQVALLGLASVIKNTPLYFADKLHQALQ
	ì		ETEPNYQVLIRILISRCETDLLSIRAEFRKKFGKSLYSSLODAV
			KGDCQSALLALCRAEDM
6417	1	845	RGESRVLWSELEGEAGGAGGWASSLNARMDNRFATAFVIACVLS
			LISTIYMAASIGTDFWYEYRSPVQENSSDLNKSIWDEFISDEAD
Ĭ			EKTYNDALFRYNGTVGLWRRCITIPKNMHWYSPPERTBSFDVVT
			KCVSFTLTEQFMEKFVDPGNHNSGIDLLRTYLWRCQFLLPFVSL
			GLMCFGALIGLCACICRSLYPTIATGILHLLAGLCTLGSVSCYV
			AGIELLHQKLELPDNVSGEFGWSFCLACVSAPLQFMASALFIWA
			AHTNRKEYTLMKAYRVA
6418	2	662	TRTRPRRPPGLGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH
			TPAPPPPPPCGGIACHGEPAKFYGYDNLQRQPIFTTQQBAELVQ
			YPDCKSSSGNIGEDPDHLNQSSSPSQMFPWMRPQAAPGRRRGRQ
			TYSRFQTLELEKEFLFNPYLTRKRRIEVSHALALTERQVKIWFQ
645.5	ļ		NRRMKWKKENNKDKFPVSRQEVKDGETKKEAQELEEDRAEGLTN
6419	1	973	PGRPRVRNFDLNSKSILQEFFCTRSIQIPANRSKTAMSKCPIFP
1	i		MARSISTSGPLDKEDTGRQKLISTGSLPATLQGATDSLGLEWHL
			PSPDPVTVPYLSPLVVWKELESLLENEGDHAITVADFVDHHPIV
			FWNLVWYFRRLDLPSNLPGLILSSEHCNKYSKIPRHCMSEDSKY VLIQMLWDNMKLHQDPGQPLYILWNAHTQKYPMVHLLQKSDNSF
			NQELLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYREI
!		1	LFLSLVALGRENIDIDAFDKEYKMAYDRLTPSQVKSTHNCDRPP
			STGVMECRKTFGEPYL
6420	207	1187	RKMIDKNOTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN
			YLLWVFTPLILLILPYFTIFLLYLTIIFLHIYKRKNVLKEAYSH
			NLWDGARKTVATLWDGHAAVWHGYEVHGMEKIPEDGPALIIFYH
			GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFKIPGFSLLLDVFC
			ALHGPREKCVEILRSGHLLAISPGGVREALISDETYNIVWGHRR
	1		GFAQVAIDAKVPIIPMFTQNIREGFRSLGGTRLFRWLYEKFRYP
	·	<u> </u>	1

Deginning   coation   corresponding   coation   corresponding   coation   corresponding   coation   corresponding   coation   corresponding   coation   corresponding   coation   corresponding   coation   corresponding   coation   corresponding   coation   corresponding   coation   corresponding   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coatio	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Sociation   Corresponding	_	1		(A=Alanine, C=Cvateine, D=Aspartic Acid, E=
Cotation   Coffret   amino acid   residue of   amino acid   amino acid   residue of   amino acid   on, V-possible nucleotide deletion, V-possible nucleotide specification   PAPMYGGPFWIKERT/IGEPTPYOPDITARSELABEKTRING/OLID   RINGELEGATION   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPORT   REPO	NO:			Glutamic Acid. F=Phenylalanine. G=Glycine
Lieuucine, M-Methionine, N-Aaparagine,		1		H=Histidine, I=Isoleugine K-Lysine
to first amino acid residue of amino acid Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TYGOFPUR, Y-TY		corresponding		L=Leucine, M=Methionine N=Asparagine
amino acid residue of amino acid sequence (amino acid sequence (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (am				P=Proline, O=Glutamine, R=Arginine
mino acid amino acid sequence    Sequence		amino acid	1	S=Serine, T=Threonine, V=Valine
amino acid sequence    Codon, /-possible nucleotide deletion,		residue of		W=Trvptophan, Y=Tvrosine, X=Unknown *=Ston
Sequence		amino acid		Codon. /=possible nucleotide deletion
FAPMYOGF PVKLETTIGGET PYDPOTTABELAEKTKNAVGALID		sequence		\=possible nucleotide insertion)
SHORI PROMINGALIBREM   SACE   MALSURAPDEMBNIKLISPIPISVVLESEFKMASSPAVLRASEL		—— <u> </u>	<del> </del>	FAPMYGGFPVKI.RTYLGDDIDYDDOLTAFFLAFYTWAVOALTA
ALSELRAÇDEMSNIKLISPIPHENVILESEFKMASSENULRISPANCES   VONSLIKSSAÇILES POLRAVOG I INVAMINATLI ILEPAGRICU   VONSLIKSSAÇILES POLRAVOG I INVAMINATLI ILEPAGRICU   VONSLIKSSAÇILES POLRAVOG I INVAMINATLI ILEPAGRICU   VONSLIKS POLRAVOG ILEVAS PLANCKOR VILLES PERMONITUS POLITICA VELEVULOGHOP POR ILLEGARE PEPUVICA PROVINCIA VELEVULOGHOP POR ILLEGARE PEPUVICA PROVINCIA VELEVULOGHOP POR ILLEGARE PEPUVICA VELEVULOGHOP POR ILLEGARE PEPUVICA VELEVULOGHOP POR ILLEGARE STYLE ILLO   ELCISMAS FLAGITAAVVINGSVANVOGI LIKKETILEPYOVAR NEI NEVIKOVADI VON INSENDIA SEPUTISHE PEPUVICA PEPUVICA PROVINCIA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUVICA PEPUV				
YQMSLKSSQFLGSPQLRQVGQIIRVPARMATILLEPARGYD DEPVITAVRGIADEPQOYTLRASIADERGALPQARAYRADTICE LDLERAPALGGSPAGLEPMGLINALEPERPLVRILVERDVETYD VELEVUDGHDEPGGILLQCTREERFYF.PPGVREREP PPVGVRRVGOT LFLPPBRGGPFGGI VDMYGTGGGLEYEASILLACKGPAVMALAYY NYEDLEKTMETHLEY SPERMANYLLSHPEVKGPGVGLIGISKOG ELCLSMASFLKGITAAVVINGSVANVGGTLRYKGGFVGILGISKOG GLCLSMASFLKGITAAVVINGSVANVGGTLRYKGGFVGILGISKOG ODDANKSEFYARBACKRICARGRRYGPICYPTGHYTEFPVG QDDANKSEFYARBACKRICARGRRYGPICYPTGHYTEFPVG PLCRASLRALVGSPIINGGEPRAHAMQVDANKGLGTFFIKHIG GREGITPSKV  EGENLSWFGFWGDIJAKEFYMKTPCPGPFLRYNFDVTKGKIFFE MKGAGTTHG CYNVLDRAVHEKELGDKVAFYWERDERGETTQITY HQLLVQVCQPSNVLRKGGIHKGDRVAFYWHTPDVTKGKIFFE MKGAGTTHG CYNVLDRAVHEKELGDKVAFYWERDERGETTQITY HQLLVQVCQPSNVLRKGGIHKGDRVAFYWHTPDVTKGKIFFE MKGAGTHICANVLLGRAVHAMAGATATICANVLLGRAVALAYMINGSCALLTREERGENTALT KELADBEALOKCQEKGFPVRCCIVVKHLGBAELGMGDSTSGSPPI KRSCPDVGISNNGGIDAMHELMGAGADECEPPREGELVANL KELADBEALOKCQEKGFPVRCCIVVKHLGBAELGMGDSTSGSPPI KRSCPDVGISNNGGIDAMHELMGAGADECEPPREADFUFTL YTSGSTGKFKGVVHTVGGYMLZVATTFKVVDFHARADVFNCTGAL GREYNTYFKFYAFYTYTGHAEDFYTTCHARDFYTGTARDFUFTL YTSGSTGKFKGVVHTVGGYMLZVATTFKVVDFHARADVFNCTGAL GREYNTYFKFYAFYTYTGHAEDFYTTCHARDFYTGTARDFUFTLANG KRSTPATFKRFPGYYVTODGCRDQDGYWLTGRIDDMINNGTHAE REPTTYFKFPGYYVTODGCRDQDGYWLTGRIDDMINNGTHAE REPTTYFKFPGYYVTODGCRDQDGYWLTGRIDDMINNGTHAE REPTTYFKFPGYYVTODGCRDQDGYWLTGRIDDMINNGTHAE REPTTYFKFPGYYVTODGCRDQDGYWLTGRIDDMINNGTHAE REPTTYFKFPGYYVTODGCRDQDGYWLTGRIDDMINNGTHAEVYGNHE REPTTYFKFPGYYVTODGCRDQDGYWLTGRIDDMINNGTHAEVYGNHE REPTTYFKFPGYYVTODGCRDQDGYWLTGRIDDMINNGTHAEVYGNHE REPTTYFKFPGYYTYTDGCRDDGATTFTTGRTTTGRTYCGNHE REPTTYFKFPGYYTYTDGCRDCDGATHAEVYGNHE REPTTYFKFPGYTYTTGRTTGATTTTGRTYTGNATATTTGRTYTTGRTTGATTGATTGATTGATTGATTGATTGATTGATTGA	6421	1844	362	
DEPUTLAVIGIAPEQ PVTLRASIGNEKASIGOARRYRADTIGE LDLERRAPIAGESPAGLEPMGLIMALE PERCHYKREDVETPLA VELEVLIGHT LOTTHERY I LPGUYRE PVEUVRENOVET L FLEPERGEP FIGHT VORHETGGGLIEVRAS, LLAGKGPANMALAY NYEDLEFMETHLILEY FERANNYLLSHPEVKGPOVGLIGISKG ELCLSMASFLKGITAAVVINGSVANVOGTLRYKGSTEPHOVGNER RIKKVKGGYADIVUNUSSPLEGEPOCKSFITVERRASSTEPLFUNG QDDIRNKSEF FARBACKRIQAHGRKRPQIICYPETGHIYEPYF PLCRASLHALUGSFII WGGEPRAHMAQVOMAKQUTFERKHIG GREGITFSKV  GERLSWFOEPWGDIAKEFYRKTPCFGFFLRYNFDVTKGKIFFE MIKGATTNIC KINLDENVIEKKLIGDKVAFYWEGNEPGETTOITY HQLLVQVCOPSINURKOGIHKGORVAIYMMIPELVVAMLACAR IGAHSIVPAGFSSESLCERILDSSCSLIITTDAF YRGERLINGL KELADBAQKOCORGP PVRCIVWILGRAELGMODSTSOSPPI KRSCPDVOISWNQGIDLWHHELMOEAGDECEPEKCDAEDPLFIL YTSGSTGKKPKGVVHTVGGYNLTKVAITFKYVFDFHAEDVFNCTAD IGWITCHSYVTYOFLANGATSVLPSGIFTIPTAHKDSOFTNERA WLWHRUVGAGROFTVOTTGGMILTPLGATPMKPGSAT FPFFGVAPATINESGELEGERAGYLVFKOPMEGIMTVVGNHE RFETTYFKKP FGYYVTOGGOGROPOVYMTKTSGKIMTKV VTKFYTAPTAI RILJKKFGDEPVTKHSRASLQVLGTVCGFPINEA WLWHRUVGAGROFTVOTTGGMILTPLGATPMKPGSAT FPFFGVAPATINESGELEGERAGYLVFKOPMEGIMTVVGNHE RFETTYFKKP FGYYVTGGOGROPOVYMTKRSGKIMTKV KUTKFYTAPTAI RILJKKFGDEPVTKHSRASLQVLGTVCGFPINEA WLAWHRUVGAGROPIOVTGTGGMILTPTKRSGKIMTKV KUTKFYTAPTAI RILJKKFGDEPVTKHSRASLQVLGTVCGFPINEA WLAWHRUVGAGROPIOVTGTGGMILTPTKSGKIMTKV KUTKFYTAPTAI RILJKKFGDEPVTKHSRASLQUGTVCGFVTLCCGHT FSPKLTELKKGITREHOT ATTADVI ONARGIDTHAMYSGHL LSTABUEGALVEHEAVARAAVVGHPHPVKGECLYCFVTLCCGHT FSPKLTELKKGITREHOT ATTADVI ONARGIDTHAMYSGKIMTS KUNGIFFIDRHAFKGVAFFLOTIDLIGDNITSTBHIFFGDLAGLEVILMS KUNGIFFIDRHAFKGVAFFLOTIDLIGDNITSTBHIFFGDLAGLEVILMS KUNGIFFIDRHAFKGVAFFLOTIDLIGNITSTBHIFFGDLAGLEVILMS KUNGIFFIDRHAFKGVAFFLOTIDLIGNITSTBHIFFGDLAGLEVILMS KUNGIFFIDRHAFKGVAFFLOTIDLIGNITSTBHIFFGDLAGUERGR FLARANDADLCHILEKHSGSTRIVLBFORKGITGBHIFFDLAGGENGA KNIKMTHAMYGNUCHGSVIKKUNGFFKORGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				YOWSI,KSSAOFI,GSPOI,ROVGOI IRVDARMANTI, II, EDAGDOOM
LDLERAPALGESPAGLEPMGLIANALEPEKPLVKERVETPLA VELEVULGHUPDEPGILLOTHERRY LEPPEGPEVBUGGURGE LFLPEBEGPFGI YOMRETGGGLLEYRASLLACKGPAVMALAYY NYEDLEKTMETHLEY FEBANIVILSHPEVKGPVGGLLGISKGG ELCLSMASFLKGITAAVVINGSVANVGGTLEYRGSTLEPFGANG QDDHANKSEFYANBACKKLQAGRGRKPGI (CYPETGHYEIPEKFTLFUNG QDDHANKSEFYANBACKKLQAGRGRKPGI (CYPETGHYEIPEKFTLFUNG QDDHANKSEFYANBACKKLQAGRGRKPGI (CYPETGHYEIPEKFTLFUNG QDDHANKSEFYANBACKKLQAGRGRKPGI (CYPETGHYEIPEKFTLFUNG QDDHANKSEFYANBACKKLQAGRGRKPGI (CYPETGHYEIPEKFTLFUNG QDDHANKSEFYANBACKKLQAGRGRKPGI (CYPETGHYEIPEKFTLFUNG QDRANKSATTNI CYNULDENNERKLIGDKVAFYMENFEGFTGTTYTY PLCASALHALVGSPI INGGEPRALMAQVDAMKQUGTFFIKKLIG GREGTIPSKY  EGENLSHFGEFWGDI AKSFYMKTFCGFFFKNFDTVRGFIFTE MKGATTNI CYNULDENNERKLIGDKVAFYMENFEGFTGTTYTY HQLLVQVCQPSNVLRKGGIHKGDRVAI YMPMI FELVVAMLACAR IGALHSI VFAGFSSESLCERI LIDSCSLLITTDAFYRREELWAL KELADARJQKCQRKOFFVRCCI VVEHIGARELIMODSTSQSPJI KRSCPDVQI SHNQGI IDIMMELMQEAGDBCEPFMCDARDLFI LI YTSGSTGKPKGVHTUGGYULYVATFFKYYPDHAEDVFMCTAB IGHITHSYVTYOFLANGATSVLFFSGI FTYPDVNRLMSI JUKYK VTKRYTAFITA RILLMKFGDBEVTKISRASLQVTMEPBPLDFECTAB IGHITHSYVTYOFLANGATSVLFFSGI FTYPDVNRLMSI JUKYK VTKRYTAFITA RILLMKFGDBEVTKISRASLQVTMEPBPLOFFCTAB HAMHVUGAQRCPI VUDFFMCTTGTGHMLTPLGATPMKNGGAT FPFFTTYFKKPPGYYVTGGCQDDDGDGYWHTGRI DDMLNWSGHL LSTABEGSALVGBRGVLFVKNGFTAGTHTVYGHRE RFFTTYFKKPPGYYVTGGCQDDDGDGYWHTGRI DDMLNWSGHL LSTABEGSALVGBRGVLFBAVAGDFD ISTGVTHAFT FSPKLTEELKKQIREKIGP IATFDYI QNABGLFKTRSGKIMRY KNGIFF IDRHAFKGVAETLQTILDLSDNRIGSVHKVAFNINKARA RIANDPHICOTTLQVULSKARANHETAHNI VETVULDEHAGRF FLANANDDHICOTTLQVULSKARANHETAHNI VETVULDEHAGRF FLANANDDHICOTTLQVULSKARANHETAHNI VETVULDEHAGRF FLANANDDHICOTTLQVULSKARANHETAHNI VETVULDEHAGRF FLANANDHHOCTTLQVULSKARANHETAHNI VETVULDEHAGRF FLANANDHHOCTTLQVULSKARANHETAHNI VETVULDEHAGRF FLANANDHHOCTTLQVULSKARANHETAHNI VETVULDEHAGRF FLANANDHHOCTTLQVULSKARANHETAHNI VETVULDEHAGR RELEPTARVILAKURSHPHAHAMARAN GGRHAFHLKHKHR FLANGARGHANDHAHAMARANHAMARANHAMARANHAMARANHAMARANHAMARANHAMARAN GGRHAFHKHKHR RICHTHAMARANHAMARANHAMARANHAMARANHAMARANHAMARAN GGRHAFHKHKHR AKSGNDHAGRE GGRGGGGGGGGGGGGGGGGGGGGGGGGGGG				DEPURTAURGI APEOPUTI PASI POPERCAL POPULA PURDOTI CE
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LFLPPBGPFPGIVDMFGTGGGLLETRSLLAKCKGAWALLAYY NYEDLPKTMETHLE FYEEANNILLSHPEKAKGGVGLLGISKGG ELCLSMASFLKGITAAVVINGSVANVGGTLRYKGERUPUVONR NRIKVYTKOVADIVDVINSPLEGPDQKS FIPVERASETFLEFLVG QDDHNNKSEFYANBACKRLQAHGRKRÇGICYPETGHYLEFPYF PLCRASLHALVGSFIINGGBPAHAMAQVDANKGLQTFFIKHLG GREGITPSKV  6422 181 2133 EGENLSWFGFWGINKSFYMKTPCGFFLKNFDYTKGKIFLE MINKGATTHICYNULDRNYHEKKLGDKVAFYWENEDFDGSTTOITY HQLLVQVCQFSNULRKQGIHKGDRVALYMMHIPELVVAMLACAR IGALHSIVPAGFSSBLCGER ILDSSCSLLITPSKREHUPKL KELADBALQKCORKGFPVRCCIVVKHLGRAELGMGDSTSQSPFI KRSCPDVQISWNQGIDLWHHELMQDAGDBCEPFWCDABDPLFIL YTGSSTGKPKGVWHYVGGYMLYVATFFKYVPDHABDVFKCTAD LGWITGHSYVYTYGFLANGATSVLPFSGIFTYPDVNRLWSTUNKYK VTKFYTAFFIA RILLMKFGDBEVTKHSRASLQVFTGFHNDYDKIK RFTTYFKKPFGYVVTGGCQRDQDGYWHTGRIDDMINNYGHL LSTAEWSALVWEHPAVKGAERGSVLVFKGFTATVGFPHREAD FFFFGVAFAILMSGGELEGERGSVLVFKGFTATVGFTNYGGNT FFFFGVAFAILMSGGELEGERGSVLVFKGFTATVGFTNYGFTANGATSVLFSGIFTYPONNLWSGHL LSTAEWSALVWEHPAVKGAERGSVLVFKGFTATVGFTNYGFTANGATSVLFFSGIFTYPONNLWSGHL KRIAQNDHDLGDMSTVADPSVISHLFSHCLTIQ  6423 614 1237 ANIXETPROLDFSTVLDIJLDSNGTTSTFNETFKDLHGLRVLNLKS KNGIFFIBHAFKGVAETLQTLDLSDNRIGSVHKXAFNNILKARA RIANNPWRCDCTLQVLKSMASHTATANIV CYVTYUPGN GEDARHLETIKLSLEFROKKABEPDLSTVT GGGGGGGGGVGDVAVVAHNRTLKQLKDFPTFGGSGGMYSPCL GGGGAGGGVAVVAHNRTLKQLKDFPTFTGGSGGMYSPCL GGGRAGGLWVAHNFTLKGLLFFTGGSGGMYSPCL GGRACHLTWRLDFSTTTLEFTGGTSGGGMYSPCL GGRACHTMFLLKGURFI IHDLKLLADVGIVGFPNAGKSLLSC VSHARPATADVATTTLKFEGLGKIMYSDFKGISVADLEGILEGENITKSL GGRKLITNFLEHKGQRFI IHDLKLALDVGIVGFPNAGKSLLSC VSHARPATADVATTTLKFEGLGKIMYSDFKGISVADLEGILEGENITKSL DEQANGENDALHKKQLLMUNSTDTNSSTEPSEFEHLMSOLLONF KUTKELLEYKEGLGVARALLANKNDLPDADGVATTSKILD CGRKLITNFLEHKGGGGFTTATTSTTSTEPSEFEHLMSOLLONF KUTKELLEYKEGLGKARALLANKNDLPDADGVATTSKML DEQANGENGARATTTLKFEGLGFTATTSTTSTSTEPSEFEMSOLLORKSLLSC VSHARPATADVATTTLKFEGGGFTATTSTTSTSTSTEPSEFEMSOLLORKSLLSC VSHARPATADVATTTLKFEGGGFTATTSTTSTSTSTEPSETTLEDGLENGCITKSL DEQANGENGARGFTATTSTHATTSTTSTTSTTSTTSTTSTTSTTSTTSTTSTTSTTSTTS				VELEVI-DGHDPDPGRI-LCOTPHEPVEL-BBCVBDEBVDVCDVBCT
NYEDLPKTMETIHLEYFERAMNYLLISHPEVKGPGYGLIGISKOG ELCLSMASPLKGITAAVVINGSVANVGGTLPKGETLPPVGVAR NRIKUTKOGYADIUVLNSPLEGEPQKSPIPVERAESTFLFLVG ODDINMKSEYYANBACKELQAHGRRKPQIICYPETGHYFYFY PLCRASLHALVGSPIIWGGEPRAHAMAVDAMKCQTFFHKHLG GREGTIPSKV  6422 181 2133 EGERLSWFQEPWGDIAKEFYWKTPCPGPFLRYNFDVTKGKIFIE WMKGATTNICYNVLDRNVHEKKLADKVAFYWSGNEPGETTOITY HQLLVQVCOPSNULRKGGIKKGDWAIYYWGGNEPGTTOITY HQLLVQVCOPSNULRKGGIKKGDWAIYYWGNEPGETTOITY HQLLVQVCOPSNULRKGGIKKGDWAIYYWGNEPGETTOITY KRSCPDVQISWNQGIDLWHHELMQAADGKEPEWCDAEDPLFIL YTSGSTGKPKGVVHTVGGYMLTVATTFKYVFDFHAEDVFMCTAD IGHITCHSTVYTOFLANGATSVLFEGEFTVDWRLLWSLUDKYK VTKFYTAPTAIRLIMKFGDEPVTKTABALGVLGTVOPDVRLWSLUDKYK VTKFYTAPTAIRLIMKFGDEPVTKTABALGVLGTVOPDVRLWSHDL ISTAEVESALVEHEAVVAEAAVVGHPHVKGGLYCFVTLCOCHT FSFKLTEELKKQIREKIGPIATPYIQNAFGLPKTRSKGKMRVV LSTAEVESALVEHEAVVAEAAVVGHPHVKGGLYCFVTLCOCHT FSFKLTEELKKQIREKIGPIATPYIQNAFGLPKTRSGKIMRVV LSTAEVESALVEHEAVVAEAAVVGHPHVKGGLYCFVTLCOCHT FSFKLTEELKKQIREKIGPIATPYIQNAFGLPKTRSGKIMRVV KRIJANDADLCHLPKKTDYAMLVTMFGWFTDVISTVYVTYVQN KNGIBFIDRAHFKGVAETAUTDLISDNIGVHONAFNILKARA RIANNPWHCOCTLQVLRSMASNIETAHNVICKTSVLDEHAGRP FLNAANDADLCHLPKKTDYAMLVTMFGWFTDVISTVYVTYVGYN KNGIBFIDRAHFKGVAETAUTDLISDNIGVHONAFNILKARA RIANNPWHCOCTLQVLRSMASNIETAHNVICKTSVLDEHAGRP FLNAANDADLCHLPKKTDYAMLVTMFGWFTDVISTVYVTYVGYN GEGGGGGGVGVVVAHARMTLKQLDEXTPKRFVAGGGGGYFRL  6424 1 1188 KKVSWFVAAMVHCSCVLFFKKTGNFTDKLEETTRVGGGGGGYFRL LKGSKKKWBIPPVVGISVTDENKKIIGELKKENDRILVAQGGL GGGLLTNFILPLKGCKRIIHLKQLDEXTPAGAKSHLSCLUAG VSHARPALADVAFTTLKPELGKIMVSDPFLOGAPNIKASSLLSC VSHARPALADVAFTTLKPELGKIMVSDPFLOGAPNIKASSLLSC VSHARPALADVAFTTLKRELGKIMVSDPFLOGAPNIKASSLLSC VSHARPALADVAFTTLKRELGKIMVSDPFLOFAPNIKASSLLSC VSHARPALADVAFTTLKRESGSRHVLRSPFRANSLOKANNOFILTG LLTKELELYKEBLYKEBLITTRULFYVDTIGGPGLSHITVYKTKMDII LLTKELELYKEBLYKEBLITTRULFYDHTVIGTDTVMATATTRTTTRUMFIT LLTKGLELYKEBLYKEBLITTRULFYTBUTTVGGTDTVMAYDASTFPGRE KRPCTSMHFQLP 1QA RREGVHGSAKFYISDLMKVTTSGYSNVIFGVPCMMAGLEKLUS CRGGLVDIGGGGGTGTLADAKKGPTAVGYELNPHLVWYSRYRA WREGVHGSAKFYISDLMKVTTSGYSNVIFGVPCMMAGLEKLUS CRGALVOGGGGTGGDTGADGGFFTSPSPEPTLEDIRR LHAEFAAERDWEGFHOPNALLALARC		1	ł	
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6424 1 1188 KKVSWPVAAMVHCSCVLFRKYGNFIDKLRLFTRGGSGGMGYPRL GGEGGKGGDVWVVAHNRMTLKQLKDRYPRKRFVAGVGANSKISA LKGSKGKDWBIPVPVGISVTDENGKIIGELNKENDRILVAQGGL GGKLLTNFLPLKGQKRIIHLDLKLIADVGLVGFPNAGKSSLLSC VSHAKPAIADVAFTTLKPELGKIMYSDFKQISVADLPGLIEGAH MNKGMGHKFLKHIERTRQLLFVVDISGFQLSSHTQYRTAFETII LLTKELELYKEELQTKPALLAVNKMDLPDAQDKFHELMSQLQNP KDFLHLFEKNMIPERTVEFQHIIPISAVTGEGIEELKNCIRKSL DEQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII LAMEGGGIPLETLKEESQSRHVLPASFEVNSLQKSNWGFLLTG LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELNPWLVWYSRYRA WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPFPHWTPDHVTGEGIDTVWAYDASTPRGRE KRPCTSMHFQLPIQA  6426 30 565 SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHAEFAAERDWEQFHQPRNLLLALVGEVGELABLFQWKTTGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST  6427 145 959 AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK				
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LKGSKGKDWBIPVPVGISVTDENGKIIGELNKENDRILVAQGGL GGKLLTNFLPLKGQKRIIHLDLKLIADVGLVGFPNAGKSSLLSC VSHAKPAIADYAFTTLKPELGKIMYSDFKQISVADLPGLISGAH MNKGMGHKFLKHIERTRQLLFVVDISGFQLSSHTQYRTAFETII LLTKELELYKEELQTKPALLAVNKMDLPDAQDKFHELMSQLQNP KDPLHLFEKNMIPERTVEFQHIIPISAVTGEGIEELKNCIRKSL DEQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII LAMEGGGIPLETLKEESQSRHVLPASFEVNSLQKSNWGFLLTG LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGPTAVGYELNPWLVWYSKYLA WRESCYHGSAAFYISDLMKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPFPHWTPDHVTGEGIDTVMAYDASTFRGRE KRPCTSMHFQLPIQA  6426 30 565 SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHAEFAAERDWEQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST  6427 145 959 AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK		_	2200	
GGKLLTNFLPLKGQKRIIHLDLKLIADVGLVGFPNAGKSSLLSC VSHAKPAIADYAFTTLKPELGKIMYSDFKQISVADLPGLIEGAH MNKGMGHKFLKHIERTRQLLFVVDISGFQLSSHTQYRTAFETII LLTKELELYKEELQTKPALLAVNKMDLPDAQDKFHELMSQLQNP KDFLHLFEKNMIPERTVEFQHIIPISAVTGEGIEELKNCIKKSL DEQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII LAMEGGGGIPLETLKEESQSRHVLPASFEVNSLQKSNWGFLLTG LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGPTAVGYELNPWLVWYSRYRA WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVLACRFPFPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA LHAEFAAERDWEQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST  6427 145 959 AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK		[		
VSHAKPAIADYAFTTLKPELGKIMYSDFKQISVADLPGLIEGAH MNKGMGHKFLKHIERTRQLLFVVDISGFQLSSHTQYRTAFETII LLTKELELYKEELQTKFALLAVNKMDLPDAQDKFHELMSQLQNP KDPLHLFEKNMIPERTVEFQHIIPISAVTGEGIEELKNCIRKSL DEQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII LAMEGGGGIPLETLKEESQSRHVLPASFEVNSLQKSNWGFLLTG LVGGTLVAVYAVATPFVTPALRKVQLPFVPATMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGPTAVGYELNPWLVWYSRYRA WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVLACRFPFPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA  6426 30 565 SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHAEFAAERDWEQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST  6427 145 959 AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK				
MNKGMGHKFLKHIERTRQLLPVVDISGFQLSSHTQYRTAFETII LLTKELELYKEELQTKPALLAVNKMDLPDAQDKFHELMSQLQNP KDPLHLFEKNMIPERTVEFQHIIPISAVTGEGIEELKNCIRKSL DEQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII LAMEGGGGIPLETLKEESQSRHVLPASFEVNSLQKSNWGFLLTG LVGGTLVAVVAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELMPWLVWYSRYRA WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVLACRFPFPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA SGGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHAEFAAERDWEQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST 6427 145 959 AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK		]		VSHAKPAIADVAFTTI,KPEIGKIMVEDEVOTEVADI DOLITEGATI
LLTKELELYKEELQTKPALLAVNKMDLPDAQDKFHELMSQLQNP KDFLHLFEKNMIPERTVEFQHIIPISAVTGEGIEELKNCIRKSL DEQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII LAMEGGGGIPLETLKEESQSRHVLPASFEVNSLQKSNWGFLLTG LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELMPWLVWYSRYRA WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLKKKLE RELEDDARVIACRFPFPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA S65 SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHAEFAAERDWEQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST 6427 145 959 AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK		[		MNKGMGHKFLKHIERTROLLFVANTSGEOLGGUTOVDERA DEBETT
KDPLHLFEKNMIPERTVEFQHIIPISAVTGEGIEELKNCIRKSL DEQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII LAMEGGGIPLETLKEESQSRHVLPASFEVNSLQKSNWGFLLTG LVGGTLVAVVAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGPTAVGYELNPWLVWYSRYRA WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPFPHWTPDHVTGEGIDTVWAYDASTPRGRE KRPCTSMHFQLPIQA  6426 30 565 SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHAEFAAERDWEQFHQPRNLLLALVGEVGELABLFQWKTTGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST  6427 145 959 AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK				LLTKELELYKEELOTKPALLAVNKMDI.DDAODKENET.MCOT OND
DEQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII  6425 1850 1144 LAMEGGGIPLETLKEESQSRHVLPASFEVNSLQKSNWGFLLTG LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGPTAVGYELNPWLVWYSRYRA WRECVHGSAKPYISDLMKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPFPHWTPDHVTGEGIDTVMAYDASTFRGRE KRPCTSMHFQLPIQA  6426 30 565 SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHAEFAAERDWEQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST  6427 145 959 AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK				
1850 1144 LAMEGGGGIPLETLKEESQSRHVLPASFEVNSLQKSNWGFLLTG LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELNPWLVWYSRYRA WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLBKKLE RELEDDARVIACRFPFPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA 6426 30 565 SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHAEFAAERDWEQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVISKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST 6427 145 959 AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK				DEOANOENDALHKKOLLNI WIGDTMSSTEDDS YUNUTUSKYDTT
LVGGTLVAVVAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELMPWLVWYSRYRA WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPFPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA  6426 30 565 SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHAEFAAERDWEQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST  6427 145 959 AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK	6425	1850	1144	
CRRGSLVDIGSGDGRIVIAAAKKGPTAVGYELNPWLVWYSRYRA WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPFPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA  6426 30 565 SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHAEFAAERDWEQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST  6427 145 959 AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK			11	LVCCTLVAVVAVATPEVTDALDEVCA DEVINATING TONTO
WREGVHGSAKPYISDLWKVTFSQYSNVVIFGVPQMMLQLBKKLE RELEDDARVLACRFPFPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA  6426 30 565 SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHAEFAAERDWEQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST  6427 145 959 AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK				CPPGGLVDTGGGDGDTVI A A KYCOTA WOUTH AND WITH COMME
RELEDDARVIACRFPFPHWTPDHVTGEGIDTVWAYDASTPRGRE KRPCTSMHFQLPIQA  6426 30 565 SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHAEFAAERDWEQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST  6427 145 959 AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK				WDECVHGSAKEVI SDI.WKWTESOVSHIRITEGIDOMIT OF STORES
KRPCTSMHFQLPIQA  6426 30 565 SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHAEFAAERDWEQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST  6427 145 959 AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK				BELEDDYBALISCHE EDEDRIMMEDIAMABE LIMINIS AUF CO-C-
6426 30 565 SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHAEFAAERDWEQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST 6427 145 959 AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK				
LHAEFAAERDWEQFHQPRNLLLALVGEVGELAELFQWKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST 6427 145 959 AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK	6426	30	565	
PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST 6427 145 959 AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK	0.20		205	
NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST 6427 145 959 AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK				DOGUGDDEDAN OFFI ODIN THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR
ST 6427 145 959 AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK			i	PUGMSPREKAALQEELSUVLIYLVALAARCRVDLPLAVISKMDI
6427 145 959 AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK				
JUDIO TITUTO CONTROL VIN TONDE PARA TRAVER	6427	145		
	044/	140	759	
		<u></u>		WINDIAMMIMIMIALARDEWATETALDILIZMEDEAAAETKWALAP

( and 1	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ ID		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	beginning nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
		Bequence	\=possible nucleotide insertion)
<b></b>	sequence		WLLSPYTKGASLLYRKFVHPSLSRHEKEIDAYIVOAKERSYETV
i i			LSFGKRGLNIAASAAVQAATKSQGALAGRLRSFSMQDLRSISDA
			PAPAYHDPLYLEDQVSHRRPPIGYRAGGLQDSDTEDECWSDTEA
1 1			VPRAPARPREKPLIRSQSLRVVKRKPPVREGTSRSLKVRTRKKT
1 1			VPSDVDS
	1002	444	SGSGGKMEDHQHVPIDIQTSKLLDWLVDRRHCSLKWQSLVLTIR
6428	1982	444	EKINAAIQDMPESEEIAQLLSGSYIHYFHCLRILDLLKGTEAST
i I			KNIFGRYSSORMKDWOEIIALYEKDNTYLVELSSLLVRNVNYEI
			PSLKKQIAKCQQLQQEYSRKEEECQAGAAEMREQFYHSCKQYGI
1 [			TGENVRGELLALVKDLPSQLAEIGAAAQQSLGEAIDVYQASVGF
1 1		İ	VCESPTEQVLPMLRFVQKRGNSTVYEWRTGTEPSVVERPHLEEL
i (			PEQVAEDAIDWGDFGVEAVSEGTDSGISAEAAGIDWGIFPESDS
			KDPGGDGIDWGDDAVALOITVLEAGTOAPEGVARGPDALTLLEY
<u> </u>			TETRNQFLDELMELEIFLAQRAVELSEEADVLSVSQFQLAPAIL
			OGOTKEKMVTMVSVLEDLIGKLTSLOLOHLFMILASPRYVDRVT
			EFLOOKLKOSQLLALKKELMVQKQQEALEEQAALEPKLDLLLEK
!			TKELQKLIEADISKRYSGRPVNLMGTSL
6429	3413	3442	EPSSWTAAPRGPLAAHPLEAAVQEDDRRALSFDSRIKVFANGTL
6423	2472	3442	VVKSVTDKDAGDYLCVARNKVGDDYVVLKVDVVMKPAKIEHKEE
j		j	NDHKVFYGGDLKVDCVATGLPNPEISWSLPDGSLVNSFMQSDDS
1 1			GGRTKRYVVFNNGTLYFNEVGMREEGDYTCFAENOVGKDEMRVR
1 1			VKVVTAPATIRNKTCLAVQVPYGDVVTVACEAKGEPMPKVTWLS
1	i		PTNKVIPTSSEKYQIYQDGTLLIQKAQRSDSGNYTCLVRNSAGE
ļ i			DRKTVWIHVNVQPPKINGNPNPITTVREIAAGGSRKLIDCKAEG
			IPTPRVLWAFPEGVVLPAPYYGNRITVHGNGSLDIRSLRKSDSV
1 1			OLVCMARNEGGEARLIVOLTVLEPMEKPIFHDPISEKITAMAGH
]			TISLNCSAAGTPTPSLVWVLPNGTDLQSGQQLQRFYHKADGMLH
			ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL
1			VSIINGETLKLPCTPPGAGQGRFSWTLPNGMHLEGPQTLGRVSL
1			LDNGTLTVREASVFDRGTYVCRMETEYGPSVTSIPVIVIAYPPR
		1	ITSEPTPVIYTRPGNTVKLNCMAMGIPKADITWELPDKSHLKAG
			VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT
			TYIHVF
6430	1946	602	RTRVSTGLRRTLLWSEAVGASSTRGDTG1PGSGEGGAGPGGGEG
} I		1	AMLEAMAEPSPEDPPPTLKPETQPPEKRRRTIEDFNKFCSFVLA
] ]		1	YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI
			QTFVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM
		[	KLKDSLFDLDGPKVASPLSPTSLTHTSRPPAALTPVPLSQGDLS
			HPPRKKDRKNRKLGPGAGAGFGVLRRPRPTPGDGEKRSRIKKSK
		1	KRKLKKAERGDRLPPPGPPQAPPSDTDSEEEEEEEEEEEMA
		1	TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE
1			TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR
			PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG
			GPPKSGEP
6431	3	605	WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR
1			LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEEGEKH
1			RELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV
}			IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER
		1	LKGQEDSLASAVDAATEQKTCDSD
6432	56	1692	GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE
6432	56	1692	DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR
6432	56	1692	DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKRQENQ
6432	56	1692	DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKRQENQ WNELLETLHKLPIPDPGVSVHLSVHSYFTVPDTRELPSIPENRN
6432	56	1692	DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKRQENQ WNELLETLHKLPIPDPGVSVHLSVHSYFTVPDTRELPSIPENRN LTEYFVAVDVNNMLHLYASMLYERRILIICSKLSTLTACIHGSA
6432	56	1692	DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKRQENQ WNELLETLHKLPIPDPGVSVHLSVHSYFTVPDTRELPSIPENRN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	Debroline, Memerino De Revisione,
ļ	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
ļ	Bequence		\=possible nucleotide insertion)
			TGDGVARAFLKAQAAFFGSYRNALKIEPEBPITFCEEAFVSHYR
			SGAMRQFLQNATQLQLFKQFIDGRLDLLNSGEGFSDVFEEEINM
1			GBYAGSDKLYHQWLSTVRKGSGAILNTVKTKANPAMKTVYKFDI
1			AENGCAPTPEEQLPKTAPSPLVEAKDPKLREDRRPITVHFGQVR
ļ			PPRPHVVKRPKSNIAVEGRRTSVPSPEQNTIATPATLHILQKSI
			THFAAKFPTRGWTSSSH
6433	1524	484	APVTKRKEVFAKDSKGSALDAGRDPKRPALPETLCESGWASNTA
l			PTTPPQPGWCLCGKDFKSSCQTPGREKERRLATMHGSCSFLMLL
			LPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDML
			HMRWDEELAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMDV
1			PLAMEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCG
	1		SHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCP
			SGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMG
			AEGPDKPSVVSGLNSGPGHVWGPLLGLLLLPPLVLAGIF
6434	40	2002	MPQLNFGMADPTQMGGLSMLLLAGEHALGTPEVFSGTCRPDVSE
			SPELRQKSPLFQFAEISSSTSHSDASTKQCQTSALFQFAEISSN
	-		TSQLGGAEPVKRCGKSALFQLAEMCLASEGMKMEESKLIKAKES
			DGGRIKELEKGKEEKEIKMEKTDETRLQKEAEFEKSAKBNLRDS
			KELRNFEALQIDDIMAIKMEDPKEIRKEELEEDHKCSHFPDFSY
	1		SASSKIIISDVPSRKDHMCHPHGIMIIEDPAALNKPEKLKKKKK
			KSKMDRHGNDKSTPKKTCKKRQSSESDIESVIYTIEAVAKGDWG
l			IEKLGDTPRKKVRTSSSGKGSILDAKPPKKKVKSREKKMSKEKS
			SDTTKESRPPDFISISASKNISGETPEGIKAEPLTPMEDALPPS
1			LSGQAKPEDSDCHRKIETCGSRKSERSCKGALYKTLVSEGMLTS
1			LRANVDRGKRSSGKGNSSDHEGCWNEESWTFSQSGTSGSKKFKK
			TKPKEDCLLGSAKLDEEFEKKFNSLPQYSPVTFDRKCVPVPRKK
			KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT
Ì			MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ
			DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA
6435	2227	657	ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE
Ì			VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEEENDIEE
			QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA
	}		VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD
i			PTRESVLQPSPQVPATTVAHTATQQPAAPAPPAVSPREALMRAM
			HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDIRNVI
			GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY
}			GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR
	İ		AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA
	l		VDENGLWLIYPALDDEGFSQEVIVLSKLNAADLSTQKETTWRTG
		1	LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR
			LLFENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY
6436	1295	341	GACRPPVRODPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVM
			YPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL
			NVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGC
			VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAG
			AFYRSYTTQLTMNVPFQAIHFMTYEFLQBHFNPQRRYNPSSHVL
			SGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMAS
			AFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLIT
			KRQEEWRAGK
6437	1828	360 .	PPAPAPPASPARHVTRTARGHLEGGSRAPPLLQAVFLQIKNMVK
			LIHTLADHGDDVNCCAFSFSLLATCSLDKTIRLYSLRDFTELPH
			SPLKFHTYAVHCCCFSPSGHILASCSTDGTTVLWNTENGQMLAV
		1	MEQPSGSPVRVCQFSPDSTCLASGAADGTVVLWNAQSYKLYRCG
			SVKDGSLAACAFSPNGSFFVTGSSCGDLTVWDDKMRCLHSEKAH
			DLGITCCDFSSQPVSDGEQGLQFFRLASCGQDCQVKIWIVSFTH
L			ILGFELKYKSTLSGHCAPVLACAFSHDGQMLVSGSVDKSVIVYD

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	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	303	\=possible nucleotide insertion)
<del></del>			THTENILHTLTQHTRYVTTCAFAPHTLLLATGSMDKTVNIWQFD
1			LETLCQARSTEHQLKQFTEDWSEEDVSTWLCAQDLKDLVGIFKM
			NNIDGKELLNLTKESLADDLKIESLGLRSKVLRKIEELRTKVKS
			LSSGIPDEFICPITRELMKDPVIASDGYSYEKEAMENWDPAKRN
			RTSPP
6438	109	901	EVQILRAKMFQTGGLIVFYGLLAQTMAQFGGLPVPLDQTLPLNV
****	100	301	NPALPLSPTGLAGSLTNALSNGLLSGGLLGILENLPLLDILKPG
	1		GGTSGGLLGGLLGKVTSVIPGLNNIIDIKVTDPQLLELGLVQSP DGHRLYVTIPLGIKLQVNTPLVGASLLRLAVKLDITAEILAVRD
ĺ			KQERIHLVLGDCTHSPGSLQISLLDGLGPLPIQGLLDSLTGILN
		İ	KVLPELVQGNVCPLVNEVLRGLDITLVHDIVNMLIHGLQFVIKV
6439	23	412	SIQTASAITTEMASQSQGIQQLLQAEKRAAEKVADARKRKARRL
""		7.1.6	VON VEEN OMBUFOVER PREPER STREET TO THE STREET STREET
			KQAKEEAQMEVEQYRREREHEFQSKQQAAMGSQGNLSAEVEQAT RRQVQGMQSSQQRNRERVLAQLLGMVCDVRPQVHPNYRISA
6440	3	517	RADVOGROSSOORINGERVLAOLIGAVCDVRPQVHPNYRISA
	1	31/	RARWINSDMGDLPGLVRLSIALRIQPNDGPVFYKVDGQRFGQNRT
		,	IKLLTGSSYKVEVKIKPSTLQVENISIGGVLVPLELKSKEPDGD
			RVVYTGTYDTEGVTPTKSGERQPIQITMPFTDIGTFETVWQVKF
6441	234	1373	YNYHKRDHCQWGSPFSVIEYECKPNETRSLMWVNKESFL
0441	234	13/3	KSGGLRRRQRPGRSAAVGEEELPPGMEKFKAAMLLGSVGDALGY
			RNVCKENSTVGMKIQEELQRSGGLDHLVLSPGEWPVSDNTIMHI
			ATAKALTTDYWCLDDLYREMVRCYVEIVEKLPERRPDPATIEGC
			AQLKPNNYLLAWHTPFNEKGSGFGAATKAMCIGLRYWKPERLET
		}	LIEVSVECGRMTHNHPTGFLGSLCTALFVSFAAQGKPLVQWGRD
			MLRAVPLAEEYCRKTIRHTAEYQEHWFYFEAKWQFYLEERKISK
			DSENKAIFPDNYDAEERBKTYRKWSSEGRGGRRGHDAPMIAYDA
			LLAAGNSWTELCHRAMFHGGESAATGTIAGCLFGLLYGLDLVPK
6442	34	706	GLYQDLEDKEKLEDLGAALYRLSTEEK
0442	34	796	AEDPAGGLAGQDTMFARGLKRKCVGHEEDVEGALAGLKTVSSYS
			LQRQSLLDMSLVKLQLCHMLVEPNLCRSVLIANTVRQIQEEMTQ
			DGTWRTVAPQAAERAPLDRLVSTEILCRAAWGQEGAHPASGLGD
			GHTQGPVSDLCPVTSAQAPRHLQSSAWEMDGPRENRGSFHKSLD
			QIFETLETKNPSCMEELFSDVDSPYYDLDTVLTGMMGGARPGPC
6443	2		EGLEGLAPATPGPSSSCKSDLGELDHVVEILVET
0443	_	555	MASPAASSVRPPRPKKEPQTLVIPKNAAEEQKLKLERLMKNPDK
			AVPIPEKMSEWAPRPPPEFVRDVMGSSAGAGSGEFHVYRHLRRR
			EYQRQDYMDAMAEKQKLDAEFQKRLEKNKIAAEEQTAKRRKKRQ
			KLKEKKLLAKKMKLEQKKQEGPGQPKEQGSSSSAEASGTEEEEE
6444	390	000	VPSFTMGR
0444	390	899	GSTPRGKMRAPIPEPKPGDLIEIFRPFYRHWAIYVGDGYVVHLA
			PPSEVAGAGAASVMSALTDKAIVKKELLYDVAGSDKYQVNNKHD
			DKYSPLPCSKIIQRAEELVGQEVLYKLTSENCEHFVNELRYGVA
6AAE	ļ	754	RSDQVRDVIIAASVAGMGLAAMSLIGVMFSRNKRQKQ
6445	2	753	AGAAGAAGAARSPRPQAHTKGVRGLPSRRRSPDCGRMELAAGSF
			SEEQFWEACAELQQPALAGADWQLLVETSGISIYRLLDKKTGLY
			EYKVFGVLEDCSPTLLADIYMDSDYRKQWDQYVKELYEQECNGB
			TVVYWEVKYPFPMSNRDYVYLRQRRDLDMEGRKIHVILARSTSM
i			PQLGERSGVIRVKQYKQSLAIESDGKKGSKVFMYYFDNPGGQIP
			SWLINWAAKNGVPNFLKDMARACQNYLKKT
6446	1	1651	RCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENEEDLPELS
			DSGDEAAWEDEDDADLPHGKQQTPCLFCNRLFTSAEBTFSHCKS
			EHQFNIDSMVHKHGLEFYGYIKLINFIRLKNPTVEYMNSIYNPV
		-	PWEKEEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS
		*	VVEKLKHMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT
			CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD
			FIYQNPHIFKDKVVLDVGCGTGILSMFAAKAGAKKVLGVDQSEI

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ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
<b>!</b>	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			LYQAMDIIRLNKLEDTITLIKGKIEBVHLPVEKVDVIISEWMGY
			FLLFESMLDSVLYAKNKYLAKGGSVYPDICTISLVAVSDVNKHA
			DRIAFWDDVYGFKMSCMKKAVIPEAVVEVLDPKTLISEPCGIKH
1		ļ	IDCHTTSISDLEFSSDFTLKITRTSMCTAIAGYFDIYFEKNCHN
ļ		ĺ	RVVFSTGPQSTKTHWKQTVFLLEKPFSVKAGEALKGKVTVHKNK
			KDPRSLTVTLTLNNSTQTYGLQ
6447	1554	1068	RLGPAEWHLSGPCHATLGAANRGRALGVRAAWRGAPLCQRVMMP
1			SRTNLATGIPSSKVKYSRLSSTDDGYIDLQFKKTPPKIPYKAIA
			LATVLFLIGAFLIIIGSLLLSGYISKGGADRAVPVLIIGILVFL
			PGFYHLRIAYYASKGYRGYSYDDIPDFDD
6448	74	559	GQVLSHCYHYRSSRWRRGGLSRGRGAGVMALVPYEETTEFGLQK
1			FHKPLATFSFANHTIQIRQDWRHLGVAAVVWDAAIVLSTYLEMG
			AVELRGRSAVELGAGTGLVGIVAALLACRIRYERDNNFLAMLER
6449	597	1876	QFIVRKVHYDPEKDVHIYEAQKRNQKEDL EYGVCENLRKLEITGVSCRDVYAKLLHRYRHILGLWOPDIGPYG
0447	391	10/6	GLLNVVVDGLFIIGWMYLPPHDPHVDDPMRFKPLFRIHLMERKA
			ATVECMYGHKGPHHGHIQIVKKDEFSTKCNQTDHHRMSGGRQEE
	i	1	FRTWLREEWGRTLEDIFHEHMQELILMKFIYTSQYDNCLTYRRI
			YLPPSRPDDLIKPGLFKGTYGSHGLEIVMLSFHGRRARGTKITG
Ì			DPNIPAGQQTVEIDLRHRIQLPDLENQRNFNELSRIVLEVRERV
			RQEQQEGGHEAGEGRGGPRESQPSPAQPRAEAPSKGPDGTPG
			EDGGEPGDAVAAAEQPAQCGQGQPFVLPVGVSSRNEDYPRTCRM
1			CFYGTGLIAGHGFTSPERTPGVFILFDEDRFGFVWLELKSFSLY
(	1	ĺ	SRVQATFRNADAPSPQAFDEMLKNIQSLTS
6450	848	269	FVPAPRTVSGKRSLPGEWEERGEGEQRTGREFSGNGGRAVEAAR
			MRLLCGLWLWLSLLKVLQAQTPTPLPLPPPMQSFQGNQFQGEWF
ļ			VLGLAGNSFRPEHRALLNAFTATFELSDDGRFEVWNAMTRGOHC
1			DTWSYVLIPAAQPGQFTVDHRVWTHEQAGRPQDQPAGQELVAAS
			RDAGPVHLPGQSSGPLG
6451	232	939	HSPTPPTSPRASTMEDVKLEFPSLPQCKEDAEEWTYPMRREMQE
ł		ľ	ILPGLFLGPYSSAMKSKLPVLQKHGITHIICIRQNIEANFIKPN
1			FQQLFRYLVLDIADNPVENIIRFFPMTKEFIDGSLQMGGKVLVH
1	İ		GNAGISRSAAFVIAYIMETFGMKYRDAFAYVQERRFCINPNAGF
			VHQLQEYEAIYLAKLTIQMMSPLQIERSLSVHSGTTGSLKRTHE
			EEDDFGTMQVATAQNG
6452	1	652	RTRGESSNMEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQ
	l		LKFLKPKINSFYAFEVKDAKGRTVSLEKYKGKVSLVVNVASDCQ
	1		LTDRNYLGLKELHKEFGPSHFSVLAFPCNQFGBSEPRPSKBVES
	1		FARKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWK
(155	ļ <u></u>		YLVNPEGQVVKFWRPEEPIEVIRPDIAALVRQVIIKKKEDL
6453	827	223	HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLAAALGSAQSGSC
	1		RDKKNCKVVFSQQELRKRLTPLQYHVTQEKGTESAFEGEYTHHK
			DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEAITFTDD
	J	]	FSYGMHRVETSCSQCGAHLGHIFDDGPRPTGKRYCINSAALSFT
	<del></del>	200	PADSSGTAEGGSGVASPAQADKAEL
6454	827	223	HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAQSGSC
	1	İ	RDKKNCKVVFSQQELRKRLTPLQYHVTQEKGTESAFEGEYTHHK
	1		DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEAITFTDD
	1		FSYGMHRVETSCSQCGAHLGHIFDDGPRPTGKRYCINSAALSFT
CARE	1040	152	PADSSGTAEGGSGVASPAQADKAEL
6455	1042	173	RVHLATVSASAAWDALGLPVRSHMQGSTRRMGVMTDVHRRFLQL
1	1	Í	LMTHGVLEEWDVKRLQTHCYKVHDRNATVDKLEDFINNINSVLE
	1		SLYIEIKRGVTEDDGRPIYALVNLATTSISKMATDFAENELDLF
	l		RKALELIIDSETGFASSTNILNLVDQLKGKKMRKKEAEQVLQKF
1	I	I	VQNKWLIEKEGEFTLHGRAILEMEQYIRETYPDAVKICNICHSL

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	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
-	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, +=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
}	-		LIQGQSCETCGIRMHLPCVAKYFQSNAEPRCPHCNDYWPHEIPK
6456	2	555	VFDPEKERESGVLKSNKKSLRSRQH
0430		555	RPQSRSISMWRNSLLQVSSGLRWLRVCAMVDILGERHLVTCKGA
			TVEAEAALQNKVVALYFAAARCAPSRDFTPLLCDFYTALVAEAR RPAPFEVVFVSADGSSQEMLDFMRELHGAWLALPFHDPYRHELR
			KRYNVTAIPKLVIVKQNGEVITNKGRKQIRERGLACFQDWVEAA
			DIFONESV
6457	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
		332	KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
1			IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
			DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
			SFLTLSSQLKPKPVGEENICLDLKS
6458	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
ł			IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
1			DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
ļ			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
6459			SFLTLSSQLKPKPVGEENICLDLKS
6459	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
İ			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
ł			IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
1			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG DLQQATEFNQWKNVVFILQFLLSCPLGFLLMYSTVLCSYYNSAL
	}		TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
	}		SFLTLSSQLKPKPVGEENICLDLKS
6460	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
			IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIPVFLND
1			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
1		•	DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
			SFLTLSSQLKPKPVGEENICLDLKS
6461	1653	360	LQQRTLRITAVGQTHPIAWMAWEPSLGAFYGPASFITFVNCMYF
			LSIFIQLKRHPERKYELKEPTEEQQRLAANENGEINHQDSMSLS
	]		LISTSALENEHTFHSQLLGASLTLLLYVALWMFGALAVSLYYPL
1			DLVFSFVFGATSLSFSAFFVVHHCVNREDVRLAWIMTCCPGRSS
			YSVQVNVQPPNSNGTNGEAPKCPNSSAESSCTNKSASSFKNSSQ
			GCKLTNLQAAAAQCHANSLPLNSTPQLDNSLTEHSMDNDIKMHV
			APLEVOFRTNVHSSRHHKNRSKGHRASRLTVLREYAYDVPTSVE
			GSVQNGLPKSRLGNNEGHSRSRRAYLAYRERQYNPPQQDSSDAC
			STLPKSSRNFEKPVSTTSKKDALRKPAVVELENQQKSYGLNLAI QNGPIKSNGQEGPLLGTDSTGNVRTGLWKHETTV
6462	3	773	SEELDREKKLKEDSPRKTPNKESGVPSLPVSLTSIKEEPKEAKH
			PDSQSMEESKLKNDDRKTPVNWKDSRGTRVAVSSPMSQHQSYIQ
			YLHAYPYPQMYDPSHPAYRAVSPVLMHSYPGAYLSPGFHYPVYG
			KMSGREETEKVNTSPSVNTKTTTESKALDLLQQHANQYRSKSPA
			PVEKATAEREREAERERDRHSPFGQRHLHTHHHTHVGMGYPLIP
1	İ		GQYDPFQGLTSAALVASQQVAAQASASGMFPGORRE
6463	2	350	VILCILGGWIFKNADRSMBKKKGEPRTRAEARPWVDEDLKDSSD
			LHQAEEDADEWQESEENVEHIPFSHNHYPEKEMVKRSQEFYELL
			NKRRSVRFISNEQVPMEVIDNVIRTAGL
6464	12	1154	GILROKEREERNRIHKKEILFLEHLLVVPSEMSSLSGKVOTVLG

SEQ	Producted	Drodieted as	I halian not I coment now the
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1	residue of amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
1		ł	LVEPSKLGRTLTHEHLAMTFDCCYCPPPPCQEAISKEPIVMKNL
1	1		YWIQKNAYSHKENLQLNQETEAIKEELLYFKANGGGALVENTTT
		İ	GISRDTQTLKRLABETGVHIISGAGFYVDATHSSETRAMSVEQL
1			TDVLMNEILHGADGTSIKCGIIGEIGCSWPLTESERKVLQATAH
1	1		AQAQLGCPVIIHPGRSSRAPFQIIRILQEAGADISKTVMSHLDR
i			TILDKKELLEFAQLGCYLEYDLFGTELLHYQLGPDIDMPDDNKR
	ł		IRRVRLLVEEGCEDRILVAHDIHTKTRLMKYGGHGYSHILTNVV
			PKMLLRGITENVLDKILIENPKQWLTFK
6465	126	1396	KMTVFFKTLRNHWKKTTAGLCLLTWGGHWLYGKHCDNLLRRAAC
		ŀ	QEAQVFGNQLIPPNAQVKKATVFLNPAACKGKARTLFEKNAAPI
	1		LHLSGMDVTIVKTDYEGQAKKLLELMENTDVIIVAGGDGTLQEV
			VTGVLRRTDEATFSKIPIGFIPLGETSSLSHTLFAESGNKVQHI
1	Ì	1	TDATLAIVKGETVPLDVLQIKGEKEQPVFAMTGLRWGSFRDAGV
			KVSKYWYLEPLKIKAAHFFSTLKEWPQTHQASISYTGPTERPPN
1			EPEETPVQRPSLYRRILRRLASYWAQPQDALSQEVSPEVWKDVQ
ì			LSTIELSITTRNNQLDPTSKEDFLNICIEPDTISKGDFITIGSR
1			KVRNPKLHVEGTECLQASQCTLLIPEGAGGSFSIDSEEYEAMPV
			EVKLLPRKLQFFCDPRKREQMLTSPTQ
6466	1134	828	VARGTELSQLEKAHPPADMGRRKSKRKPPPKKKMTGTLETQFTC
			PFCNHEKSCDVKMDRARNTGVISCTVCLEEFQTPITYLSEPVDV
			YSDWIDACEAANQ
6467	301	2571	GELRVLALAHGELACHAVLTASLLSLRSRLMDSDMDYERPNVET
j	,		IKCVVVGDNAVGKTRLICARACNATLTQYQLLATHVPTVWAIDQ
•			YRVCQEVLERSRDVVDDVSVSLRLWDTFGDHHKDRRFAYGRSDV
ł			VVLCFSIANPNSLHHVKTMWYPEIKHFCPRAPVILVGCQLDLRY
1			ADLEAVNRARRPLARPIKPNEILPPEKGREVAKELGIPYYETSV
			VAQFGIKDVFDNAIRAALISRRHLQFWKSHLRNVQRPLLQAPFL
Ì			PPKPPPPIIVVPDPPSSSEECPAHLLEDPLCADVILVLQERVRI
1			FAHKIYLSTSSSKFYDLFLMDLSEGELGGPSEPGGTHPEDHQGH
	<b>f</b>		SDQHHHHHHHHHGRDFLLRAASFDVCESVDEAGGSGPAGLRAST
			SDGILRGNGTGYLPGRGRVLSSWSRAFVSIQEEMAEDPLTYKSR
			LMVVVKMDSSIQPGPFRAVLKYLYTGELDENERDLMHIAHIAEL
			LEVFDLRMMVANILNNEAFMNQEITKAFHVRRTNRVKECLAKGT
	ĺ		FSDVTFILDDGTISAHKPLLISSCDWMAAMFGGPFVESSTREVV
			FPYTSKSCMRAVLEYLYTGMFTSSPDLDDMKLIILANRLCLPHL
			VALTEQYTVTGLMEATQMMVDIDGDVLVFLELAQFHCAYQLADW
			CLHHICTNYNNVCRKFPRDMKAMSPENQEYFEKHRWPPVWYLKE
	1		EDHYQRARKEREKEDYLHLKRQPKRRWLFWNSPSSPSSSAASSS
			SPSSSSAVV
6468	3	1374	DAWAGTNMAALAPVGSPASRGPRLAAGLRLLPMLGLLQLLAEPG
			LGRVHHLALKDDVRHKVHLNTFGFFKDGYMVVNVSSLSLNEPED
			KDVTIGFSLDRTKNDGFSSYLDEDVNYCILKKQSVSVTLLILDI
			SRSEVRVKSPPEAGTQLPKIIFSRDEKVLGQSQBPNVNPASAGN
1			QTQKTQDGGKSKRSTVDSKAMGEKSFSVHNNGGAVSFQFFFNIS
			TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA
			GEIPLPKLYISMAFFFFLSGTIWIHILRKRRNDVFKIHWLMAAL
			PFTKSLSLVFHAIDYHYISSQGFPIEGWAVVYYITHLLKGALLF
			ITIALIGTGWAFIKHILSDKDKKIFMIVIPRRVLANVAYIIIES
1	1		TEEGTTEYGLWKDSLFLVDLLCCGAILFPVVWSIRHLQEASATD
			GKGKFSRAHFVLLSLL
6469	3	1374	DAWAGTNMAALAPVGSPASRGPRLAAGLRLLPMLGLLQLLAEPG
			LGRVHHLALKDDVRHKVHLNTFGFFKDGYMVVNVSSLSLNEPED
			KDVTIGFSLDRTKNDGFSSYLDEDVNYCILKKQSVSVTLLILDI
			SRSEVRVKSPPEAGTQLPKIIFSRDEKVLGQSQEPNVNPASAGN
	1		QTQKTQDGGKSKRSTVDSKAMGEKSFSVHNNGGAVSFQFFFNIS
			TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
		1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
_			GEIPLPKLYISMAFFFFLSGTIWIHILRKRRNDVFKIHWLMAAL
	1		PFTKSLSLVFHAIDYHYISSQGFPIEGWAVVYYITHLLKGALLF
	ļ		ITIALIGTGWAFIKHILSDKDKKIFMIVIPRRVLANVAYIIIES
			TEEGTTEYGLWKDSLFLVDLLCCGAILFPVVWSIRHLQEASATD
	i	Į.	GKGKFSRAHFVLLSLL
6470	2726	1437	AAASGVSSRADAPVLAOSPASAGNGRPSTPRVPGSRRHPSAPRS
6470	1 2728	1437	GPLPREDGCRTPGPQLLPLPGALLRPRTLLSSAAETGRSRHPDT
			_
			QHPSSGGRCRGGTESPSSAAGRPASMAEAEEDCHSDTVRADDDE
	1	ł	ENESPAETDLQAQLQMFRAQWMFELAPGVSSSNLENRPCRAARG
	1	1	SLOKTSADTKGKQEQAKEEKARELFLKAVEEEQNGALYEAIKFY
			RRAMQLVPDIEFKITYTRSPDGDGVGNSYIEDNDDDSKMADLLS
			YFQQQLTFQESVLKLCQPELESSQIHISVLPMEVLMYIFRWVVS
	1		SDLDLRSLEQLSLVCRGFYICARDPEIWRLACLKVWGRSCIKLV
	1	1	PYTSWREMFLERPRVRFDGVYISKTTYIRQGEQSLDGFYRAWHQ
			VEYYRYIRFFPDGHVMMLTTPEEPQSIVPRLRTR
6471	1750	299	FFFDKMAAGGSGVGGKRSSKSDADSGFLGLRPTSVDPALRRRRR
04/1	1,50		GPRNKKRGWRRLAGEPLGLEVDQFLEDVRLQERTSGGLLSEAPN
			EKLFFVDTGSKEKGLTKKRTKVQKKSLLLKKPLRVDLILENTSK
		ļ	VPAPKDVLAHQVPNAKKLRRKEQLWEKLAKQGELPREVRRAQAR
		)	LLNPSATRAKPGPQDTVERPFYDLWASDNPLDRPLVGQDEFFLE
			1
		Į.	QTKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSFEDHQTLLS
	1		AAHEVELQRQKEAEKLERQLALPATEQAATQESTFQELCEGLLE
	ı	i	ESDGEGEPGQGEGPEAGDAEVCPTPARLATTEKKTEQQRRREKA
	(		VHRLRVQQAALRAARLRHQELFRLRGIKAQVALRLAELARRQRR
			ROARREAEADKPRRLGRLKYQAPDIDVQLSSELTDSLRTLKPEG
			NILRDRFKSFQRRNMIEPRERAKFKRKYKVKLVEKRAFREIQL
6472	3	897	SCGSDRAQWAMEFPFDVDALFPERITVLDQHLRPPARRPGTTTP
			ARVDLQQQIMTIIDELGKASAKAQNLSAPITSASRMQSNRHVVY
ļ	1		ILKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAHNEVEPLCIL
		1	DFYIHESVQRHGHGRELFQYMLQKBRVEPHQLAIDRPSQKLLKF
	Į.		LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATRHSRAA
			AVDPTPAAPARKLPPKRAEGDIKPYSSSDREFLKVAVEPPWPLN
			RAPRRATPPAHPPPRSSSLGNSPERGPLRPFVP
			SSAVE FVWEGEKMAAE PNKTE I OTL FKRLRAVPTNKACFDCGAK
6473	22	912	-
ĺ		}	NPSWASITYGVFLCIDCSGVHRSLGVHLSFIRSTELDSNWNWFQ
			LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ
		1	LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAW
ł	1	Ĭ	DAPATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKASLEL
	Ĭ		KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSEIERQAQVAE
			KLREQQAADAKKQAEESMVASMRLAYQELQIDR
6474	3	462	LOROROHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS
	1		KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA
1			KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP
1			PSTLSVKGQIETVRVKGTEN
CA35		462	LORGROHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS
6475	3	402	1
ļ .		1	KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA
1	1	1	KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP
	1		PSTLSVKGQIETVRVKGTEN
6476	106	1090	ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL
			KSQVDKRFSAHYDAVEAELKSSTVGLVTLNDMKARQEALVRERE
ł	1		ROLAKROHLEEORLOGERORBOEORRERKRKISCLSFALDDLDD
1			QADAAEARRAGNLGKNPDVDTSFLPDRDREEEENRLREELRQEW
l			EAQREKVKDEEMEVTFSYWDGSGHRRTVRVRKGNTVQQFLKKAL
		1	
		i	I OCI, DKINET, ET, DO ACUEOT MET KENT TI BUVUTEVOET TABABCE
			QGLRKDFLELRSAGVEQLMFIKEDLILPHYHTFYDFIIARARGK
			QGLRKDFLELRSAGVEQLMFIKEDLILPHYHTFYDFIIARARGK SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF PASRWEAYDPEKKWDKYTIR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
}	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		residue of	S=Serine, T=Threonine, V=Valine,
	amino acid		
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į.	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
6477	227	915	LOGHLMGIMAASRPLSRFWEWGKNIVCVGRNYADHVREMRSAVL
1 04,,,	22,		SEPVLFLKPSTAYAPEGSPILMPAYTRNLHHELELGVVMGKRCR
			AVPEAAAMDYVGGYALCI;DMTARDVQDECKKKGLPWTLAKSFTA
1	1	i	
			SCPVSAFVPKEKIPDPHKLKLWLKVNGELRQEGETSSMIFSIPY
		i	IISYVSKIITLEEGDIILTGTPKGVGPVKENDEIEAGIHGLVSM
i		ļ	TFKVEKPEY
6478	2	1495	FVSSRILPESLASSEASTLEAMGRKEEDDCSSWKKQTTNIRKTF
04,0	_	1 2123	IFMEVLGSGAFSEVFLVKORLTGKLFALKCIKKSPAFRDSSLEN
1			BIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILE
			RGVYTEKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPE
)		1	ENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQKPYSKA
ļ			VDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFW
1			DDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDI
1			YPSVSLQIQKNFAKSKWRQAFNAAAVVHHMRKLHMNLHSPGVRP
			EVENRPPETOASETSRPSSPEITITEAPVLDHSVALPALTQLPC
i	I		QHGRRPTAPGGRSLNCLVNGSLHISSSLVPMHQGSLAAGPCGCC
Ì	1		SSCLNIGSKGKSSYCSEPTLLKKANKKQNFKSEVMVPVKASGSS
ł			HCRAGQTGVCLIM
6479	3	949	SCRGPGWHPAGGQAGAMELLSALSLGELALSFSRVPLFPVFDLS
01/2	(	1	YFIVSILYLKYEPGAVELSRRHPIASWLCAMLHCFGSYILADLL
1			LGEPLIDYFSNNSSILLASAVWYLIFFCPLDLFYKCVCFLPVKL
1	<b>,</b>	1	
	ł	ļ	IFVAMKEVVRVRKIAVGIHHAHHHYHHGWFVMIATGWVKGSGVA
		ļ	LMSNFEQLLRGVWKPETNEILHMSFPTKASLYGAILFTLQQTRW
1	1		LPVSKASLIFIFTLFMVSCKVFLTATHSHSSPFDALEGYICPVL
1			FGSACGGDHHHDNHGGSHSGGGPGAQHSAMPAKSKEELSEGSRK
	1	l	KKAKKAD
6480	192	514	DFMSIYFPIHCPDYLRSAKMTEVMMNTQPMEEIGLSPRKDGLSY
0400	192	324	QIFPDPSDFDRCCKLKDRLPSIVVEPTEGEVESGELRWPPEEFL
1	ļ.		
		<u> </u>	VQEDEQDNCEETAKENKEQ
6481	110	1131	KSRMDLDVVNMFVIAGGTLAIPILAFVASFLLWPSALIRIYYWY
	i		WRRTLGMQVRYVHHEDYQFCYSFRGRPGHKPSILMLHGFSAHKD
	}	İ	MWLSVVKFLPKNLHLVCVDMPGHEGTTRSSLDDLSIDGQVKRIH
l	1		OFVECLKLNKKPFHLVGTSMGGQVAGVYAAYYPSDVSSLWLVCP
1	1		AGLOYSTDNOFVQRLKELQGSAAVEKIPLIPSTPEEMSEMLQLC
1	1		SYVRFKVPQQILQGLVDVRIPHNNFYRKLFLEIVSEKSRYSLHQ
	i		
i			NMDKIKVPTQIIWGKQDQVLDVSGADMLAKSIANCQVELLENCG
			HSVVMERPRKTAKLIIDFLASVHNTDNNKKLD
6482	2517	568	EPVSKVSQSRRKAGVPTANIEESQAVEAAMANVPWAEVCEKFQA
1	1		ALALSRVELHKNPEKEPYKSKYSARALLEEVKALLGPAPEDEDE
			RPEAEDGPGAGDHALGLPAEVVEPEGPVAORAVRLAVIEFHLGV
			NHIDTEELSAGEEHLVKCLRLLRRYRLSHDCISLCIQAQNNLGI
1	1	1	
			LWSEREEIETAQAYLESSEALYNQYMKBVGSPPLDPTERFLPEE
		1	EKLTEGERSKRFEKVYTHNLYYLAQVYQHLEMFEKAAHYCHSTL
		1	KRQLEHNAYHPIEWAINAATLSQFYINKLCFMEARHCLSAANVI
			FGQTGKISATEDTPEAEGEVPELYHQRKGEIARCWIKYCLTLMQ
1			NAOLSMODNIGELDLDKOSELRALRKKELDEEESIRKKAVQFGT
]		1	GELCDAISAVEEKVSYLRPLDFEEARELFLLGQHYVFEAKEFFQ
l		1	
1			IDGYVTDHIEVVQDHSALFKGLAFFETDMERRCKMHKRRIAMLE
			PLTVDLNPQYYLLVNRQIQFEIAHAYYDMMDLKVAIADRLRDPD
1			SHIVKKINNLNKSALKYYQLFLDSLRDPNKVFPEHIGEDVLRPA
1			MLAKFRVARLYGKIITADPKKELENLATSLEHYKFIVDYCEKHP
1		1	EAAOEIEVELELSKEMVSLLPTKMERFRTKMALT
6402	<del></del>	(22	NSHLLCGLRARAPLSANGREARAMEQRLAEFRAARKRAGLAAQP
6483	3	623	
	1		PAASQGAQTPGEKAEAAATLKAAPGWLKRPLVWKPRPASARAQP
[			GLVQEAAQPQGSTSETPWNTAIPLPSCWDQSFLTNITFLKVLLW
1			LVLLGLFVELEFGLAYFVLSLFYWMYVGTRGPEEKKEGEKSAYS
			. h

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No.   nucleotide   location   corresponding   to first   amino acid   residue of   residue of   residue of   amino acid   sequence   sequence   sequence   sequence   sequence   sequence   verified of   sequence   verified of   sequence   verified of   sequence   verified of   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verified   verifie		1		
Location   Corresponding   to first   amino acid			1	
Leleucine, M-Methiodine, N-Asparagine, proline, of cirst amino acid residue of amino acid residue of amino acid sequence   S-Serine, T-Threonine, V-Valine, metadue of amino acid sequence   S-Serine, T-Threonine, V-Valine, amino acid sequence   S-Serine, T-Threonine, V-Valine, metadue of amino acid sequence   S-Serine, T-Threonine, V-Valine, metadue of amino acid sequence   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOLEREKOLRPIAGE   VPNPGCEATGOTITAEOL	NO:			
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amino acid sequence   Codon, /-possible nucleotide deletion,    -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion	i	4	amino acid	
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GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS  6491 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL				APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD
NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS  6491 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL	1		1	DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL
NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS  6491 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL				GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD
KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS  6491 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH  KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT  HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG  QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE  APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD  DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL	ì			_
6491 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL				-
KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL		1	<del> </del>	
HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL	6491	3	1183	
QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL	1	1		
APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL				HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG
APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL				QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE
DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL	1 .	1	1	
	1			
	]		1	77
	1		1	GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD
NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL	L	1		NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Clubania haid D. Phanalalanda G. Glassina
MO:	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
i		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l .	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
	<del> </del>		KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS
6492	34	2573	IPFLKSCCCCCLFDFPPPPLDQVQEEECEVERVTEHGTPKPFRK
"	1	1 23/3	PDSVAFGESQSEDEQFENDLETDPPNWQQLVSREVLLGLKPCEI
	ì	ł	****
	1	İ	KRQEVINELFYTERAHVRTLKVLDQVFYQRVSREGILSPSELRK
ł	ł	}	IFSNLEDILQLHIGLNEQMKAVRKRNETSVIDQIGEDLLTWFSG
Į.		1	PGEEKLKHAAATFCSNQPFALEMIKSRQKKDSRFQTFVQDAESN
			PLCRRLQLKDIIPTQMQRLTKYPLLLDNIATYTEWPTEREKVKK
			AADHCRQILNYVNQAVKEAENKQRLEDYQRRLDTSSLKLSEYPN
	1	1	VEELRNLDLTKRKMIHEGPLVWKVNRDKTIDLYTLLLEDILVLL
		l	QKQDDRLVLRCHSKILASTADSKHTFSPVIKLSTVLVRQVATDN
ſ		1	KALFVISMSDNGAQIYELVAQTVSEKTVWQDLICRMAASVKEQS
1			TKPIPLPQSTPGEGDNDEEDPSKLKEEQHGISVTGLQSPDRDLG
i			LESTLISSKPQSHSLSTSGKSEVRDLFVAERQFAKEQHTDGTLK
İ		1	EVGEDYQIAIPDSHLPVSEERWALDALRNLGLLKQLLVQQLGLT
ł		<b>,</b>	EKSVQEDWQHFPRYRTASQGPQTDSVIQNSENIKAYHSGEGHMP
		į.	
1		1	FRIGTGDIATCYSPRISTESFAPRDSVGLAPQDSQASNILVMDH
		İ	MIMTPEMPTMEPEGGLDDSGEHFFDAREAHSDENPSEGDGAVNK
	Į.	ţ	EEKDVNLRISGNYLILDGYDPVQESSTDEEVASSLTLQPMTGIP
i		ł	AVESTHQQQHSPQNTHSDGAISPFTPEFLVQQRWGAMEYSCFEI
1			QSPSSCADSQSQIMEYIHKIEADLEHLKKVEESYTILCQRLAGS
	· ·		ALTDKHSDKS
6493	557	1147	TPARMAYQGSSTSDCMSKTLDSASAHFAASAVVSAPVPSRSEVA
1	1		KEQNTGHNNINGVVQPSGTSKTLYSTNMALSSSPGISAVQLVRT
İ		ŀ	VGHTTTNHLIPALCTSSPQTLPMNNSCLTNAVHLNNVSVVSPVN
1			VHINTRTSAPSPTALKLATVAASMDRVPKVTPSSAISSIARENH
[			EPERLGLNGIABTTVAMEVT
6494	2425	1052	AVAGGARPCSTPSSPHRRCRRHRPRPLPRPPAAIMSASAVYVLD
			LKGKVLICRNYRGDVDMSEVEHFMPILMEKEEEGMLSPILAHGG
			VRFMWIKHNNLYLVATSKKNACVSLVFSFLYKVVQVFSEYFKEL
		1	EEESIRDNFVIIYELLDELMDFGYPQTTDSKILQEYITQEGHKL
	}	į.	ETGAPRPPATVTNAVSWRSEGIKYRKNEVFLDVIBSVNLLVSAN
1			
			GNVLRSEIVGSIKMRVFLSGMPELRLGLNDKVLFDNTGRGKSKS
		}	VELEDVKFHQCVRLSRFENDRTISFIPPDGEFELMSYRLNTHVK
ŀ			PLIWIESVIEKHSHSRIEYMIKAKSQFKRRSTANNVEIHIPVPN
1			DADSPKFKTTVGSVKWVPENSEIVWSIKSFPGGKEYLMRAHFGL
			PSVEAEDKEGKPPISVKFEIPYFTTSGIQVRYLKIIEKSGYQAL
			PWVRYITQNGDYQLRTQ
6495	2425	1052	AVAGGARPCSTPSSPHRRCRRHRPRPLPRPPAAIMSASAVYVLD
			LKGKVLICRNYRGDVDMSEVEHFMPILMEKEEEGMLSPILAHGG
1			VRFMWIKHNNLYLVATSKKNACVSLVPSFLYKVVQVFSEYFKEL
			EEESIRDNFVIIYBLLDELMDFGYPQTTDSKILQEYITQEGHKL
ļ		į	ETGAPRPPATVTNAVSWRSEGIKYRKNEVFLDVIESVNLLVSAN
			GNVLRSEIVGSIKMRVFLSGMPELRLGLNDKVLFDNTGRGKSKS
		1	VELEDVKFHQCVRLSRFENDRTISFIPPDGEFELMSYRLNTHVK
			-
1	1		PLIWIESVIEKHSHSRIEYMIKAKSQFKRRSTANNVEIHIPVPN
1			DADSPKFKTTVGSVKWVPENSBIVWSIKSFPGGKEYLMRAHFGL
1			PSVEAEDKEGKPPISVKFEIPYFTTSGIQVRYLKIIEKSGYQAL
	<del></del>		PWVRYITQNGDYQLRTQ
6496	247	559	LRAVSLLPLQLVLPEYSIHSLPCIMFLCAQEWLTLGLNVPLLFY
}			HFWRYFHCPADSSELAYDPPVVMNADTLSYCQKEAWCKLAFYLL
L			SFFYYLYCMIYTLVSS
6497	1053	352	ANTQICRLCPRRHLHPPCGAKMGNGTEEDYNFVFKVVLIGESGV
i			GKTNLLSRFTRNEFSHDSRTTIGVEFSTRTVMLGTAAVKAQIWD
1			
			TAGLERYRAITSAYYRGAVGALLVFDI.TKHOTYAVVERWI.KFI.V
			TAGLERYRAITSAYYRGAVGALLVFDLTKHQTYAVVERWLKELY DHAEATIVVMLVGNKSDLSOAREVPTEFARMFAFNNGLLFLETS
			TAGLERYRAITSAYYRGAVGALLVFDLTKHQTYAVVERWLKELY DHAEATIVVMLVGNKSDLSQAREVPTEEARMFAENNGLLFLETS ALDSTNVELAFETVLKEIFAKVSKQRQNSIRTNAITLGSAQAGQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	to first		S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			BPGPGEKRACCISL
6498	2636	272	SLRLCPWGTHLAGPTTMRLSSLLALLRPALPLILGLSLGCSLSL
			LRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLDQSDEDFKPRI
			VPYYRDPNKPYKKVLRTRYIQTELGSRERLLVAVLTSRATLSTL
			AVAVNRTVAHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLM
			SETLRHLHTHFGADYDWFFIMQDDTYVQAPRLAALAGHLSINQD
		į	LYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
			DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPB
	1		KEGSSAFLSAFAVHPVSEGTLMYRLHKRFSALELERAYSEIEQL
		1	OAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEVLGWDYFTE
			OHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRYQPRLRF
		1	OKORLLNGYRRFDPARGMEYTLDLLLECVTQRGHRRALARRVSL
			LRPLSRVEILPMPYVTEATRVQLVLPLLVAEAAAAPAFLEAFAA
			NVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAAELERRY
			PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPG
			PEVLNRCRMNAISGWOAFFPVHFQEFNPALSPQRSPPGPPGAGP
	i		DPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAARARLAG
		,	ELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRD
			CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQANST
	<u> </u>	2040	SCSADTRPSGOAWPTVGLRAAAGAFRTGSPLALGPETPQVACLP
6499	3	2040	-
			GHPPVRPQVSGGPGAMPDPAAHLPFFYGSISRAEAEEHLKLAGM
			ADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNGTYAIAG
ļ			GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQPGVFDC
		}	LRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKLIATTAHERM
			PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYALSLIYG
1		1	KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVBYLKLKADGLIYC
			LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTLNSDGYT
į			PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLFLKRDNL
			LIADIELGCGNFGSVRQGVYRMRKKQIDVAIKVLKQGTEKADTE
			EMMREAQIMHQLDNPYIVRLIGVCQAEALMLVMEMAGGGPLHKF
			LVGKREEIPVSNVAELLHQVSMGMKYLEEKNFVHRDLAARNVLL
			VNRHYAKISDFGLSKALGADDSYYTARSAGKWPLKWYAPECINF
			RKFSSRSDVWSYGVTMWEALSYGQKPYKKMKGPEVMAFIBQGKR
			MECPPECPPELYALMSDCWIYKWEDRPDFLTVEQRMRACYYSLA
			SKVEGPPGSTQKAEAACA
6500	1773	726	TGPTHASADAWGLVRSVTBWCANVRGNPCAAALSCPQAVLDAGK
			MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHL
			QAPNKEDILKISEDERMELSKSFRVYCIILVKPKDVSLWAAVKE
			TWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRKAYKYAFDK
		[	YRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHTIKSG
1			DLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEQGGMIWKISED
1	1		KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN
			QVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGPYFQ
65'01	1	570	LVGMSGGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLIIKDLGE
""	_	1	IHSRLLDHRPVIQGETRYFVKEFEEKRGLREMRVLENLKNMIHE
			TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQERKKI
			HSDHLVASEKQHMLQWDNFMKEQPNKRAEVDEEHRKAMERLKEQ
Ì		1	YAEMEKDLAKFSTF
	+	1650	AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE
6502	213	1620	
		1	KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS
İ			SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT
		1	AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLBEK
1		1	KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ.
			EQARRDALKQRAEQSISEEPGWEEEEEBLMGISPISPKEAKVPV
1			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide location		Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
:	corresponding to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	amino acid	1	
ŀ		sequence	Codon, /=possible nucleotide deletion, \-possible nucleotide insertion)
<b>.</b>	sequence		1
t	}		IHSKPLTPAGHTGGPEPRPPARVETLREEAPTDLRVFELNSDSG
			KSTPSNNGKKGSSTDISEDWEKDFDLDMTEEEVQMALSKVDASG
6503	713	1650	EVSGPGGSEGSEPNGPGCESSPQPAQLSPQEGPCSCLR
6503	213	1630	AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS
		1	
			SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT
		Ï	AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK
l	}		KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ
ŀ			EQARRDALKQRAEQSISEEPGWEEEEEELMGISPISPKEAKVPV
			AKISTFFEGEPGPQSPCEENLVTSVEPPAEVTPSESSESISLVT
1			QIANPATAPEARVLPKDLSQKLLEASLEEQGLAVDVGETGPSPP
			IHSKPLTPAGHTGGPEPRPPARVETLREEAPTDLRVFELNSDSG
		1	KSTPSNNGKKGSSTDISEDWEKDFDLDMTBEEVQMALSKVDASG EVSGPGGSEGSEPNGPGCESSPOPAOLSPOEGPCSCLR
6504	2131	1294	<u> </u>
0504	2131	1294	GKVCLVAHWVCLSILSPPPAGMKTPNAQEAEGQQTRAAAGRATG SANMTKKKVSQKKQRGRPSSQPCRNIVGCRISHGWKEGDEPITO
		i	WKGTVLDQVPINPSLYLVKYDGIDCVYGLELHRDERVLSLKILS
1			DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAOA
			PIMKAWFYITYEKDPVLYMYQLLDDYKEGDLRIMPESSESPPTE
1			REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF
			DDDFHIYVYDLVKKS
6505	2131	1294	GKVCLVAHWVCLSILSPPPAGMKTPNAOEAEGOOTRAAAGRATG
8303	2131	1234	SANMTKKKVSQKKQRGRPSSQPCRNIVGCRISHGWKEGDEPITO
1		}	WKGTVLDQVPINPSLYLVKYDGIDCVYGLELHRDERVLSLKILS
ļ			DRVASSHISDANLANTI I GKAVEHMFEGEHGSKDEWRGMVLAQA
1			PIMKAWFYITYEKDPVLYMYQLLDDYKEGDLRIMPESSESPPTE
			REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF
			DDDFHIYVYDLVKKS
6506	1	1350	EVSPPTSCCLTVAVADPGVSEGFRGFGAGCEMPGRGRCPDCGST
1 0000	-	1	ELVEDSHYSQSQLVCSDCGCVVTEGVLTTTFSDEGNLREVTYSR
Į.		1	STGENEQVSRSQQRGLRRVRDLCRVLQLPPTFEDTAVAYYQQAY
			RHSGIRAARLQKKEVLVGCCVLITCRQHNWPLTMGAICTLLYAD
			LDVFSSTYMQIVKLLGLDVPSLCLAELVKTYCSSFKLFQASPSV
1		1	PAKYVEDKEKMLSRTMQLVELANETWLVTGRHPLPVITAATFLA
			WQSLQPADRLSCSLARFCKLANVDLPYPASSRLQELLAVLLRMA
		1	EQLAWLRVLRLDKRSVVKHIGDLLQHRQSLVRSAFRDGTAEVET
		1	REKEPPGWGQGQGEGEVGNNSLGLPQGKRPASPALLLPPCMLKS
	ļ	1	PKRICPVPPVSTVTGDENISDSEIEQYLRTPQEVRDFQRAQAAR
1		1	OAATSVPNPP
6507	1878	929	RSHASRLPELPSGCLVLQVQELVQMSGMEATVTIPIWQNKPHGA
		1	ARSVVRRIGTNLPLKPCARASFETLPNISDLCLRDVPPVPTLAD
			IAWIAADEEETYARVRSDTRPLRHTWKPSPLIVMQRNASVPNLR
			GSEERLLALKKPALPALSRTTELQDELSHLRSQIAKIVAADAAS
		1	ASLTPDFLSPGSSNVSSPLPCFGSSFHSTTSFVISDITEETEVE
1		1	VPELPSVPLLCSASPECCKPEHKAACSSSEEDDCVSLSKASSFA
			DMMGILKDFHRMKQSQDLNRSLLKEEDPAVLISEVLRRKFALKE
			EDISRKGN
6508	862	342	WEARKRPORWPSERREVRVPPPHLORGRSGLEPGTFRKMAAARP
-555			SLGRVLPGSSVLFLCDMQEKFRHNIAYFPQIVSVAARMLKNTTL
	1		DLLDRGLQVHVVVDACSSRSQVDRLVALARMRQSGAFLSTSEGL
		1	ILQLVGDAVHPQFKEIQKLIKEPAPDSGLLGLFQGQNSLLH
6509	2	1053	FVWNPRGGRKRROAAVTQAATRASGTPSPRDGTMTQGKLSVAN
5505	1	1000	KAPGTEGQQQVHGEKKEAPAVPSAPPSYEEATSGEGMKAGAFPP
1	1		APTAVPLHPSWAYVDPSSSSSYDNGFPTGDHELFTTPSWDDQKV
1		i	RRVFVRKVYTILLIQLLVTLAVVALFTFCDPVKDYVQANPGWYW
			ASYAVFFATYLTLACCSGPRRHFPWNLILLTVFTLSMAYLTGML
L	_l	<u> </u>	Thi dicebelificit Familian At 1 moistiff Confi

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
ļ- <del></del>			SSYYNTTSVLLCLGITALVCLSVTVFSFQTKFDFTSCQGVLFVL
			LMTLFFSGLILAILLPFQYVPWLHAVYAALGAGVFTLFLALDTQ
			LLMGNRRHSLSPEEYIFGALNIYLDIIYIFTFFLQLFGTNRE
6510	37	1156	PCALDGCPQRGAVHPLLSSAMGLLAFLKTQFVLHLLVGFVFVVS
			GLVINFVQLCTLALWPVSKQLYRRLNCRLAYSLWSQLVMLLEWW
			SCTECTLFTDQATVERFGKBHAVIILNHNFEIDFLCGWTMCERF
		}	GVLGSSKVLAKKELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVV
			EGLRRLSDYPEYMWFLLYCEGTRFTETKHRVSMEVAAAKGLPVL
			KYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGIL
			YGKKYEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIY
			NQKGMFPGEQFKPARRPWTLLNFLSWATILLSPLFSFVLGVFAS
			GSPLLILTFLGFVGAGNGHCR
6511	2541	1425	GEEQPLAAAPTECLEQVIGGAGDPGTWASFPSPLPGPAPLKGGK
			TMATNFSDIVKQGYVKMKSRKLGIYRRCWLVFRKSSSKGPQRLE
	ł	1	KYPDEKSVCLRGCPKVTEISNVKCVTRLPKETKRQAVAIIFTDD
1			SARTFTCDSELEAEEWYKTLSVECLGSRLNDISLGEPDLLAPGV
			QCEQTDRFNVFLLPCPNLDVYGECKLQITHENIYLWDIHNPRVK
ļ		}	LVSWPLCSLRRYGRDATRFTFRAGRMCDAGEGLYTFQTQEGEQI
			YQRVHSATLAIAEQHKRVLLEMEKNVRLLNKGTEHYSYPCTPTT
1			MLPRSAYWHHITGSQNIAEASSYAGEGYGAAQASSETDLLNRFI
			LLKPKPSQGDSSEAKTPSQ
6512	159	807	FGKKSTWFPLSRSLRVASGRSCKLGHGGYTGSGPGFGEPRDSGA
ŀ		i	EVPSGSGRATGCERGGVRGARQGRAPGSSIWRKEPRMVCTRKTK
l	1		TLVSTCVILSGMTNIICLLYVGWVTNYIASVYVRGQEPAPDKKL
1			EEDKGDTLKIIERLDHLENVIKQHIQEAPAKPEEAEAEPFTDSS
			LFAHWGQELSPEGRRVALKQFQYYGYNAYLSDRLPLDRP
6513	2	756	FVSPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTA
l			LFPDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQV
			AAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQ
			GVPLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPV
	}		LQQDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSF
			SPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALF
İ			PDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQVAA
			PYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQGV
1			PLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPVLQ
	1		QDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSFSP
1			EPGFSLAQLNLIWQLTDTRQLVHSFTEGR
6514	985	302	VGIPGPTISSAAEMEDLLDLDEELRYSLATSRAKMGRRAQQESA
1			QAENHLNGKNSSLTLTGETSSAKLPRCRQGGWAGDSVKASKFRR
			KASEBIEDFRLRPQSLNGSDYGGDIPIIPDLEEVQEEDFVLQVA
		.[	APPSIQIKRVMTYRDLDNDLMKYSAIQTLDGEIDLKLLTKVLAP
		1	. EHEVRERNPSWQDDVGWDWDHLFTEVSSEVLTEWDPLQTEKEDP
l			AGQARHT
6515	1345	305	GRVGSRRRGAAVPGGCGAGSTQLEVSASASCGALGSADMNPIVV
]	l		VHGGGAGPISKDRKERVHQGMVRAATVGYGILREGGSAVDAVEG
1	1		AVVALEDDPEFNAGCGSVLNTNGEVEMDASIMDGKDLSAGAVSA
1	1		VQCIANPIKLARLVMEKTPHCFLTDQGAAQFAAAMGVPEIPGEK
1	1		LVTERNKKRLEKEKHEKGAQKTDCQKNLGTVGAVALDCKGNVAY
}			ATSTGGIVNKMVGRVGDSPCLGAGGYADNDIGAVSTTGHGESIL
	1		KVNLARLTLFHIEQGKTVEEAADLSLGYMKSRVKGLGGLIVVSK
1	1		TGDWVAKWTSTSMPWAAAKDGKLHFGIDPDDTTITDLP
6516	1	1402	FRRLRYLGQDATAAARDLRTRGLQGYCPSATARQQVLVSALQQL
	_	'	KGRRSEHRNENOEMPYSTNKELILGIMVGTAGISLLLLWYHKVR
			KPGIAMKLPEFLSLGNTFNSITLQDEIHDDQGTTVIFQERQLQI
			LEKLNELLTNMERLKEEIRFLKEAIPKLEEYIQDELGGKITVHK
ł	1		ISPOHRARKRRLPTIQSSATSNSSEEAESEGGYITANTDTEEQS
ŀ			

Deginning   Cocation   Cocation   Cocation   Cocation   Corresponding   Coffice   Cocation   Corresponding   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffi	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Sociation   Cocration   Corresponding	_			(A=Alanine, C=Cysteine D=Aspartic Acid S=
Coctation   Corresponding   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffre	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine
LeLeucine, M-Methionine, N-Asparagine, periodine, of first amino acid residue of amino acid sequence   S-Serine, T-Threonine, V-Valine, amino acid sequence   S-Serine, T-Threonine, V-Valine, w-Tryptophan, Y-Tyrosine, K-Unknown, *-Stop Coden, /-possible nuclectide deletion, v-possible nuclectide deletion, v-possible nuclectide deletion, v-possible nuclectide insertion   PFVPKAFFIKWELINLDVLLGWUPHLEWSESSKSSFELLEDHK KERPER SERVEN	1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine.
to first amino scid residue of amino acid amino acid sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence sequence  sequence  sequence  sequence  sequ	İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
amino acid residue of amino acid sequence	i		amino acid	P=Proline, Q=Glutamine, R=Arginine,
main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main acid sequence   main ac		amino acid	residue of	S=Serine, T=Threonine, V=Valine.
sequence    Codon, /-possible nuclectide deletion,		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence   N-possible nuclectide insertion	1	amino acid	sequence	Codon, /=possible nucleotide deletion.
EKFRDE I EPMMRPARAGOMYSLISTITGEKKHYANIGKTISEST ( RIALIPEEPPLYILKGRYCYTVEKLSWIEKKHYANTLFGKIESSTY)  (BALHAFILKABELCOGYSNIPMYLLACTTOLEENQNALKFCNL)  ALLLIPTYTKEDKEAQKEMQKIHTSLKR  GEWÄGGSSINANYVYKGHAEDYERWQRQGAGKWIDTALCIPYFR  HAQGHELGASRYRGADGPLRVSGKTMIPLHCAFLEATOQAGYP  LTEDMAGFQGEFGMIMMT IHEGKRISAACATHIPALSKTNILAC  ALTUSANLFERITANGVEYVKHOGSGSHAYAKSVILSGGAIN  SPOLIMLSGIGNADDLKKLGIPWYCHLIPYGONLODHLEITYGI  ACTRIPTHEAGKOPRIRWCIGLERUKSTOGGATAHLETGGFIR  SQROVBRIDDIOPHIPLPSQUIDHGRVPTOQBAYQWIVOPWRGTSY  GUKLKISANIPODHYOIQPHILSTIDI IEDPRILCHTEIFAGO  ALAPFRGELQPOSHIQSKEIDAFVRAKADSAYHPSCTCKMO  GUKLKISANIPODHYOIQPHILSTIDI IEDPRILCHTEIFAGO  ALAPFRGELQPOSHIQSKEIDAFVRAKADSAYHPSCTCKMO  GUKLKISANIPODHYOIQPHILSTIDI IEDPRILCHTEIFAGO  ALAPFRGELQPOSHIQSKEIDAFVRAKADSAYHPSCTCKMO  GUKLKISANIPODHYOIQPHILSTIDI IEDPRILCHTEIFAGO  ALAPFRGELQPOSHIQSKEIDAFVRAKADSAYHPSCTCKMO  GEKANDI KIGGPALMBKUPVYKRPTLAYOR  BANDI KIGGPALMBKUPVYKRPTLAYOR  EKANDI KIGGPALMBKUPVYKRPTLAYOR  EKANDI KIGGPALMBKUPVYKRPTLAYOR  EKANDI KIGGPALMBKUPVYKRPTLAYOR  LCKKCRAPGKKOPDDSARESHSOGDLFSEETISDINNITSIT  TPTLSPSQOPLPPELNYTSPSKEECOFCTDIANYSLITPTKRSIC  GTDSGSENEASPYKRRPLLENTERSEETISSKOKSRRRCFQCOTT  KIELVQOSLOSKCRGVYFOMHALPOGROCHOPKOLSTITPTKRSIC  GTDSGSENEASPYKRRPLLENTERSEETISSKOKSRRRCFQCOTT  KIELVQOSLOSKCRGVYFOMHALPOGROCHOPKOLSTITPTKRSIC  GTDSGSENEASPYKRRPLLENTERSEETISSKOKSRRRCFQCOTT  KIELVQOSLOSKCRGVYFOMHALPOGROCHOPKOLSTITPTKRSIC  GTDSGSENEASPYKRRVNOEGGGGORGKQLOPPARSPOGSYGSPAS  WSFAPLSAAPGSSSRSSFSSFSKSSRSSFSFSKOKSRRKKKKKKKKKKKKK		sequence		\=possible nucleotide insertion)
EKFRDE I EPMMRPARAGOMYSLISTITGEKKHYANIGKTISEST ( RIALIPEEPPLYILKGRYCYTVEKLSWIEKKHYANTLFGKIESSTY)  (BALHAFILKABELCOGYSNIPMYLLACTTOLEENQNALKFCNL)  ALLLIPTYTKEDKEAQKEMQKIHTSLKR  GEWÄGGSSINANYVYKGHAEDYERWQRQGAGKWIDTALCIPYFR  HAQGHELGASRYRGADGPLRVSGKTMIPLHCAFLEATOQAGYP  LTEDMAGFQGEFGMIMMT IHEGKRISAACATHIPALSKTNILAC  ALTUSANLFERITANGVEYVKHOGSGSHAYAKSVILSGGAIN  SPOLIMLSGIGNADDLKKLGIPWYCHLIPYGONLODHLEITYGI  ACTRIPTHEAGKOPRIRWCIGLERUKSTOGGATAHLETGGFIR  SQROVBRIDDIOPHIPLPSQUIDHGRVPTOQBAYQWIVOPWRGTSY  GUKLKISANIPODHYOIQPHILSTIDI IEDPRILCHTEIFAGO  ALAPFRGELQPOSHIQSKEIDAFVRAKADSAYHPSCTCKMO  GUKLKISANIPODHYOIQPHILSTIDI IEDPRILCHTEIFAGO  ALAPFRGELQPOSHIQSKEIDAFVRAKADSAYHPSCTCKMO  GUKLKISANIPODHYOIQPHILSTIDI IEDPRILCHTEIFAGO  ALAPFRGELQPOSHIQSKEIDAFVRAKADSAYHPSCTCKMO  GUKLKISANIPODHYOIQPHILSTIDI IEDPRILCHTEIFAGO  ALAPFRGELQPOSHIQSKEIDAFVRAKADSAYHPSCTCKMO  GEKANDI KIGGPALMBKUPVYKRPTLAYOR  BANDI KIGGPALMBKUPVYKRPTLAYOR  EKANDI KIGGPALMBKUPVYKRPTLAYOR  EKANDI KIGGPALMBKUPVYKRPTLAYOR  EKANDI KIGGPALMBKUPVYKRPTLAYOR  LCKKCRAPGKKOPDDSARESHSOGDLFSEETISDINNITSIT  TPTLSPSQOPLPPELNYTSPSKEECOFCTDIANYSLITPTKRSIC  GTDSGSENEASPYKRRPLLENTERSEETISSKOKSRRRCFQCOTT  KIELVQOSLOSKCRGVYFOMHALPOGROCHOPKOLSTITPTKRSIC  GTDSGSENEASPYKRRPLLENTERSEETISSKOKSRRRCFQCOTT  KIELVQOSLOSKCRGVYFOMHALPOGROCHOPKOLSTITPTKRSIC  GTDSGSENEASPYKRRPLLENTERSEETISSKOKSRRRCFQCOTT  KIELVQOSLOSKCRGVYFOMHALPOGROCHOPKOLSTITPTKRSIC  GTDSGSENEASPYKRRVNOEGGGGORGKQLOPPARSPOGSYGSPAS  WSFAPLSAAPGSSSRSSFSSFSKSSRSSFSFSKOKSRRKKKKKKKKKKKKK				FPVPKAFNTRVEELNLDVLLQKVDHLRMSESGKSESFELLRDHK
INRAPMINGHEMYAULGYVSEFEGLOMKINYGHLYKEHLIG RILLPEPFFLYLKGRYCTYVSKIN MISKMANTIJGKIFSSTV QEALMHPIKAEELCGYSHNYMMILAKCYTDLEBOONALHFCNL ALLLPYVKGUSSSINAMVYNGHAEDYERMORGAGGOVYAHCLPYCNL ROWGGSSSINAMVYNGHAEDYERMORGAGGOVYAHCLPYCH ROQHBLGARSTWADDLKKICI IPVVCHLGRYOMLOGHISVAFORDY LITEMMGFOOGGGGMIDMT HIRGKRISAACAYLHDALSRYNLKA RAETLUSKULFEGTBAUVYEVKUNGGHRAYASKEVILLGGOAN ACTEPITIHBAQKPIRKVCIGLEMIMKFIGGATAHLETOGFI SQRUPPFDIQFFILDSQVIDIBERVFTOQBAYAYOPMGTISV GWIKLRSANFQDHEVIQPWISTETDIEDFFLCVKITREIFFOG ALAPFRGERUPGSSIIGSKELDGAVRAADSFRANGSHAPSTTMIA ACADII KOGGALHARVONDOVAVKPHSTETDIEDFFLCVKITREIFFOG BEDTAVVUPCUTKULGVEHLAVUDASIHPSWYSGNIMATTMIA EKAADII KIGGALHARVONDOVAVKPHTATOR PANNFGSEFFTRVERRARSFPLPPPRAPRRRRIKHLRAVFGES RHCGRRAPPPSFNICHMONDOVAVKPHTATOR RHCGRRAPPSFNICHMONDOVAVKPHTATOR RHCGRRAPPSFNICHMONDOVAVKPHTATOR RHCGRRAPPSFNICHENVTSPSKEEGFGCTOTIANVITTKRSG GTDSGSENBASPVRRPALLEPTERSESTISSKOKSRRFCFQCOT KLELVQGELGSCGCOVFCMILHIPGGHCTPDHMGGREBAIM MONKLDRKVORSCORIGEGCS KLENGAPSFNICHVARADFTATVSEKEPPGKUCISSRDPFGSIS AKKVATTERKAPRRVNGEGGGGNERULGPPANPPQSVGGPA MSEADJAADSISSRSSFSFSSAATAVSSAASALGOGPOFRIL VPPTLLHAQPHILLIPAAJAASANAKSRRPKERKERERHGLI GGARBAGGASREENGEVKPLPRKYNIEDIGLKKKKKKKKKIK KUNDITKYTOSKI PENNSEPPFVSLKERPRQNINLKHICHIEPKOLI HIEHOPNGGASVIHCIQ GRARGAGASREENGEVKPLPRKYRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK				EKFRDEIEFMWRFARAYGDMYELSTNTQEKKHYANIGKTLSERA
ORALHAPIKABELCPGYSNPNYMYLAKCYTÜLEENQNALKPCNL				INRAPMNGHCHLWYAVLCGYVSEFEGLQNKINYGHLFKEHLDIA
6517  3 1414 GRWGGSSINANYTYGHADEYERKQRGARGMDYAHCLPYFE KAQGHELGASRYRGADGLRYSGKITNPLHCAPLERTOQAGYP LTERMGFOGGGGGFGWMDTHLHEKRHSAACAYLPHALSRTHLKA EAETLVSRYLFEGTRAVGUFYVKNQGSHRAYASKEVILSGGAIN SPQLIMISGIGNADDLKKLGIPVVCHUPGVGQNIQDHLEHTQQ ACTHPITHESAQKPERKVGQEHRAYASKEVILSGGAIN SPQLIMISGIGNADDLKKLGIPVVCHUPGVGQNIQDHUPTQQRAYAKADSAYHPSCTCKMGQ PSPDFTAVVDPODPFVQPNIQDHUPTQPNIJSTETILEPFRGAULHFTTGPIFLE SQREVPHDIQFHFLPSQVIDHGRUPTQQBAYQHVVDWSPHRGTSV GWLKLESANPQDPFVQPNIVTDASIMPPMIKANADAYHPSCTCKMGQ PSPDFTAVVDPODPFVQPNIVTDASIMPPMIKANADAYHPSCTCKMGQ PSPDFTAVVDPOTRYGVGVNIVTDASIMPPMIKANADAYHPSCTCKMGQ PSPDFTAVVDPOTRYGVGVNIVTDASIMPPMIKANADAYHPSCTCKMGQ PSPDFTAVVDPOTRYGVGVNIVTDASIMPPMIKANADAYHPSCTCKMGQ PSPDFTAVVDPOTRYGVGVNIVTDASIMPPMIKANADAYHPSCTCKMGQ PSPDFTAVVDPOTRYGVGVNIVTDASIMPPMIKANADAYHPSCTCKMGQ PSPDFTAVVDPOTRYGVGVNIVTDASIMPPMIKANADAYHPSCTCKMGQ PSPDFTAVVDPOTRYGVGALAYANADAYHPSCTCKMGQ PSPDFTAVVDPOTRYGVGALAYANADAYHPSCTCKMGQ PSPDFTAVVDPOTRYGVALAYANADAYHPSCTCKMGQ PSPDFTAVVDPOTRYGVALAYANADAYHPSCTCKMGQ PSPDFAVDPOTRYGVALAYANADAYHPSCTCKMGQ PSPDFAVDPOTRYGVALAYANADAYHTATVSKEGGCGCTUTAHVSLITTTTKRSC GTTOSGSENEASPVKRPRILENTERSEETSRSKQKSRRRCFQCCOT KLELVQGSLGSCCGVYFOCHKRLPEGCGCTTDHMSGRGEBGAIN MWKLDRXVGTSCGRIGGGCS  6519 3 1113 ERKMAPPSFSVENGGGGGGGSNRQLQPPAAPSPQSYGSPAS MSFAPLSAAPSBSSSRSSFFFFAGTAVPSSASASLSQGPGFKLL VPPTLIHAQPHHILLIPAAAAANANAKSRRVKRKKKKKKK WNEIKKRKGKVKKKKKKKKKK WNEIKKRKKKKKKKK WNEIKKRKKKKKKKK WNEIKKRKKKKKKKKK WNEIKKRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ł			IKLLPEEPFLYYLKGRYCYTVSKLSWIEKKMAATLFGKIPSSTV
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ACTRITILISAGKPIRKVCIGLEMIKKPTOGGATANLETGGFIR SQPGVVPPDIOPHILPSGVJDHGRVPTQGATVQVHVGPRGTSV GWLKLRSAMPQDHPVIQPNYLSTETDIEDFRLCVKLTREIFAGE ALAPFRGKELQPGSHIQSKKELDAFVRAKADSAYHPSCTCKMGQ PSDPTAVVDPQTRVLGVENLRVVDASHMSMSMYHPSCTCKMGQ PSDPTAVVDPQTRVLGVENLRVVDASHMSMSMYHPSCTCKMGQ PSDPTAVVDPQTRVLGVENLRVVDASHMSMSMYHPSCTCKMGQ PSDPTAVVDPQTRVLGVENLRVVDASHMSMSMYHPSCTCKMGQ PSDPTAVVDPQTRVLGVENLRVVDASHPSTGNDASHTINAN EKAADIIKGQPALMBKDVPVYKPRTLATQR PAMMPDSSEPTRVERPRAFSPFDJPPDRAPRRERHRLLRAVPGPSE RHRCRRRAPPPSTMCDAGSBRSKAPSLPPRCPCGFMGSSKTMN LCSKCFADFQKKQPDDDASBRSKAPSLPPRCPCGFMGSSKTMN LCSKCFADFQKKQPDDDASBRSKAPSLPPRCPCGFMGSSKTMN LCSKCFADFQKKQPDDDASBPSTNSQSDLFSETTSDNNTSIST TPPLSPSQPLPTELNVTSPSKEEGGFCTDTARVSLITPTKRSC GTDSGSENBASPVKRPRLLENTERSEETSSKKKSRRRCCPCCT KLELVQOELGSCRCGVYFCMLRRLEDGCTPTDHMSRGREEAIM MMVKLDRKVGRSCGRIGEGCS AKKVRTEEKKAPRRVSGEGSGGNSCLQPPAAPSPQSYGSPAS WSFADLSAAPSPSSRSSFSFSAGTAVPSSASASLSQFGPRKLL VPPTLHAQPHHLLIPAAAAASANARFPKEKKEKERRRHGL GGAREAGGASREENGEVKPLRPADIKTDLIKVKKKKKKKKK WMSEIKKRGEVKILLKSKCKERPKTNELDLIKKVKKKKKKKKK WMSEIKKRGEVKILLKSKCKERPKTNELDLIKVKKKKKKKKKK ENEKRRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIHDVVG KNLDTKNTDSKIPENGEGSGGNSGROLQPPAAPSPQSYGSPAS WSFAPLSAAPSPSSRSSFSFSAGTAVPSSASASLSQFGPRKLL VPPTLHAQPHHLLIPAAAAASANAKSRRPKKREKRRRIGL GGAREAGGASREENGEVKPLPRDKIKTOKIKTEDGLEKKKKKK VNNEIKERNGEVKILLKSGKEKPFTNIEDLGIKKVKKKKKKKKK WNNEIKERNGEVKILLKSGKEKPFTNIEDLGIKKVKKKKKKKKKK WNNEIKENGEVKILLKSGKEKPFTNIEDLGIKKVKKKKKKKKKK WNNEIKENGEVKILLKSGKEKPFTNIEDLGIKKVKKKKKKKKKK WNNEIKENGEVKILLKSGKEKPFTNIEDLGIKKVKKKKKKKKK WNNEIKENGEVKILLKSGKEKPFTNIEDLGIKKVKKKKKKKKKK WNNEIKENGEVKILLKSGKEKPFTNIEDLGIKKVKKKKKKKKK WNNEIKENGEVKILLKSGKEKPFTNIEDLGIKKVKKKKKKKKK WNNEIKENGEVKILLKSGKEKPFTNIEDLGIKKVKKKKKKKKK WNNEIKENGEVKILLKSGKEKPTNIEDLGIKKVKKKKKKKKK WNNEIKENGEVKILLKSGKEKPTNIEDLGIKKVKKKKKKKK WNNEIKENGEVKILLKSGKEKPTNIEDLGIKKVKKKKKKKKH ENEKKRFRAMYSKSIGTICSGLIDTUDGAARGINDNITHDVO KLUDTKNYDSKIPENSEPPFVSKLAGGGGGGNAGGNETURDLIKDVO KNLDTKNYTGSKIPPSKERESENSESSTVEGESVTVEGGENE IRTUNSTRETPFKSKLAGGEGENFERDELEENSSTURKVENSAVDFEGGVALE COURTER PPATSSESERGEPPFFFEREKENKESSETKGBEVGLGSLM	1			EAETLVSRVLFEGTRAVGVEYVKNGQSHRAYASKEVILSGGAIN
SQPGVPRPDIGPHIPSQVIBINGPTQCAYQVHVGPMRGTSV GWLKLRSARPQOHPV1QPNILSTETIDEPRCVKLTREIFAQE ALAPFRGKELQPGSHIQSDKEIDAFVRAKADSAYHPSCTCKMGQ PSDPTAVVDPQTRVLGVENLRVVDASIMPSMYGSGLINAPTIMIA EKAADII KOQPALMBKUDVYVKPRILARUYGS EKAADII KOQPALMBKUDVYVKPRILARUYGS EKAADII KOQPALMBKUDVYVKPRILARUYGSSINAPTIMIA EKAADII KOQPALMBKUDVYVKPRILARUYGSSINAPTIMIA LCSKCFADFQKKQPDDDSAPSTSNSQSDLFSEETTSDNNITSIT TPTLSPSQQPLPTEINVTSPSKEEGGCTDTAHVSLITPTKRSC GTDSQSEWBASPYVKRPKLENTERSEETSSSKQKSRRRCPCQT KLELVQQELGSCRGYVFCMLKRLPEQHDCTFDHMSRGREEAIM MWKLDRAWGRSCORI LOEGGS  6519 3 1113 EKKMAPPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSLS AKKVRTEEKKAPRRVNGEGGSGNSRQLQPPAAPSPQSYGSPAS WSPAPLSAAPSPSSSRSSFSFSAGTAVPSSASASLSQGGPRKLL VPPTLLHAQPHHLLIPAAAAASANAXSRPPEKREKERRRHGL GGAREAGGASREENGEVKPLPRDKIKDKIKKERDKEKERRKKHK VMNEIKKSNGEVKILLKSKKEKPKTNIEDLQIKKVKKKKKKKKK ENEKKRRPKMYSKSIOTICSGLITDVSDQAARGILNDNIKDVYG KNLDTINTDSKIPENSEPFFVSLKEPRVQNNLKRLDTLEFKQLI HIEHQPNGGASVHCLQ UPPTLHAQPHHLLIPAAAAASANAKPREKKEKERRRHGL GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKERERKKHK VMNEIKENGEVKILLKSRKEKPKTNIEDLQIKKVKKKKKKKK ENEKKRRPKMYSKSIOTICSGLITDVSDQAARGILNDNIKDVG WSFAPLSAAPSPSSSSSSFSFSAGTAVPSSASASLSQGGRKLL UPPTLHAQPHHLLIPAAAAASANAKPREKKEKERERRHGL GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEKERRRHGL GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEKERRERHGL GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEKEKERRERGG WSFAPLSAAPSPSSSSSSFSFSAGTAVPSSASASLSQGGRKLL UPPTLHAQPHLLLIPAAAAASANAKFREKKEKERERRIGL GGAREAGGASREENGEVKPLPRDKIKDKIKEKCKKKKKKKK WNNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKK  EENEKKRRPKMYSKSIOTICSGLITDVEDQAARGINDNIKDVG KALUTKNYTORSIPPSSSSSSSSFSFSAGTAVPSSSASSLSQGGEKEL GGAREAGGASREENGEVKPLPPBUKSEESVTVECQSNE TPPATSSEAEQPRGFEENEKENSESETKKDEKDGSKEKEK VKNTIPSSATLASAGLARRQKOTFMASSPRPMBALITEAIKAC FOKSGASVVAIRKYIIHKYPSILLERGFULKQALKREINRGVI KQVKGKGASGSFVVVQKSRKTPQKSRNKNRSSAVDPEPQVKLE DVLPLAFTRLCEPKERSYSSLIRKYVSQYYPKLRVIPRLDELDLKNA LQRAVERGQILGOTTOKRSAGFGFOLKAGSKPLLGSLIMBVALLS AIAANNBFKTCSTTALKKYVLENPGTNSNYOMHLIKKTLARCE KNGMMEDISGKGFGGTPOLKSGERFLLGGSLMBVALDA LQRAVERGQILGOTTOKRSAGFGFOLKSGERFLLGGSLMBVALDA LQRAVERGQILGOTTOKRSAGFTGLKKSG	-			SPOLLMLSGIGNADDLKKLGIPVVCHLPGVGQNLQDHLEIYIQQ
GWLKLRSAMPODHPVIQPNYLISTETILIDERLCVALTREIFAGE ALAPFREKELOPGSHIGSDKEIDAPVARADSAYHSCTCKMGG PSDPTAVVDPOTRVLGUENLRVVDASIMPSMVSGNINAPTIMIA EKAADIIKGOPALMOKDVVVKPRTLATQR  PAWMPGSEPRTRVERPARSEPDLPPRAPARPRRERILLRAVPGPSR RHRCRRRAPPPPSTMGDASSRSKAPSLPPRCTOCPMGSSKTNN LCSKCTRAPPOKOPODDBASPSTMSGSDLFSEETTSDNNTSIT TPTLSPSQOPLPTELNVTSPSKEEGGPCTDTAHVSLITPTKRSC GTDSQSENEASPVKRPRLLENTERSEETSRSKOKSRRCRCPQCTT KLELVQQELGSCRGGYVFCMLRRIPEGHDCTFPHMGRGREEAIM KMVKLDRKVGRSCQRIGEGCS RKMASPPSPFWICVANAAPTATVSEKEPFGKLQLSSRDPPGSLS AKKVRTEEKKAPRRVNGEGGSGNSRQLQPPAAPSPQSYGSPAS WSFAPLSAAPSPSSRSSSPSFSAGTAVPSSASSLSQFGPRKLL VPPTLLHAQPHHLLLPAAAAAASANAKSRPPKEKEEKERRHGL GGAREAGGASREENGEVKPLPRDKIKOKIKERDKKEKEKKKHK VMSEIKKREPKWIKSKSICTICSGLLTDVSDQAARGLINDNIKDYVG KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKKKHKKKKKK ENEKRRPRMYSKSICTICSGLLTDVSDQAARGLINDNIKDYVG KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKREDLEFKQLI HIEHQPNGGASVHCLQ  3 1113 ERRMAEPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPFGSLS AKKVATTEEKKAPRRVNGGGSGGSNSRCLQPPAAPSPGNSSSPAS WSFAPLSAAPSPSSSRSSFSFSAGTAVPSSASALSQFGPRKLL VPPTLHAQPHILLLPAAAAAASANAKSRPKKRERRRRIGL GGAREAGGASREENGEVKPLPROKIKOKIKERDKKKKKKKKKKK ENEKKRRPKYSKSICTICSGLLTDVSDQAARGINDNIKDTVG KVNNEIKKSNGEVKILLKSGKEEPFTNIEDLQIKKVKKKKKKKKK VNNEIKKSNGEVKILLKSGKEEPFTNIEDLQIKKVKKKKKKKKK HENEKKRRPKYMSKSICTICSGLLTDVSDQAARGINDNIKDTVG KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI HEHQPNGGASVHLCQ  6521 184 1798 KLFWAATDTSGGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP IRRTVNSTRETPFKSKLAEGEEERPFPDISSESSVSVEGENE ENEKKRRPKYSKSICTICSGLLTDVSTADAGRINDNIKDTVG KNLDTKNYDSKIPENSEFPFVSKLERRRYSLKKREKKRRING VKNTIPSWATLASSQLARRQKOTPMASSPRPOMALTRAIKAC POKSGASVAVAIRYIIHKYPSLELERRGYLLKQALKREINRGVI KQVKGKGASGSFVVVQKSRKTPGKSRNRKNSSAVPEEQONE TPPATSSERDEPRGFENEKEENNSSTKORKOGSKEKK VKNTIPSWATLASSQLARRQKOTPMASSPRPOMALTRAIKAC POKSGASVAVAIRYIIHKYPSLELERRGYLLKQALKREINRGVI KQVKGKGASGSFVVVQKSRKTPGKSRNRKNSSAVPEPGVKLE DULPLAFTR.CEPKERSYSLIRKYVSGYYPLKUPDLISGLLENG LQRAMERGOLEQTTORGASGFTCLKKSGEKPLLGGSLMBYALLS ALAANDBFKTCSTTALKKYVLENPGTNSNOMBLLKKTLQKCE KRGMMEDISGKGFSGTFCLKKSGEKPLLGGSLMBYALLS ALAANDBFKTCSTTALKKYVLENPGTNSOMOMBLLKKTLOR	1			ACTRPITCHSAQKPLRKVCIGLEWLWKFTGEGATAHLETGGFIR
ALAPFRCKELQPGSHIQSDKRIDAFVRAKABASYNPSCTCKMGQ PSDPTAVVPOOTRYLQSVENIRVUDASIMPSMYSGNINAPTIMIA EKAADIIKGOPALMUKDUPVYKPRTLATQR  6518  242  1098  PAWNPGSERPTRVERPÄKSFPLPPPRAPRREHKLLRAVEGESR RHRCRRAPPPSTINGDAGSERSKAEDPPRCPCOPMGSSKTMN LCSKCFADPOKKOPDDDSABTSINSGSLIPSETTSDNINTSIT TPTLSPSQOPLPTELENTYSPSKEECGFCTDTAHVSLITPTKRSC GTDSQSENEASPVKRPRLLENTERSEETSRKOKSRRRCPCCTT KLELVQOELGSCRCYVYCHHRLPPEQHDCTTPDIMMGREEAIM KMYKLDRKVGRSCORIGEGGS  86519  3 1113  ERKMASPFSPVICVAANAPTATVSEKEPPGKLQLGSRDPPGSLS AKKVRTEEKKAPRRVNGEGGSGGNSRQLQPPAAPSPQSYGSPAS WSFAPLSAAPSPSSSRSSFSFSAGTAVPSSASASLSQPGPRKLL VPPTLLHAQPHHLLIPAAAAASANAKSRRPKKREKERERRHGL GGAREAGGASREENGEVKPLDPROKIKDLKTKKKKKKKKKK ENEKRKRPKMYSKSIQTICSGLITUVEDQAAKGILNDNIKDVVG KNLDTINNDSKIPENSSPPVSLKERPRVQNNLKRLDTLEFKGLI HIEHQPNGASVIHCLQ  ERMMASPPSPVGVAAAAPTATVSEKEPPGKLQLSSRDPPGSLS AKKVRTEEKKAPRRVNGEGGSGGNSRQLQPPAAPSPQSYGSPAS WSFAPLSAAPSPSSSRSSFSFSAGTAVPSSASASLSQPGPRKLL VPPTLLHAQPHHLLIPAAAAASANAKSRRPKKREKERERRIGL GGAREAGGASREENGEVKPLPROKIKDLTSERVCHTERVCH WHEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKK ENEKRKRPKMYSKSIQTICSGLITUVEDQAAKGILNDNIKDVVG KNLDTKNTDSKIPLAAAAAPSANAKSRRPKKREKERERRIGL GGAREAGGASREENGEVKPLPROKIKDKIKEREKKERERKIGL WHEILKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKK ENEKRRPKMYSKSIQTICSGLITUVEDQAAKGILNDNIKDVVG KNLDTKNTDSKIPSNSEFPPVSLKEPRVQNNLKRLDTLEFKQLI HEEQPMGAGSVIHCLQ  VAMEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKKK ENEKRRPKMYSKSIQTICSGLITUVEDQAAKGILNDNIKDVVG KNLDTKNTDSKIPSNSEFPPVSLKERPRVQNNLKRLDTLEFKQLI HEEQPMGAGSVIHCLQ  KLFKMATDTSGGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP IRRTVNTSTRETPPKSKLAEGEEKPPPDISSEESVSTVEEGENE TPPATSSEAGQAVAIRKYIHKYPSLELERRGYLLKQALKERELINGVI KQVKGKGASGSFVVVQKSRKTPQKSRRKNRSSAVDPEPQVKLE DVLPLAFTILEPKEASYSLIRKYVSGYYEKKEVIRROLLKRAL LGRAVERGQLEQITIGKAGSGFTGALKFEVIRFURIRTQLLKNA LORAVERGQLEQITIGKAGSGFTGALKFEVILFORLUFNA LORAVERGQLEQITIGKAGSGFTGALVFPKKEPDDSRDEDE  DEDESSEEDSEDEEPPPKRRLPENGSVLIPPKKEPDDSRDEDE  DEDESSEEDSEDEEPPPKRRLPENGSVLIPPKKEPDDSRDEDE  DEDESSEEDSEDEEPPPKRRLPENGSVLIPPKKEPDDSRDEDE  DEDESSEEDSEDEEPPPKRRLPENGSVLIPPKKEPDDSRDEDEDE  RYSNAGGRARAPLPKKAPPKAKTPAKKTRPSSTVIKK				SQPGVPRPDIQFHFLPSQVIDHGRVPTQQEAYQVHVGPMRGTSV
### PSDPTAVVDPQTRVLGVENLRVUDASINENWIGNILNAPTIMIA ### EKAADI IKGOPALMUKDVPV KUPTLATOR  ### PAWNPGSEPTTRVRPRARSFPLPPPRAPRRERHELLRAVPGPSR RHRCRRAPPPSTMGDAGSERSKAPSLPPRCPCGPMGSSKTM LCSKCFADPGKKQPDDDSAPSTBNOSDLPSETTSINNTSITI TPPTLSPSQOPLPTELLNYTSPSKEECGFCTDTAHVSLITPTKRSC GTDSQSENEASPVKRPRLLENTERSETSRSKGSRRRCFQCOT KLELVQQELGSCRCGYVFCMLHELPRGHDCTFDIMMGREEAIM KMYKLDRKVGRSCORIGEGCS  #### AKVATEEKKAPRRVNGEGGSGNSRQLQPPAAPSPQSYGSPAS WSFAPLSAAPSPSSSRSSFSFSAGTAVPSSASASLSQOFGPKIL VPPTLHAPAPHHLLPAAAAAPANAKGRPKEKREKERRHGL GGAREAGGASREENGEVKPLDFRDKIKDKIKKKKKKKKKK VMNEIKKENGEVKILLKSGKEKPKTNIEDLGIKKVKKKKKKKKK ENEKRRPRMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG KNLDTKNYDSKIPENSFPPVSLKEPFVQNNLKRLDTLEFKQLI HIEHQPNGGASVIHCLQ  ###################################	1			ALADERCKEL ODGGULGODVILSTETDIEDFRLCVKLTREIFAGE
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AKKVRTEEKKAPRRVNGEGGSGGNSRQLGPPAAPSPQSYGSPAS WSFAPLSAAPSPSSRSSRSFSPSAGTAVPSSASASLSOPGPRKLL VPPTLLHAQPHHLLLIPAAAAASANAKSRRPKEKERRRHGL GGAREAGGASREENGEVKPLPRDKIKDKIKGKEKEKEKKKKK VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKKK ENEKRRPKMYSKSIOTICSGLITDVEDQAAKGILNDNIKDYVG KNLDTKNYDSKIPENSBFPFVSLKEPRVQNNLKRLDTLBFKQLI HIEHQPNGGASVIHCLQ  6520 3 1113 ERMMAEPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSLS AKKVRTEEKKAPRRVNGEGGSGGNSRQLQPPAAPSPQSYGSPAS WSFAPLSAAPSPSSSRSSFSFSAGTAVPSSASASLSQPGPRKLL VPPTLLHAQPHHLLLPAAAAAANAKSRPJKKREKERRHGL GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEREKKHK VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKK ENEKRRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG KNLDTKNYDSKIPENSEPFFVSLKEPRVQNNLKRLDTLEFKQLI HIEHQPNGGASVIHCLQ  6521 184 1798 KLFKMATDTSQGELVHPKALPLIVGAQLTHADKLGEKVEDSTMP IRRTVNSTRETPPKSKLAEGEEKPPDISSEESVSTVEPQENE TPPATSSEAEOPKGEPENBEKEENKSSEETKKDEKDQSKEKEK VKKTIPSWATLSASQLARAQKOTPMASSPRPMDAILTEAIKAC FQXSGASVVAIRKYIIHKYPSLELEERRGYLLQALKREINRGVI KQVKGKGASGSFVVVQKSRKTPQKSGNRRNRSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA LQRAVERGQLEQITIGKGASGTFQLKKSGEKPLLGGSLMEYAILS AIAAMNEPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEEDE DEDESSEEDSEDEEPPPKRRLQKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE	6519	3	1113	
WSFAPLSAAPSFSSRSFSFSAGTAVPSSASASLSQPGPRKLL VPPTLLHAQPHHLLLPAAAAASANAKSRRPKEKRERRHGL GGAREAGGASREENGEVKPLPRDKI KDKI KERDKEKEREKKHK VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKKK ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG KNLDTKNYDSKI PENSFPVSLKEPRVQNNIKRLDTLEFKQLI HIEHQPNGGASVIHCLQ  6520 3 1113 ERKMAEPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSLS AKKVRTEEKKAPRRVNGEGGSGGNSRQLQPPAAPSFQSYGSPAS WSFAPLSAAPSFSSSRSSFSFSAGTAVPSSASASLSQPGPRKLL VPPTLLHAQPHHLLLPAAAAASANAKSRRPKEKREKERRHGL GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEREKKHK VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKHK ENEKRRRPKMYSKSIQTICSGLLTDVEDQAAKGIINDNIKDYVG KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI HIEHQPNGGASVIHCLQ  6521 184 1798 KLFKMATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP IRRTVNSTRETPPKSKLAEGEEEKPEPDISSEESVSTVEEQENE TPPATSSEAEQPKGEPENBEKEENKSSETKKDEKDQSKEKEKK VKKTIPSWATLSASQLARAQKOTPMASSPRPMDAILTEAIKAC FOKSGASVVAIRKYI HKYPSLBLERRGYLLKQALKRELNRGVI KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRRYVSQYYPKLRVDIRPQLLKNA LQRAVERGQLEQITGKGASGSTFQLKKSGEKPLLGSILMEYALLS AIAAMNEPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE DEDESSEEDSEDEEPPPKRRLQKKTPAKSFGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE	į.	i i		AKKVRTEEKKAPRRVNGEGGSGGNSRQLQPPAAPSPOSYGSPAS
VPPTLLHAQPHHLLLPAAAAASANAKSRRPKEKREKERRHGL GGAREAGGASREENGEVKPLPROKIKOKIKERDKEKEREKKKHK VMMEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKK ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILMDNIKDYVG KNLDTKNYDSKIPENSBFPPVSLKEPRVQNNLKRLDTLBFKQLI HIEHQPNGGASVIHCLQ 6520 3 1113 ERMAEPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSLS AKKVRTEEKKAPRRVNGBGGSGGNSRQLQPPAAPSFQSYGSPAS WSFAPLSAAPSFSSSRSSFSFSAGTAVPSSASASLSQPGPRKLL VPPTLLHAQPHHLLLPAAAAASANAKSRRPKEKKEKERRHGL GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEREKKKHK VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKH ENEKRRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI HIEHQPNGGASVIHCLQ  6521 184 1798 KLFKMATDTSQGELVHPKALPLTVGAQLIHADKLGEKVEDSTMP IRRTVNSTRETPPKSKLAEGEEEKPEPDISSEESVSTVEEQENE TPPATSSEASQPKGEPENBEKENKSSEETKKDEKDQSKEKEKK VKKTIPSWATLSASQLARAQKQTPMASSPRPKMDAILTEAIKAC FQKSGASVVAIRKYIIHKYPSIELERRGYLLKQALKREINRGVI KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS AIAAMBPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE				WSFAPLSAAPSPSSSRSSFSFSAGTAVPSSASASLSOPGPRKLL
VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKHK ENEKRKRPKMYSKSIQTICSGLITDVEDQAAKGILNDNIKDYVG KNLDTKNYDSKIPENSBFPFVSLKEPRVQNNLKRLDTLBFKQLI HIEHQPNGGASVIHCLQ  3 1113 ERKMAEPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDFPGSLS AKKVRTEEKKAPRRVNGBGGSGGNSRQLQPPAAPSPQSYGSPAS WSFAPLSAAPSPSSSRSSFSFSAGTAVPSSASASLSQPGPRKLL VPPTLLHAQPHHLLLPAAAAAASANAKSRPKKKREKERRHGL GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEERKKHK VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKHK ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG KNLDTKNYDSKIPENSEPFFVSLKEPRVQNNLKRLDTLEFKQLI HIEHQPNGGASVIHCLQ  6521 184 1798 KLFKMATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP IRRTVNSTRETPPKSKLAEGEEEKPEPDISSESVSTVEEQENE TPPATSSEAEQPKGEPENBEKEENKSSEETKKDEKDQSKEKEKK VKKTIPSWATLSASQLARAQKOTPMASSPRPKMDAILTEAIKAC FQKSGASVVAIRKYIIHKYPSLELERRGYLLKQALKRELNRGVI KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA LQRAVERGQLEDJTGKGASGTFQLKKSGEKPLLGGSLMEYAILS AIAAMNEPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE	į			VPPTLLHAQPHHLLLPAAAAAASANAKSRRPKEKREKERRRHGI.
ENEKRKEPEMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG KNLDTKNYDSKIPENSEFFFVSLKEPRVQNNLKRLDTLEFKQLI HIEHQPNGGASVIHCLQ  ERMMAEPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSLS AKKVRTEEKKAPRRVNGEGGSGGNSRQLQPPAAPSPQSYGSPAS WSFAPLSAAPSPSSSRSSFSFSAGTAVPSSASASLSQPGPRKLL VPPTLLHAQPHHLLLPAAAAASANAKSRPKKKEKERRRHGL GGAREAGGASRBENGEVKPLPRDKIKDKIKERDKKEKEREKKKKK VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKHK ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI HIEHQPNGGASVIHCLQ  KLFKMATDTSQEELVHPKALPLIVGAQLIHADKLGEKVEDSTMP IRRTVNSTRETTPKSKLAEGEEEKPEPDISSESVSTVEEQENE TPPATSSEAEQPKGEPENBEKEENKSSETKKDEKDGSKEKEKK VKKTIPSWATLSASQLARAQKOTPMASSPRPMDAILTEAIKAC FQKSGASVVAIRKYIHKYPSLELERRGYLLKQALKRELNRGVI KQVKGKGASGSFVVVSRKTPQKSRNRNKNSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS AIAAMNEPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGMMEQISGKGFSGTFQLCFPYYPSFGVLFFKKEPDDSRDEDE DEDESSEEDSEDEEPPPKRRLQKKTPAKSPCKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE	ľ	İ		GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEREKKKHK
KNIDTKNYDSKI PENSEFPFVSLKEPRVQNNIKRLDTLEFKQLI HIEHQPNGGASVIHCLQ  ERMMÆFPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDFPGSLS AKKVRTEEKKAPRRVNGEGGSGGNSRQLQPPAAPSPQSYGSPAS WSFAPLSAAPSPSSSRSSFSFSAGTAVPSSASASLSQPGPRKLL VPPTLLHAQPHHLLLPAAAAASANAKSRRPKBKREKERRHGL GGAREAGGASREENGEVKPLPRDKI KDKI KERDKEKEREKKRHK VMNE I KKENGEVKI LLKSGKEKPKTNI EDLQI KKVKKKKKKHK ENEKRKPKMYSKSIQTI CSGLLTDVEDQAAKGI LMDNI KDYVG KNLDTKNYDSKI PENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI HIEHQPNGGASVIHCLQ  KLFKMATDTSQGELVHPKALPLI VGAQLIHADKLGEKVEDSTMP IRRTVNSTRETPPKSKLAEGEEEKPEPDI SSEESVSTVEEQENE TPPATSSEAEQPKGEPENBEKEENKSSEETKKDEKDQSKEKEKK VKKTI PSWATLSASQLARAQKQTPMASSPRPKMDAILTEAIKAC FQKSGASVAIRKYI IHKYPSLELERRGYLLKQALKRELNRGVI KQVKGKGAGSGFVVVQKSRKTPQKSRNRKNRSSADPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDI RPQLLKNA LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGS LMEYAILS AIAAMNEPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGWMEQI SGKGFSGTFOLCFPYYPSPGVLFPKKEPDDSRDEDE DEDESSEEDSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE				VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKKK
HIEHQPNGGASVIHCLQ  ERKMAEPPSPVHCVAAAAPTATVSEKEPPGKLQLSSRDPPGSLS AKKVRTEEKKAPRRVNGEGGGGGNSRQLQPPAAPSPQSYGSPAS WSFAPLSAAPSPSSSRSSFSFSAGTAVPSSASASLSQPGPRKLL VPPTLLHAQPHHLLLPAAAAASANAKSRPKEKKEKERRRHGL GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEREKKKHK VMNEIKKEMGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKHK ENEKRKPKMYSKSIQTICSGLJTDVEDQAAKGILNDNIKDYVG KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI HIEHQPNGGASVIHCLQ  6521  184  1798  KLFKMATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP IRRTVNSTRETPPKSKLAEGEEEKPEPDISSEESVSTVEEQENE TPPATSSEAEQPKGEPENBEKEENKSSEETKKDEKDQSKEKEKK VKKTIPSWATLSASQLARAQKOTPMASSPRPKMDAILTEAIKAC FQKSGASVVAIRKYIIHKYPSLELERRGYLLKQALKRELNRGVI KQVKGKGASGSFVVVVQKSRKTPQKSRNRKNRSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS AIAAMMEPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFSGTFQLCFPYYPSFGVLFPKKEPDDSRDEDE DEDESSEEDSEDEEPPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKKATPAKKTRPSSTVIKKPSGGSS KKPATSARKE				ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG
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AKKVRTEEKKAPRRVNGEGGSGGNSRQLQPPAAPSPQSYGSPAS WSFAPLSAAPSPSSRSSFSFSAGTAVPSSASASLSQPGPRKILL VPPTLLHAQPHHLLLPAAAAASANAKSRPKEKREKERRHGL GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEREKKKHK VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKHK ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI HIEHQPNGGASVIHCLQ  6521 184 1798 KLFKMATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP IRRTVNSTRETPPKSKLAEGEEEKPEPDISSEESVSTVEEQENE TPPATSSEAEQPKGEPENBEKEENKSSEETKKDEKDQSKEKEKK VKKTIPSWATLSASQLARAQKOTPMASSPRPKMDAILTEAIKAC FQKSGASVVAIRKYIIHKYPSLELERRGYLLKQALKRELNRGVI KQVKGKGASGSFVVVQKSRKTPQKSRNKRNSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS AIAAMNSPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE	6520	<u> </u>	1112	
WSFAPLSAAPSPSSRSSFSFSAGTAVPSSASASLSQPGPRKLL VPPTLHAQPHHLLLPAAAAASANAKSRRPKBKREKERRHGL GGAREAGGASRBENGEVKPLPRDKIKKDKKEREKKEKKHK VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKHK ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI HIEHQPNGGASVIHCLQ  KLFKMATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP IRRTVNSTRETPPKSKLAEGEEEKPEPDISSESVSTVEEQENE TPPATSSEAEQPKGEPENBEKEENKSSETKKDEKDQSKEKEKK VKKTIPSWATLSASQLARAQKQTPMASSPRPKMDAILTEALKAC FQKSGASVVAIRKYIHKYPSLELERRGYLLKQALKRELNRGVI KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS AIAAMMEPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE	0.220	,	1113	EKKMAEPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSLS
VPPTLLHAQPHHLLLPAAAAASANAKSRRPKBKREKERRHGL GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEREKKHK VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKHK ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG KNLDTKNYDSKIPENSEPPFVSLKEPRVQNNLKRLDTLEFKQLI HIEHQPNGGASVIHCLQ  6521 184 1798 KLFKMATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP IRRTVNSTRETPPKSKLAEGEEEKPEPDISSEESVSTVEEQENE TPPATSSEAEQPKGEPENBEKEENKSSEETKKDEKDQSKEKEKK VKKTIPSWATLSASQLARAQKOTPMASSPRPKMDAILTEAIKAC FQKSGASVVAIRKYIIHKYPSLELERRGYLLKQALKRELNRGVI KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLIKNA LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS AIAAMNSPKTCSTTALKKYVLENNPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFSTFQLCFPYYPSPGVLFPKKEPDDSRDEDE DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE				AAAVKTEEKKAPRRVNGEGGGGGNSRQLQPPAAPSPQSYGSPAS
GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEREKKKHK VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKHK ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI HIEHQPNGGASVIHCLQ  6521 184 1798 KLFKMATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP IRRTVNSTRETPPKSKLAEGEEEKPEPDISSEESVSTVEEQENE TPPATSSEAEQPKGEPENBEKEENKSSEETKKDEKDQSKEKEKK VKKTIPSWATLSASQLARAQKOTPMASSPRPKMDAILTRAIKAC FQKSGASVVAIRKYIIHKYPSLELERRGYLLKQALKRELNRGVI KQVKGKGASGSFVVVQKSRKTPQKSRNKRNSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS AIAAMNSPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE				UDDITE LUNODULL LENNANDA DE COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DEL COMPANIO DEL COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DEL COMPANIO DEL COMPANIO DE LA ANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL
VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKHK ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGIINDNIKDYVG KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI HIEHQPNGGASVIHCLQ  KLFKMATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP IRRTVNSTRETPPKSKLAEGEEEKPEPDISSEESVSTVEEQENE TPPATSSEAEQPKGEPENBEKEENKSSEETKKDEKDQSKEKEKK VKKTIPSWATLSASQLARAQKOTPMASSPRPKMDAILTEAIKAC FQKSGASVVAIRKYIIHKYPSLELERGYLLKQALKREINRGVI KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLIKNA LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS AIAAMNSPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE		Ì		GGAPFAGGASPRENGEURDI BERTARANAKSKRPKEKERRRHGL
ENEKRKPFKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG KNLDTKNYDSKIPENSEFFFVSLKEPRVQNNLKRLDTLEFKQLI HIEHQPNGGASVIHCLQ  KLFKMATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP IRRTVNSTRETPPKSKLAEGEEEKFEPDISSESSVSTVEEQENE TPPATSSEAEQPKGEPENBEKEENKSSEETKKDEKDQSKEKEKK VKKTIPSWATLSASQLARAQKOTPMASSPRPKMDAILTEAIKAC FQKSGASVVAIRKYIIHKYPSLELERRGYLLKQALKREINRGVI KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS AIAAMNEPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE				WWILL KKENGEAKTI'I KECKEADAMITEDI OTAMIAMI
KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI HIEHQPNGGASVIHCLQ  KLFKMATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP IRRTVNSTRETFPKSKLAEGEEEKPEPDISSESVSTVEEQENE TPPATSSEAEQPKGEPENBEKEENKSSEETKKDEKDQSKEKKK VKKTIPSWATLSASQLARAQKQTPMASSPRPKMDAILTEAIKAC FQKSGASVVAIRKYIIHKYPSLELERRGYLLKQALKRELNRGVI KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS AIAAMNEPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE	1			ENEKERE PRMYSKSIOTIOSGLI TOUTON A KOLINDULKOVIK
HIEHQPNGGASVIHCLQ  KLFKMATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP IRRTVNSTRETPPKSKLAEGEEEKPEPDISSESVSTVEEQENE TPPATSSEAEQPKGEPENBEKEENKSSEETKKDEKDQSKEKK VKKTIPSWATLSASQLARAQKQTPMASSPRPKMDAILTEAIKAC FQKSGASVVAIRKYIHKYPSLELERRGYLLKQALKRELNRGVI KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS AIAAMNEPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE	1 1			KNLDTKNYDSKIPENSEEDEVSLVEDDVONNI VDI DTI EEVOLI
184 1798 KLFKMATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP IRRTVNSTRETPPKSKLAEGEEEKPEPDISSEESVSTVEEQENE TPPATSSEAEQPKGEPENBEKEENKSSEETKKDEKDQSKEKEKK VKKTIPSWATLSASQLARAQKOTPMASSPRPKMDAILTEAIKAC FQKSGASVVAIRKYIIHKYPSLELERRGYLLKQALKREINRGVI KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS AIAAMNSPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE				HIEHOPNGGASVIHCLO
IRRTVNSTRETPPKSKLAEGEEEKPEPDISSEESVSTVEEQENE TPPATSSEAEQPKGEPENBEKEENKSSEETKKDEKDQSKEKEKK VKKTIPSWATLSASQLARAQKOTPMASSPRPKMDAILTEAIKAC FQKSGASVVAIRKYIIHKYPSLELERRGYLLKQALKRELNRGVI KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS AIAAMNSPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE	6521	184	1798	KLFKMATDTSOGELVHPKALPLIVGAOLTHADKI.GEVIPDOWARD
TPPATSSEAEQPKGEPENBEKEENKSSEETKKDEKDQSKEKEKK VKKTI PSWATLSASQLARAQKOTPMASSPRPKMDAILTEAIKAC FQKSGASVVAIRKYI IHKYPSLELERGYLLKQALKREINRGVI KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLIKNA LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS AIAAMNSPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE		,		IRRTVNSTRETPPKSKLAEGEERKPEPDISSERSVSTVPFORME
VKKTIPSWATLSASQLARAQKOTPMASSPRPKMDAILTEAIKAC FQKSGASVVAIRKYIIHKYPSLELERRGYLLKQALKRELNRGVI KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS AIAAMNEPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFSGTFQLCFPYYPPSPGVLFPKKEPDDSRDEDE DEDESSEBDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE				TPPATSSEAEOPKGEPENBEKEENKSSEETKKDRKDOGVEVEVV
FQKSGASVVAIRKYIIHKYPSLELERRGYLLKQALKRELNRGVI KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS AIAAMNEPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFSGTFQLCFPYYPPSPGVLFPKKEPDDSRDEDE DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE			ļ	VKKTIPSWATLSASQLARAQKQTPMASSPRPKMDATLTFATVAC
KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS AIAAMBPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFSGTFQLCFPYYPPSPGVLFPKKEPDDSRDEDE DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE		ĺ		FQKSGASVVAIRKYIIHKYPSLELERRGYLLKOALKPEINDGUT
DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA LQRAVERQQLEQITOKGASGTFQLKKSGEKPLLGGSLMEYAILS AIAAMNEPKTCSTTALKKYVLENHPGTINSNYQMHLLKKTLQKCE KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE			ļ	KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPOVKI.E
LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS AIAAMNSPKTCSTTALKKYVLENNPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE				DVLPLAFTRLCEPKEASYSLIRKYVSOYYPKLRVDIRPOLLKNA
AIAAMNEPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE				LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSIMEVATIS
KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE				ALAAMNEPKTCSTTALKKYVLENHPGTNSNYOMHLLKKTLOKCE
DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE				KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE
PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS KKPATSARKE		1		DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA
KKPATSARKE				PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS
5522 1042 391 NKWLRPSPRSHRTPESGRVLSLFRLPPPGMALSGSTPAPCWEED				KKPATSARKE
	6522	1042	391	NKWLRPSPRSHRTPESGRVLSLFRLPPPGMALSGSTPAPCWEED

	·	1 5 . 1/	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
	· · · · · · · · · · · · · · · · · · ·		ECLDYYGMLSLHRMFEVVGGQLTECELELLAFLLDEAPGAAGGL
ĺ			SRARSGLKLLLELERRGQCDESNLRLLGQLLRVLARHDLLPHLA
			RKRRPVSPERYSYGTSSSSKRTEGSCRRRQSSSSANSQQGSP
		}	PTKRORRSRGRPSGGARRRRRGPQPHPSSSQSPPDLPLKAK
6523		1097	ASCOTRRTAALDSGERIAGRRSPIALAMASNFNDIVKOGYVKI
6523	2	1097	<del>-</del>
ĺ			RSRKLGIFRRCWLVFKKASSKGPRRLBKFPDEKAAYFRNFHKVT
		1	ELHNIKNITRLPRETKKHAVAIIFHDETSKTFACESELEAEEWC
i			KHLCMECLGTRLNDISLGEPDLLAAGVQREQNERFNVYLMPTPN
			LDIYGECTMQITHENIYLWDIHNAKVKLVMWPLSSLRRYGRDST
			WFTFESGRMCDTGEGLFTFQTREGEMIYQKVHSATLAIAEQHER
1		1	LMLEMEQKARLQTSLTEPMTLSKSISLPRSAYWHHITRQNSVGE
l		1	IYSLQGNHENRHSDLTGKSCKTSENRFLEENAPLVMYGITHHLF
i			MDTSTCKVVHDLE
6524	2	1097	ASCOTRRTAALDSGERIAGRRSPIALAMASNFNDIVKQGYVKI
	_		RSRKLGIFRRCWLVFKKASSKGPRRLEKFPDEKAAYFRNFHKVT
			ELHNIKNITRLPRETKKHAVAIIFHDETSKTFACESELEAEEWC
	ł		KHLCMECLGTRLNDISLGEPDLLAAGVOREONERFNVYLMPTPN
]			LDIYGECTMQITHENIYLWDIHNAKVKLVMWPLSSLRRYGRDST
			WFTFESGRMCDTGEGLFTFQTREGEMIYQKVHSATLAIAEQHER
Į.			LMLEMEQKARLQTSLTEPMTLSKSISLPRSAYWHHITRQNSVGE
1			IYSLQGNHENRHSDLTGKSCKTSENRFLEENAPLVMYGITHHLF
			MDTSTCKVVHDLE
6525	1	1859	GESPFSEBESIEFNPSSSGRSARTVSSNSFCSDDTGWPSSQSVS
			PVKTPSDAGNSPIGFCPGSDEGFTRKKCTIGMVGEGSIQSSRYK
	ì		KESKSGLVKPGSEADFSSSSSTGSISAPEVHMSTAGSKRSSSSR
			NRGPHGRSNGASSHKPGSSPSSPREKDLLSMLCRNQLSPVNIHP
i		1	SYAPSSPSSSNSGSYKGSDCSPIMRRSGRYMSCGENHGVRPPNP
ŀ			EQYLTPLQQKEVTVRHLKTKLKESERRLHERESEIVELKSQLAR
İ			MREDWIEEECHRVEAQLALKEARKEIKQLKQVIETMRSSLADKD
			KGIQKYFVDINIQNKKLESLLQSMEMAHSGSLRDELCLDFPCDS
			PEKSLTLNPPLDTMADGLSLEEOVTGEGADRELLVGDSIANSTD
l		1	LFDEIVTATTTESGDLELVHSTPGANVLELLPIVMGQEEGSVVV
			ERAVQTDVVPYSPAISELIQSVLQKLQDPCPSSLASPDESEPDS
			MESFPESLSALVVDLTPRNPNSAILLSPVETPYANVDAEVHANR
	1		LMRELDFAACVEERLDGVIPLARGGVVROYWSSSFLVDLLAVAA
ľ	İ	ì	PVVPTVLWAFSTQRGGTDPVYNIGALLRGCCVVALHSLRRTAFR
			IKT
6526	2	2034	SGRAGEPEEWRGRQIIDSKETWIPFNSEDSQQLEEAYSSGKGCN
	1		GRVVPTDGGRYDVHLGERMRYAVYWDELASEVRRCTWFYKGDKD
			NKYVPYSESFSQVLEETYMLAVTLDEWKKKLESPNREIIILHNP
1	1		KLMVHYQPVAGSDDWGSTPMEQGRPRTVKRGVENISVDIHCGEP
			LQIDHLVFVVHGIGPACDLRFRSIVQCVNDFRSVSLNLLQTHFK
	1		KAQENQQIGRVEFLPVNWHSPLHSTGVDVDLQRITLPSINRLRH
		1	FTNDTILDVFFYNSPTYCQTIVDTVASEMNRIYTLFLQRNPDFK
1 .			GGVSIAGHSLGSLILFDILTNOKDSLGDIDSEKGSLNIVMDQGD
	1		TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQBIGIP
			LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN
			TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL
			KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI
			PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY
1			PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPINV
1			GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV
			LKEIYQTQGIFLDQPLQ
6527	1	922	GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCQRGDLS
1			FIFNGDAAPSESFVVLDNEQKVYQRIHHEESEMBTEEEVDILMS
		Į.	SDIYSATLSTKSISFTRAQTGWLFREDKTERVGNFLADFYLVNG

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
<b></b>			LVLESRKRREHLSEEDILRNKAIMESLSKGGNIMEONFEPIRRO
ĺ			SLTPPPONTITWEEYISAENGKAPHLGRELVCKESKKTFKATIA
1			MSQEFPLGIELLLNVLEVVAPFKHFNKLREFVQMKLPPGFPVKL
ļ			DIPVFPTITATVTFOEFRYDEFDGSIFTIPDDYKEDPSRFPDL
6528	1 1	1073	LTGPAAAEPRCAADAGMKRALGRRKGVWLRLRKILFCVLGLYIA
""	_		IPFLIKLCPGIQAKLIFLNFVRVPYFIDLKKPQDQGLNHTCNYY
Ì	1		LOPEEDVTIGVWHTVPAVWWKNAQGKDQMWYEDALASSHPIILY
)		Ì	LHGNAGTRGGDHRVELYKVLSSLGYHVVTFDYRGWGDSVGTPSE
			RGMTYDALHVFDWIKARSGDNPVYIWGHSLGTGVATNLVRRLCE
			RETPPDALILESPFTNIREEAKSHPFSVIYRYFPGFDWFFLDPI
1		1	TSSGIKFANDENVKHISCPLLILHAEDDPVVPFQLGRKLYSIAA
]			PARSFRDFKVQFVPFHSDLGYRHKYIYKSPELPRILREFLGKSE
			PEHOH
6529	363	2215	THIRYNKIGVVKTMSCGNEFVETLKKIGYPKADNLNGEDFDWLF
0329		****	EGVEDESFLKWFCGNVNEQNVLSERELEAFSILQXSGKPILEGA
			ALDEALKTCKTSDLKTPRLDDKELEKLEDEVOTLLKLKNLKIOR
	1		RNKCOLMASVTSHKSLRLNAKEEEATKKLKQSQGILNAMITKIS
			NELQALTDEVTQLMMFFRHSNLGQGTNPLVFLSQFSLEKYLSQE
			EOSTAALTLYTKKOFFOGIHEVVESSNESOFFNFLKIOTPSICD
}			NOEILEERRLEMARLQLAYICAQHQLIHLKASNSSMKSSIKWAE
			ESLHSLTSKAVDKENLDAKISSLTSEIMKLEKEVTQIKDRSLPA
			VVRENAQLLNMPVVKGDFDLQIAKQDYYTARQELVLNQLIKQKA
ł			SFELLQLSYEIELRKHRDIYRQLENLVQELSQSNMMLYKQLEML
ļ			TDPSVSQQINPRNTIDTKDYSTHRLYQVLEGENKKKELFLTHGN
ŀ			LEEVAEKLKQNISLVQDQLAVSAQEHSFFLSKRNKDVDMLCDTL
			YQGGNQLLLSDQELTEQFHKVESQLNKLNHLLTDILADVKTKRK
ļ			TLANNKLHQMEREFYVYFLKDEDYLKDIVENLETQSKIKAVSLE
		L	D
6530	128	2986	GAAHHGAIVQVHPLLPGSSTIMIHDLCLVFPAPAKAVVYVSDIQ
1 .	.}		ELYIRVVDKVEIGKTVKAYVRVLDLHKKPFLAKYFPFMDLKLRA
1			ASPIITLVALDEALDNYTITFLIRGVAIGQTSLTASVTNKAGQR
			INSAPQQIEVFPPFRLMPRKVTLLIGATMQVTSEGGPQPQSNIL
ļ			FSISNESVALVSAAGLVQGLAIGNGTVSGLVQAVDAETGKVVII
			SQDLVQVEVLLLRAVRIRAPIMRMRTGTQMPIYVTGITNHQNPF
	1		SFGNAVPGLTFHWSVTKRDVLDLRGRHHEASIRLPSQYNFAMNV
			LGRVKGRTGLRAVVKAVDPTSGQLYGLARELSDEIQVQVFEKLQ
			LLNPEIEAEQILMSPNSYIKLQTNRDGAASLSYRVLDGPEKVPV
			VHVDEKGFLASGSMIGTSTIEVIAQEPFGANQTIIVAVKVSPVS
			YLRVSMSPVLHTQNKEALVAVPLGMTVTFTVHFHDNSGDVFHAH
			SSVLNFATNRDDFVQIGKGPTNNTCVVRTVSVGLTLLRVWDAKH
			PGLSDFMPLPVLQAISPELSGAMVVGDVLCLATVLTSLEGLSGT
1	ļ		wsssansilhidpktgvavaravgsvtvyyevaghlrtykevvv
			SVPQRIMARHLHPIQTSFQEATASKVIVAVGDRSSNLRGECTPT
1			QREVIQALHPETLISCQSQFKPAVFDFPSQDVFTVEPQFDTALG
			QYFCSITMHRLTDKQRKHLSMKKTALVVSASLSSSHFSTEQVGA
}		1	EVPFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGS
}			PAVLAFAKEKSFGWPSFITYTVGVLDPAAGSQGPLSTTLTFSSP
1	1	1	VTNQAIAIPVTVAFVVDRRGPGPYGASLFQHFLDSYQVMFFTLF
			ALLAGTAVMIIAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS
1		1	SPTSPNALPPARKASPPSGLWSPAYASH
1			
6531	845	1,425	PSASTPPSASPDPVPDIRTCHFCLVEDDSVGCTSGSEKCTTSSS
6531	845	1425	FSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS
6531	845	1425	SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFAEYWYQA
6531	845	1425	SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFAEYWYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL
6531	845	1425	SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFAEYWYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS
6531	845	1425	SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFAEYWYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL

	·	Daniel Brass and	Amino acid segment containing signal peptide
SEQ	Predicted beginning	Predicted end nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid'		Codon, /=possible nucleotide deletion,
1	1	sequence	\=possible nucleotide insertion)
	sequence		ITDSTGTHLVLTVTNKNAHSPGLSRGSPQQPSSQPGSPAPAPSA
1		}	OMDLEHPLOPLFGTPTSLLKKEPPGYEEAMSQQPKQQENGSSSQ
ì			OMDDLFDILIOSGEISADFKEPPSLPGKEKPSPKTVCWSPLAAQ
ŀ	ļ	1	PSPSAELPQAAPPPPGSPSLPGRLEDFLESSTGLPLLTSGHDGP
i	1		EPLSLIDDLHSQMLSSTAILDHPPSPMDTSELHFVPEPSSTMGL
	}		DLADGHLDSMDWLELSSGGPVLSLAPLSTTAPSLFSTDFLDGHD
		Í	LOLHWDSCL
L	1700		STISWLARVEPPRRSSGVGAARLRPPGGSRPLRARACVLALAVL
6533	1798	373	STISWLARVEPPRRSSGVGAARLRFPGGSRPLRARACVLALAVL ALLERNNADSMSAHSMLCERIAIAKELIKRAESLSRSRKGGIEG
	1	1	GAKLCSKLKAELKFLOKVEAGKVAIKESHLOSTNLTHLRAIVES
	1	1	AENLEEVVSVLHVFGYTDTLGEKQTLVVDVVANGGHTWVKAIGR
	1	!	KAEALHNIWLGRGQYGDKSIIEQAEDFLQASHQQPVQYSNPHII
1	1	i	FAFYNSVSSPMAEKLKEMGISVRGDIVAVNALLDHPEELQPSES
			ESDDEGPELLOVTRVDRENILASVAFPTEIKVDVCKRVNLDITT
1		1	LITYVSALSYGGCHFIFKEKVLTEQAEQERKEQVLPQLEAFMKD
		1	KELFACESAVKDFQSILDTLGGPGERERATVLIKRINVVPDQPS
1	1		ERALRIVASSKINSRSLTIFGTGDTLKAITMTANSGFVRAANNQ
1			GVKFSVFIHOPRALTESKEALATPLPKDYTTDSEH
6537	4.7	596	KATRFISAAFVVLNKQGVSPAKLPHTSWSWSLQTLSFLFSGDLA
6534	47	596	EKSLOCFPCSAMLLELIPLLGIHFVLRTARAQSVTQPDIHITVS
1			EGASLELRCNYSYGATPYLFWMERTVEEAFILLVCLKPWRVASS
1			LEKKEKEDESFOLLLGSRYNVLKAHCLLPLIRWLTSGDSLLSAQ
			PHCPOGL
6535	250	964	LIKTFFRDVAIORDLLPKEKNLETLLTLAFLEIDKAFSSHARLS
6535	250	704	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL
			TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD
1			LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW
			DFVNOCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN
1			SEINFSFSRSFASSGRWA
6536	242	1174	SLVKEMTNOYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS
0536	-72		LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS
			LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV
1		<b>\</b>	GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI
		1	INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK
1			IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW
			DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC
		1	PI
6537	1638	921	NRFNPPPTQGPDPSLVYRPDVDPEVAKDKASFRNYTSGPLLDRV
6531	1020	321	FTTYKLMHTHQTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV
1			DESDPDVDFPNSFHAFQTAEGIRKAHPDKDWFHLVGLLHDLGKV
			LALFGEPQWAVVGDTFPVGCRPQASVVFCDSTFQDNPDLQDPRY
	1		STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG
			AEAVPAGDTLSPQSTCTR
6538	3345	2412	PYLYDFLDALITCOTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE
6538	3343	2412	ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYPMV
Ì	(		EKIFRKSVEFCNDHDVWKLNVAHVLFMQENKYKEAIGFYEPIVK
1			KHYDNILNVSAIVLANLCVSYIMTSQNEKAEELMRKIEKEEEQL
1	[		SYDDPNRKMYHLCIVNLVIGTLYCAKGNYBFGISRVIKSLEPYN
			KKLGTDTWYYAKRCFLSLLENMSKHMIVIHDSVIQECVQFLGHC
1	1	1	ELYGTNIPAVIEQPLEEERMHVGKNTVTDESRQLKALIYEIIGW
			NK NK
(530	1-316	770	FLGAASPHPHFSSLAPHPDQPEFTPVQDELEAMELWGPGV
6539	218	339	
6540	3	391	LERLWILLLRRPEDAMAECPTLGEAVTDHPDRLWAWEKFVYLDE KOHAWLPLTIEIKDRLQLRVLLRREDVVLGRPMTPTQIGPSLLP
1	1		
L	<u> </u>		IMWQLYPDGRYRSSDSSFWRLVYHIKIDGVEDMLLELLPDD

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	n=nistidine, i=isoleucine, k=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of		S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6541	1165	536	RTLVQRRILMLLRKPARGRDLRGRGRGTPRGGRKGLLPTPDEFP
	j		RFEGGRKPDSWDGNREPGPGHEHFRDTPRPDHPPHDGHSPASRE
			RSSSLQGMDMASLPPRKRPWHDGPGTSBHREMEAPGGPSEDRGG
			KGRGGPGPAQRVPKSGRSSSLDGEHHDGYHRDEPFGGPPGSGTP
			SRGGRSGSNWGRGSNMNSGPPRRGASRGGGRGR
6542	3	3775	SWPRGRGETGGHPGALRTRTMQKSVRYNEGHALYLAFLARKEGT
1			KRGFLSKKTAEASRWHEKWFALYQNVLFYFEGEQSCRPAGMYLL
			EGCSCERTPAPPRAGAGQGGVRDALDKQYYFTVLFGHEGQKPLE
			LRCEEEQDGKEWMEAIHQASYADILIERBVLMQKYIHLVQIVET
1			EKIAANQLRHQLEDQDTEIERLKSEIIALNKTKERMRPYQSNQE
}			DEDPDIKKIKKVQSFMRGWLCRRKWKTIVQDYICSPHAESMRKR
			NQIVFTMVEAESEYVHQLYILVNGFLRPLRMAASSKKPPISHDD
			VSSIFLNSETIMFLHEIFHQGLKARIANWPTLILADLFDILLPM
1			LNIYQEFVRNHQYSLQVLANCKQNRDFDKLLKQYEANPACEGRM
ļ			LETFLTYPMFQIPRYIITLHELLAHTPHEHVERKSLEFAKSKLE
			ELSRVMHDEVSDTENIRKNLAIERMIVEGCDILLDTSOTFIROG
1			SLIQVPSVERGKLSKVRLGSLSLKKEGERQCFLFTKHFLICTRS
)			SGGKLHLLKTGGVLSLIDCTLIEEPDASDDDSKGSGQVFGHLDF
ł			KIVVEPPDRAAFTVVLLAPSRQEKAAWMSDISQCVDNIRCNGLM
1			TIVEEENCE TO THE TOTAL OF THE PROPERTY
			TIVFEENSKVTVPHMIKSDARLHKDDTDICFSKTLNSCKVPQIR
			YASVERLLERLTDLRFLSIDFLNTFLHTYRIFTTAAVVLGKLSD
Í			IYKRPFTSIPVRSLELFFATSQNNRGEHLVDGKSPRLCRKFSSP
ŀ			PPLAVSRTSSPVRARKLSLTSPLNSKIGALDLTTSSSPTTTTQS
j			PAASPPPHTGQIPLDLSRGLSSPEQSPGTVEENVDNPRVDLCNK
			LKRSIQKAVLESAPADRAGVESSPAADTTELSPCRSPSTPRHLR
l			YRQPGGQTADNAHCSVSPASAFAIATAAAGHGSPPGFNNTERTC
			DKEFIIRRTATURVLUVLRHWVSKHAQDFELUNELKMUVLULLE
			EVLRDPDLLPQERKAAANILMALSQDDQDDIHLKLEDIIQMTDC
1		l	MKAECFESLSAMELAEQITLLDHVIFRSIPYEEFLGQGWMKLDK
			NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIEKWVAV
	}		ADICRCLHNYNGVLEITSALNRSAIYRLKKTWAKVSKQTKALMD
1	1	+	KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAFIEEGT
1	İ		PNFTEEGLVNFSKMRMISHIIREIRQFQQTSYRIDHQPKVAOYL
			LDKDLIIDEDTLYELSLKIEPRLPA
6543	1857	950	FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCTHPLDL
1			LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASLCRQMT
			YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLAGGFVG
			TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEGLRRLF
			SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIFTHFVA
		•	SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVETAKLGP
			LAFYKGLVPAGIRLIPHTVLTFVFLEQLRKNFGIKVPS
6544	630	79	
		,,	PSPCFIRSRLDGQPWMAGLEAWLSQNFSLHQPQSRVRVRRASIS EPSDTDPEPRTLNPSPAGWFVQQHPBLELMSSFRERFGRNWLQY
			DEAL BECKEL DESERVATION DOT BETT COCCUSION SELECTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
			RSHLBPSGNPLPATPTTSAPSAPPASSQGPDTAPRPSPPQBEAR
[ ·		1	GPQESPQKMSEEVRAEPQEEEE3KEGKEEKEEGEMAPLPEAHLG
6545	177		EGKQKECP
0345	176	560	PPHSHAALLPAAMTPLLTLILVVLMGLPLAQALDCHVCAYNGDN
[		Ì	CFNPMRCPAMVAYCMTTRTYYTPTRMKVSKSCVPRCFETVYDGY
			SKHASTTSCCQYDLCNGTGLATPATLALAPILLATLWGLL
6546	1657	364	HLLNGLDEVAAFFVADLGAIVRKHFCFLKCLPRVRPFYAVKCNS
		ļ	SPGVLKVLAQLGLGFSCANKAEMELVQHIGIPASKIICANPCKQ
			IAQIKYAAKHGIQLLSFDNEMELAKVVKSHPSAKMVLCIATDDS
1	1		HSLSCLSLKFGVSLKSCRHLLENAKKHHVEVVGVSFHIGSGCPD
			PQAYAQSIADARLVFEMGTELGHKMHVLDLGGGFPGTEGAKVRF
			EEIASVINSALDLYFPEGCGVDIFAELGRYYVTSAFTVAVSIIA
			KKEVLLDQPGREEENGSTSKTIVYHLDEGVYGIFNSVLFDNICP
			The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s

SEQ Predicted Predicted end Amino acid segment containing s	
ID beginning nucleotide (A=Alanine, C=Cysteine, D=Aspar	tic Acid E-
NO: nucleotide location Glutamic Acid, F=Phenylalanine,	G-Glycine
location corresponding H=Histidine, I=Isoleucine, K=Lys	d-drycine,
corresponding to first L=Leucine, M=Methionine, N=Aspar	sine,
to first amino acid P=Proline, Q=Glutamine, R=Argin:	ragine,
amino acid residue of S=Serine, T=Threonine, V=Valine	ine,
residue of amino acid W=Trvptophan. Y=Tvrosine, X=Unks	,
	nown, *=Stop
amino acid sequence Codon, /=possible nucleotide de	letion,
sequence \=possible nucleotide insertion	
TPILQKKPSTEQPLYSSSLWGPAVDGCDCVA	
LVFDNMGAYTVGMGSPFWGTQACHITYAMSR	VAWEALRRQLMAA
EQEDDVEGVCKPLSCGWEITDTLCVGPVFTP	
6547 1 541 LHSKYLAPALCSQPGMMRCCRRRCCCRQPPHI	ALRPLLLLPLVLL
PPLAAAAAGPNRCDTIYQGFAECLIRLGDSMC	GRGGELETICRSW
NDFHACASQVLSGCPEEAAAVWESLQQRARQI	APRPNNLHTLCGA
PVHVRERGTGSETNQETLRATAPALPMAPAP	
RPLA	
6548 2 219 FVSRLSVRDVRFPTFLGGHGADAMHTDPDYS	AVVDIETDAEDG
IKGCGITFTLGKGTEVGELKILSRFONA	DILVI INIDANDO
6549 73 1490 ETGRVCEDARPACGSRSRRRRKEAAPGIPTPS	December
ARAFSKAPARLSRPRAREEPPDPGRRYIQEE	
SSVAAKLWFLTDRRIREDYPQKEILRALKAKO	
DEVVLTIEQGNLGLRINGELITAYPQVVVVRV	
VLRHLEKMGCRLMNRPQAILNCVNKFWTFQEI	
YGGHENFAKMIDEAEVLEFPMVVKNTRGHRGI	
DLSHLIRHEAPYLFQKYVKESHGRDVRVIVVC	
DGRMQSNCSLGGVGMMCSLSEQGKQLAIQVSN	
MKDDGSFCVCEANANVGFIAFDKACNLDVAG	
RLTRRMSLLSVVSTASETSEPELGPPASTAVI	
PESTERELLTKLPGGLFNMNQLLANEIKLLVI	
6550 2293 922 FRVSRDGAPDCGIEQMGLAMEHGGSYARAGGS	SRGCWYYLRYFF
LFVSLIQFLIILGLVLFMVYGNVHVSTESNLQ	ATERRAEGLYSQ
LLGLTASQSNLTKELNFTTRAKDAIMQMWLNF	ARRDLDRINASFR
QCQGDRVIYTNNQRYMAAIILSEKQCRDQFKI	MNKSCDALLFML
NQKVKTLEVEIAKEKTICTKDKESVLLNKRVA	EEQLVECVKTRE
LQHQERQLAKEQLQKVQALCLPLDKDKFEMDI	RNLWRDSIIPRS
LDNLGYNLYHPLGSELASIRRACDHMPSLMSS	
IERVARENSDLQRQKLEAQQGLRASQEAKQKV	
AECSRQTQLALEEKAVLRKERDNLAKELEEKK	
RNSALDTCIKTKSQPMMPVSRPMGPVPNPQPI	
LESQRPPAGIPVAPSSG	DIJEGUAL INCOME
6551 157 748 IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFI	ADDI.MECCVEVE
ADTVDLNWCVISDMEVIELNKCTSGQSFEVIL	
ASLPRRRDPSLEEIQKKLEAAEERRKYQEAEL	
EVIQKAIEENNNFIKMAKEKLAQKMESNKENR EKDKHAEEVRKNKELKERASR	PYUTHWAITEKTÖ
	3 D D 3 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
TO THE TOTAL PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION OF THE PARTICULAR DESIGNATION	
ADTVDLNWCVISDMEVIBLNKCTSGQSFEVIL	
ASLPRRRDPSLEEIQKKLEAAEERRKYQEAEL	
EVIQKAIEENNNFI KMAKEKLAQKMESNKENR	EAHLAAMLERLQ
EKDKHAEEVRKNKELKEEASR	
6553 2 1807 FVWSKMAAHLSYGRVNLNVLREAVRRELREFL	
EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRL	
RPRLELMDIIAENVLSEDRRGPTRDFHILFVP	
LGVLGSFIHREEYSLDLIPFDGDLLSMESEGA	
LYHAAKGLMTLQALYGTIPQIFGKGECARQVA	NMMIRMKREFTG
SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYE	GLIDEIYGIONS
. YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNS	
FNAVGSVLSKKAKIISAAFEERHNAKTVGEIK	
RGSLANHTSIAELIKDVTTSEDFFDKLTVEQE	1
YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQK	
YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIR	
QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSI	
EERQPLPTGLQKKRQPGENRVTLIFFLGGVTF.	
	" TOOUT LIDOU
EDGGTEYVIATTKLMNGTSWIEALMEKPF	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	bequeee	\=possible nucleotide insertion)
6554	119	1244	FEMGSQVSVESGALHVVIVGGGFGGIAAASQLQALNVPFMLVDM
6554	113	1	KDSFHHNVAALRASVETGFAKKTFISYSVTFKDNFRQGLVVGID
			LKNOMVLLOGGEALPFSHLILATGSTGPFPGKFNEVSSQQAAIQ
\			AYEDMVROVORSRFIVVVGGGSAGVEMAABIKTEYPEKEVTLIH
			SOVALADKELLPSVRQEVKEILLRKGVQLLLSERVSNLEELPLN
	}	}	EYREYIKVOTDKGTEVATNLVILCTGIKINSSAYRKAFESRLAS
			SGALRVNEHLOVEGHSNVYAIGDCADVRTPKMAYLAGLHANIAV
	1		ANIVNSVKORPLOAYKPGALTFLLSMGRNDGVGQISGFYVGRLM
			VRLTKSRDLFVSTSWKTMRQSPP
6555	1552	498	IHMALLRKINOVLLFLLIVTLCVILYKKVHKGTVPKNDADDESE
9355	1332	170	TPEELEEEIPVVICAAAGRMGATMAAINSIYSNTDANILFYVVG
]			LRNTLTRIRKWIEHSKLREINFKIVEFNPMGLKGKIRPDSSRPE
	1	•	LLOPLNFVRFYLPLLIHOHEKVIYLDDDVIVQGDIQELYDTTLA
		•	LGHAAAFSDDCDLPSAQDINRLVGLQNTYMGYLDYRKKAIKDLG
<b>{</b>		1	ISPSTCSFNPGVIVANMTEWKHQRITKQLEKWMQKNVEENLYSS
[			SLGGGVATSPMLIVFHGKYSTINPLWHIRHLGWNPDARYSEHFL
ł			OEAKLLHWNGRHKPWDFPSVHNDLWESWFVPDPAGIFKLNHHS
6556	241	1449	ASLCKGCFFVTHVLVIILPSLQSPPTFGFLLDIDGVLVRGHRVI
0556	241	1117	PAALKAFRRLVNSOGOLRVPVVFVTNAGNILOHSKAQELSALLG
Ì			CEVDADQVILSHSPMKLFSEYHEKRMLVSGQGPVMENAQGLGFR
			NVVTVDELRMAFPLLDMVDLERRLKTTPLPRNDFPRIEGVLLLG
			EPVRWETSLOLIMDVLLSNGSPGAGLATPPYPHLPVLASNMDLL
ł			WMAEAKMPRFGHGTFLLCLETIYOKVTGKELRYEGLMGKPSILT
			YQYAEDLIRRQAERRGWAAPIRKLYAVGDNPMSDVYGANLFHQY
i			LOKATHDGAPELGAGGTRQQQPSASQSCISILVCTGVYNPRNPQ
Ť	i .		STEPVLGGGEPPFHGHRDLCFSPGLMEASHVVNDVNEAVQLVFR
			KEGWALE
6557	2598	1534	RMCGRTSCHLPRDVLTRACAYQDRRGQQRLPEWRDPDKYCPSYN
0337	1000		KSPOSNSPVLLSRLHFEKDADSSERIIAPMRWGLVPSWFKESDP
			SKLOFNTTNCRSDTVMEKRSFKVPLGKGRRCVVLADGFYEWQRC
1			QGTNQRQPYFIYFPQIKTEKSGSIGAADSPENWEKVWDNWRLLT
			MAGIFDCWEPPEGGDVLYSYTIITVDSCKGLSDIHHRMPAILDG
1	Ì	Ì	EEAVSKWLDFGEVSTQEALKLIHPTENITFHAVSSVVNNSRNNT
			PECLAPVDLVVKKELRASGSSQRMLQWLATKSPKKEDSKTPQKE
			ESDVPQWSSQFLQKSPLPTKRGTAGLLEQWLKREKEEEPVAKRP
			YSQ
6558	21	1138	FHGRRRGGRKMELGSCLEGGREAAEEBGEPEVKKRRLLCVEFAS
		1	VASCDAAVAQCFLAENDWEMERALNSYFEPPVEESALERRPETI
			SEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSLITWNID
		I	GLDLNNLSERARGVCSYLALYSPDVIFLQEVIPPYYSYLKKRSS
1		1	NYEIITGHEEGYFTAIMLKKSRVKLKSQEIIPFPSTKMMRNLLC
1	1		VHVNVSGNELCLMTSHLESTRGHAAERMNQLKMVLKKMQEAPES
1	1	İ	ATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWD
			TOMNSNLGITAACKLRFDRIFFRAAAEEGHIIPRSLDLLGLEKL
		1	DCGRFPSDHWGLLCNLDIIL
6559	3	364	GPELSGLPTRPKKLKANQTPIAMDCCASRSCSVPTGPATTICSS
			DKSCRCGVCLPSTCPHTVWLLEPTCCDNCPPPCHIPQPCVPTCF
I		1	LLNSCQPTPGLETLNLTTFTQPCCEPCLPRGC
6560	3	1435	TATSGGIWLRRKWRCHWPRPLPQSCVGTEGGLQVRDTSSRIAKG
1			GVDHTKMSLHGASGGHERSRDRRRSSDRSRDSSHERTESQLTPC
1	1		IRNVTSPTRQHHVEREKDHSSSRPSSPRPQKASPNGSISSAGNS
			SRNSSQSSSDGSCKTAGEMVFVYENAKEGARNIRTSERVTLIVD
			NTRFVVDPSIFTAQPNTMLGRMFGSGREHNFTRPNEKGEYEVAB
1			GIGSTVFRAILDYYKTGIIRCPDGISIPELREACDYLCISFEYS
			TIKCRDLSALMHELSNDGARRQFEFYLEEMILPLMVASAQSGER
	1		ECHIVVLTDDDVVDWDEEYPPQMGEEYSQIIYSTKLYRFFKYIE
		<del></del>	

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	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,    -possible nucleotide insertion)
	sedgetice		NRDVAKSVLKERGLKKIRLGIEGYPTYKEKVKKRPGGRPEVIYN
			YVQRPFIRMSWEKEEGKSRHVDFQCVKSKSITNLAAAAADIPQD
			QLVVMHPTPQVDBLDILPIHPPSGNSDLDPDAQNPML
6561	3	1086	PGRRFRRKESSSSRWFPADCLLGLRGPASSLLSPEPSPSWPSHS
			PCPMAALTDLSFMYRWFKNCNLVGNLSEKYVFITGCDSGFGNLL
	1		AKQLVDRGMQVLAACFTEEGSQKLQRDTSYRLQTTLLDVTKSES
			IKAAAQWVRDKVGEQGLWALVNNAGVGLPSGPNEWLTKDDFVKV
			INVNLVGLIEVTLHMLPMVKRARGRVVNMSSSGGRVAVIGGGYC
	İ		VSKFGVEAFSDSIRRELYYFGVKVCIIEPGNYRTAILGKENLES
			RMRKLWERLPQETRDSYGEDYFRIYTDKLKNIMQVAEPRVRDVI NSMEHAIVSRSPRIRYNPGLDAKLLYIPLAKLPTPVTDFILSRY
			LPRPADSV
6562	1	1562	MSTLYDIRAHKAQLLRFFASSDSNKALEQRRTLHTPKLEHLDRV
	_		LYEWFLGKRSEGVPVSGPMLIEKAKDFYEQMQLTEPCVFSGGWL
			WRFKARHGIKKLDASSEKQSADHQAAEQFCAFFRSLAAEHGLSA
			EQVYNADETGLFWRCLPNPTPEGGAVPGPKQGKDRLTVLMCANA
			TGSHRLKPLAIGKCSGPRAFKGIQHLPVAYKAQGNAWVDKEIFS
			DWFHHIFVPSVREHFRTIGLPEDSKAVLLLDSSRAHPQEAELVS
			SNVFTIFLPASVASLVQPMEQGIRRDFMRNFINPPVPLQGPHAR
			YNMNDAIFSVACAWNAVPSHVFRRAWRKLWPSVAFAEGSSSEEE
			LEAECFPVKPHNKSFAHILELVKEGSSCPGQLRQRQAASWGVAG REAEGGRPPAATSPAEVVWSSBKTPKADQDGRGDPGEGEEVAWE
			QAAVAFDAVLRFAERQPCFSAQEVGQLRALRAVFRSOOOVRRRR
		ļ	GALGAVVKVEALQEGPGGCGATAQSPLPCSSTAGDN
6563	1319	2694	LARPAQPVLLREPEGAGPPVPAGHLVHHLQGGHLRERAHPDLEA
		ļ	HEHPLPCDQMFWRQMGGHLRMVBANSRGVVWGIGYDHTAWVYTG
			GYGGGCFQGLASSTSNIYTQSDVKCVHIYENQRWNPVTGYTSRG
İ			LPTDRYMWSDASGLQECTKAGTKPPSLQWAWVSDWFVDFSVPGG
			TDQEGWQYASDFPASYHGSKTMKDFVRRRCWARKCKLVTSGPWL
		}	EVPPIALRDVSIIPESPGAEGSGHSIALWAVSDKGDVLCRLGVS
			ELNPAGSSWLHVGTDQPFASISIGACYQVWAVARDGSAFYRGSV
			YPSQPAGDCWYHIPSPPRQRLKQVSAGQTSVYALDENGNLWYRQ GITPSYPQGSSWEHVSNNVCRVSVGPLDQVWVIANKVQGSHSLS
			RGTVCHRTGVQPHEPKGHGWDYGIGGGWDHISVRANATRAPRSS
			SQEQEPSAPPEAHGPVCC
6564	1	975	APGSCALWSYCGRGWSRAMRGCQLLGLRSSWPGDLLSARLLSOE
	!		KRAAETHFGFETVSEEEKGGKVYQVFESVAKKYDVMNDMMSLGI
	1		HRVWKDLLLWKMHPLPGTQLLDVAGGTGDIAFRFLNYVQSQHQR
			KQKRQLRAQQNLSWEEIAKEYQNEEDSLGGSRVVVCDINKEMLK
	1		VGKQKALAQGYRAGLAWVLGDAEELPFDDDKFDIYTIAFGIRNV
			THIDQALQEAHRVLKPGGRFLCLEFSQVNNPLISRLYDLYSFQV
	İ		IPVLGEVIAGDWKSYQYLVESIRRFPSQEEFKDMIEDAGFHKVT
6565	1464	999	YESLTSGIVAIHSGFKL RSAVANGLTKRRMGLKLNGRYISLILAVQIAYLVQAVRAAGKCD
	-30.		AVFKGFSDCLLKLGDSMANYPOGLDDKTNIKTVCTYWEDFHSCT
			VTALTDCQEGAKDMWDKLRKESKNLNIQGSLFELCGSGNGAAGS
	1		LLPAFPVLLVSLSAALATWLSF
6566	3	1385	KYESAQPGGTQPEPGLGARMAIHKALVMCLGLPLFLFPGAWAQG
			HVPPGCSQGLNPLYYNLCDRSGAWGIVLEAVAGAGIVTTFVLTI
			ILVASLPFVQDTKKRSLLGTQVFFLLGTLGLFCLVFACVBKPDF
			STCASRRFLFGVLFAICFSCLAAHVFALNFLARKNHGPRGWVIF
	1		TVALLLTLVEVIINTEWLIITLVRGSGEGGPQGNSSAGWAVASP
			CAIANMDFVMALIYVMLLLLGAFLGAWPALCGRYKRWRKHGVFV
			LLTTATSVAIWVVWIVMYTYGNKQHNSPTWDDPTLAIALAANAW
			AFVLFYVIPEVSQVTKSSPEQSYQGDMYPTRGVGYETILKEQKG
L	L		QSMFVENKAFSMDEPVAAKRPVSPYSGYNGQLLTSVYQPTEMAL

NO: nu lo co to am	edicted ginning cleotide cation	Predicted end nucleotide location	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
lo co to am		location	Glutamic Acid F-Phenylalanina C-Glucia
co to am	cation		orgenize vera, r-riterlyrarantine, G=GlyClne,
to am		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
am	rresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
! !	ino acid	residue of	S=Serine, T=Threonine, V=Valine,
i re	sidue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
am	ino acid	sequence	Codon, /=possible nucleotide deletion,
se	quence	_	\=possible nucleotide insertion)
			MHKVPSEGAYDIILPRATANSQVMGSANSTLRAEDMYSAQSHQA
			ATPPKDGKNSQVFRNPYVWD
6567	125	863	TKRSNLKAYACSIHHIRTMSYVFVNDSSQTNVPLLQACIDGDFN
			YSKRLLESGFDPNIRDSRGRTGLHLAAARGNVDICQLLHKFGAD
			LLATDYQGNTALHLCGHVDTIQFLVSNGLKIDICNHQGATPLVL
			AKRRGVNKDVIRLLESLEEQEVKGFNRGTHSKLETMQTAESESA
1			MESHSLLNPNLQQGEGVLSSFRTTWQEFVEDLGFWRVLLLIFVI
			ALLSLGIAYYVSGVLPFVENQPELVH
6568	3	1183	HASDRLLVLPDNYSHFSQASANLQGPSRTTELFHPTLASISSPM
			LEGAELYFNVDHGYLEGLVRGCKASLLTQQDYINLVQCETLEDL
			KIHLQTTDYGNFLANHTNPLTVSKIDTEMRKRLCGEFBYFRNHS
			LEPLSTFLTYMTCSYMIDNVILLMNGALQKKSVKEILGKCHPLG
			RFTEMEAVNIAETPSDLFNAILIETPLAPFPQDCMSENALDELN
			IELLRNKLYKSYLEAFYKFCKNHGDVTAEVMCPILEFEADRRAF
			IITLNSFGTELSKEDRETLYPTFGKLYPEGLRLLAQAEDFDQMK
			NVADHYGVYKPLFEAVGGSGGKTLEDVFYEREVQMNVLAFNRQF
1			HYGVFYAYVKLKEQEIRNIVWIAECISQRHRTKINSYIPIL
6569	205	1532	RRRGPORLGHGRPTPLLCRWRTAGPSHWEKQARAFQGLRPVDPR
			RMSWLFPLTKSASSSAAGSPGGLTSLQQQKQRLIESLRNSHSSI
			AEIQKDVEYRLPFTINNLTININILLPPQFPQEKPVISVYPPIR
			HHLMDKQGVYVTSPLVNNFTMHSDLGKIIQSLLDEFWKNPPVLA
i I			PTSTAFPYLYSNPSGMSPYASQGFPFLPPYPPQEANRSITSLSV
			ADTVSSSTTSHTTAKPAAPSFGVLSNLPLPIPTVDASIPTSQNG
1			FGYKMPDVPDAFPELSELSVSQLTDMNEQEEVLLEQFLTLPQLK
1			QIITDKDDLVKSIEELARKNLLLEPSLEAKRQTVLDKYELLTQM
			KSTFEKKMQRQHELSESCSASALQARLKVAAHEAEEESDNIAED
			FLEGKMEIDDFLSSFMEKRTICHCRRAKEEKLQQAIAMHSQFHA
			PL
6570	330	1304	ARLPRLTFLREGFLYVLLSHWVFVGAPRPPASDSWKKGLVPSAP
1			PASRKMGSKALPAPIPLHPSLQLTNYSFLQAVNTFPATVDHLQG
			LYGLSAVQTMHMNHWTLGYPNVHEITRSTITEMAAAQGLVDARF
l 1			PFPALPFTTHLFHPKQGAIAHVLPALHKDRPRFDFANLAVAATQ
			EDPPKMGDLSKLSPGLGSPISGLSKLTPDRKPSRGRLPSKTKKE
			FICKFCGRHFTKSYNLLIHERTHTDERPYTCDICHKAFRRQDHL
			RDHRYIHSKEKPFKCQECGKGFCQSRTLAVHKTLHMQTSSPTAA
			SSAAKCSGETVICGGT
6571	169	656	APDMNRKKLQKLTDTLTKNCKHLFRGFDKDNDGCVNVLEWIHGL
			SLFLRGSLEEKMKYCFEVFDLNGDGFISKEEMFHMLKNSLLKQP
			SEEDPDEGIKDLVEITLKKMDHDHDGKLSFADYBLAVREETLLL
L			EAFGPCLPDPKSQMEFEAQVFKDPNEFNDM
6572	49	1646	TPERAQPGALLGAAGCCVCGGRWWPRSHERGYFSSAKMGSKRRN
			LSCSERHQKLVDENYCKKLHVQALKNVNSQIRNQMVQNENDNRV
			QRKQFLRLLQNEQFELDMEEAIQKAEENKRLKELQLKQEEKLAM
			ELAKLKHESLKDEKMRQQVRENSIELRELEKKLKAAYMNKERAA
			QIAEKDAIKYEQMKRDAEIAKTMMEEHKRIIKEENAAEDKRNKA
1			KAQYYLDLEKQLEBQEKKKQBAYEQLLKEKLMIDEIVRKIYBED
1			QLEKQQKLEKMNAMRRYIEEFQKEQALWRKKKREEMEEENRKII
			EFANMQQQREEDRMAKVQENBEKRLQLQNALTQKLEEMLRQRED
]			LEQVRQELYQEEQAEIYKSKLKEEAEKKLRKQKEMKQDFEEQMA
j			LKELVLQAAKEEEENFRKTMLAKFAEDDRIELMNAQKQRMKQLE
			HRRAVEKLIEERRQQFLADKQRELEEWQLQQRRQGFINAIIEEE
			RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI
			CEEK
6573	767	275	GGGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK
			LFLDFFRRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL
1			TRKLSQRPTVEELRERKILIRFSDYVEVADAQDYDRRADKPWTR

			1 2 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
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			LTAADKVSRGECWRVGGRTVCWVSLGSPLGSV
6574	204	1159	LESSVPVSVGVFWACGVSWTGAAGLQDGALSDTMARNAEKAMTA
55.1			LARFROAQLEEGKVKERRPFLASECTBLPKAEKWRRQIIGEISK
	1		KVAOIQNAGLGEFRIRDLNDEINKLLREKGHWEVRIKELGGPDY
	ì		GKVGPKMLDHEGKEVPGNRGYKYFGAAKDLPGVRELFEKEPLPP
			PRKTRAELMKAIDFEYYGYLDEDDGVIVPLEQEYEKKLRAELVE
			KWKAERBARLARGEKEEEEEEEEEINIYAVTEEESDEEGSQEKG
			GDDSQCKFIAHVPVPSQCEIEEALVRRKKMELLQKYASETLQAQ
			SEEARRLLGY
<u> </u>		000	
6575	117	820	SPALASQSGGITEBKMLEPQENGVIDLPDYEHVEDBTFPPFPPP
		1	ASPERODGEGTEPDEESGNGAPVPVPPKRTVKRNIPKLDAQRLI
]		1	SERGLPALRHVFDKAKFKGKGHEAEDLKMLIRHMEHWAHRLFPK
1		1	LQFEDFIDRVEYLGSKKEVQTCLKRIRLDLPILHEDFVSNNDEV
l		1	AENNEHDVTSTELDPFLTNLSESEMFASELSISLTEEQQQRIER
L			NKQLALERRQAKLP
6576	1	1060	PEPQALVGQKRGALRLLVARLVLTVSAPAEVRRRVLRPVLSWMD
1			RETRALADSHFRGLGVDVPGVGQAPGRVAFVSEPGAFSYADFVR
			GFLLPNLPCVFSSAFTQGWGSRRRWVTPAGRPDFDHLLRTYGDV
}			VVPVANCGVQEYNSNPKEHMTLRDYITYWKEYIQAGYSSPRGCL
1			YLKDWHLCRDFPVEDVFTLPVYFSSDWLNEFWDALDVDDYRFVY
		ì	AGPAGSWSPFHADIFRSFSWSVNVCGRKKWLLFPPGQBEALRDR
			HGNLPYDVTSPALCDTHLHPRNQLAGPPLBITQEAGEMVFVPSG
			WHHQVHNLVMCCFSCPLSGAFLQEDGSTTSPLSQPELGWNGVAH
ļ			G
6577	2271	987	SDRMASDDFDIVIEAMLEAPYKKEEDEQQRKEVKKDYPSNTTSS
			TSNSGNETSGSSTIGETSNRSRDRDRYRRRNSRSRSPGRQCRHR
			SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF
			REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV
İ			GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG
l			VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED
Ī			MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL
			EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG
l			RFQLMAKLAEGAGIQLPSTAAAAAAAAAAAAAAAALQLNGAVPLGA
		J	LNPAALTALSPALNLASQCLQLSSLFTPQTM
6578	377	1489	PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA
53,6	]		LOIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL
1			VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFIG
			MITPNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA
			LLTCGIIIGGFWLGVDQBGAEGTLSWLGTVFGVLASLCVSLNAI
			YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLLGELQALRDF
			AOLGSAHFWGMMTLGGLFGFAIGYVTGLOIKFTSPLTHNVSGTA
			KACAQTVLAVLYYEETKSFLWWTSNMMVLGGSSAYTWVRGWEMK
	<u> </u>	ļ- <del></del>	KTPEEPSPKDSEKSAMGV
6579	2	711	RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYFTSSSVNSSAYT
			IYMGKDKYENEDLIKHGWPEDIWFHVDKLSSAHVYLRLHKGENI
			EDIPKEVLMDCAHLVKANSIQGCKMNVNVVYTPWSNLKKTADM
			DVGQIGFHRQKDVKIVTVBKKVNEILNRLEKTKVERFFDLAAEK
}			ECRDREERNEKKAQIQEMKKREKEEMKKKREMDELRSYSSLMKV
		<u></u>	ENMSSNQDGNDSDEFM
6580	62	1571	LVALKNWKPKGTNIPAPQSPVFGEAVSGVYMMTKVLGMAPVLGP
			RPPQEQVGPLMVKVEEKEEKGKYLPSLEMFRQRFRQFGYHDTPG
			PREALSQLRVLCCEWLRPEIHTKEQILELLVLEQFLTILPQELQ
1		}	AWVQEHCPESAERAVTLLEDLERELDEPGHQVSTPPNEQKPVWE
			KISSSGTAKESPSSMQPQPLETSHKYESWGPLYIQESGEEQEFA
			QDPRKVRDCRLSTQHEESADEQKGSEAEGLKGDIISVIIANKPE
			ASLERQCVNLENEKGTKPPLQEAGSKKGRESVPTKPTPGERRYI
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Deginning nucleotide location corresponding to first amino acid amino acid sequence to first amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequenc	SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
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TGEKPYKCKECKAPNISSNYNKHRITITEGKPYMCHICGKTPC SKSNLSKHQRVITORGSAP  87681 228 476 RVPLKDLSSTPMASNYTASIAQARKLVEQLMEANIDERKYSKA AADLAMYCEHARAKEPLLITYPVASEPPREKKEPCAIL  6582 1428 718 CFFTKTHCSPVSVPYLSPLVLRKELESILENEGDQVIHTSSFIN QHPITFMILWYFRILDLSNLPGLIHITSECKEVQLPLSSFIN QHPITFMILWYFRILDLSNLPGLIHITSECKEVQLPLSSFIN QHPITFMILWYFRILDLSNLPGLIHITSECKEVQLPLSSFIN QHPITFMILWYFRILDLSNLPGLHVSNLNSHSEKSSLLSEE QQETSTLVETIRGSIQHNNUKPINLLSQMKKEGKKRQRSLSFIN ELSLUSLGERUDININLHGEPREPICVSNNNINSSELBELGKQLDAB ELSLUSLGERUDI IREATMENT SANNINSSELBELGKQLDAB PSASVEMCRCRAPAEL  6583 487 41 RIFFMISGLRFRACTWRPATALWSASLALGISSMHPSPRSISLP LSPMISPDINTGGLSFTALFRSPOSEHATSCPRLHLWRCRAPA RSPSIGERLQVINPSPLINHTHINSGKVLIGUOGRSGGFOBAC SQAGSGAVQGGWNCIF RSPSIGERLQVINPSPLINHTHINSGKVLIGUOGRSGGFOBAC SQAGSGAVQGGWNCIF FSAMLSPSIGERLGVINPSPLINHTHINSGKVLIGUOGRSGGFOBAC SQAGSGAVGGWNCIF FSAMLSPSIGERLGVINPSPLINHTHINSGKVLIGUOGRSGGFOBAC SQAGSGAVGGWNCIF FSAMLSPSIGERLGVINPSPLINHTHINSKYNIMAFNAADKWNFAT MNQARLEBDLSNKKI YQEEEMPESGAGSEFNRKLERBARKKVLINH FSIMQQRRLIDCHOMSONSEKVIGUEGERKSKGGRAGASELRIHDLBDLMSK SDASSAGEGGFOVFREKKSKGRIKASELRIHDLBDLMS SDASSAGGGGVFVFRAKKKAPILKRGGIKKGKKKKKKNSDDEAFFDLS DLDDFSGQEVDYMSDSSSSGBEBESKARAPQGEBGRGVUNG SDASSGEGERKPPEDENSE SDLDSEASSAFFMAKKKTPPKRERKPSGSSGSRSPROTTSPS DLDDFSGGEVDYMSKSSSSGBEBESKARAPQGEBGRKGVDGE DSEESEERKPPEDEKSEERKRAPPGGKKRKRKSSBEDSSE ESDIDSEASSAFFMAKKKTPPKRERKPSGSSRGSRSPROTTSPS GSTSTRAASSALEGGKVSSKAMTNOKHFISHA GSTSTRAASSALEGGKVSSKAMTNOKHFISHA GSTSTRAASSALEGGKVSSKAMTNOKHFISHA GSTSTRAASSALEGGKVSSKAMTNOKHFISHA GSTSTRAASSALEGGKVSSKAMTNOKHFISHA HKKGRAAQKADVILTGARNYQCKINNITVGRAPLLVQDVV TDEMAHFDRRRTPERVVHAKGGAAFGYFEVYHDITKKYSKAKVPE HIGKKTPILAVRSTVAGEGGSADTAVTDRPGFAVYTAVTDRPGFAVYTAVT HKKRTPLAVRSTVAGEGGSADTAVTDRPGFAVYTAVTAVTAVT PURMATPROAETFPRIPTDLITKWPHKNYFILTVOKLVINN PVYTFAVEGLIAPTVTAGSGCGSTSGSKMCGGGGSGCKSC FPYKTDGGIKNASVAGAAFGYFEVYHDITKKYSKAKVPE HIGKKTPILAVRSCHAMTVTGGGGGSSSGKMCGGGGGSGCC GSGGGAGGGCHAUTTGARTYTGGGGGGSSSGC GAGGGGGGGGGGGGGGGGGGGGGGGGGG				
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AADLMAYCEAHAKEDPLUTEVPASEINPFREKKFFCAIL  6582  1428  718  CFTKTHCSPVSVYISGLUKRELESLENEGOVYLTHTSSFIN  QHPIIFWTILWYFRELDLPSNLDGLITTSFHCNEGVQLPLSSLS  QDSKLVYIQLLIMNINLHQEPREPLYVSWENNINSEKSESLISBE  QOESTILVETIRGSIQHNNUTKINLINGQMREGMKRQRSLYRE  ILFLSLVSLGRENIDIEAFDNEYGIAVNSLSSEILBERLGKIDAP  PSASVENCKKCROGAPLI  RIFFMTSGRIENRCTWREPTALWSASILGITSSMHEPSRSISLP  LSMMLSPIPSMTSGLSPTALFREPDISHERTSCPHILLWRCRAPL  RSFSPLGRLQVLPRSPLWYTHNSGKEVLGLQVQRSRSGTGPAC  SQAGSGAVQGSNWCIF  WINQARLERDLSNKKIYQEEEMPSGASSEFNRKKREBARKKYG  IVLKFERFEDDPHLRWNGSGRKFKSKIKKGSDEBAFRKYG  IVLKFERFEDDPHLRWNGSGRKFKSKIKKGSDEBAFRES  PEDHAALGEPSSOWYTEYVVRVPRNTTKKYNIMAFNAADKVNFAT  WINQARLERDLSNKKIYQEEEMPSGASSEFNRKKREBARKKYG  IVLKFERFEDDPHLRWNGSGRKFKKIKKGKGNDEAFPLSYLFITC  CPODAPEAFPVHWYNTFTLARHRITLTAEBAEEEMERRIKVINH  FSI MQORALKDODOEDEEEKBERGRKRASSLHURSTYLFTG  CPODAPEAFPVHWWNTFTPLARHRITLAEBAEEEMERRIKVINH  FSI MQORALKDODOEDEESKERKGRKASSLHURSTYSTYLFTG  CPODAPEAFPVHWWNTFTPLARHRITLAEBAEEEMERRIKYGN  BSADASGEEGGRYVKAKKAPLAKGGKKKKKKKGSDDEAFPDS  GGSTSTLRAAASKLEQGKKWSMSPAARKRIHURJENSTYLFTG  GSSTSTLRAAASKLEQGKKWSMSPAARKRIHURJENSUSSESDISSE  ESDIDSEASSAFPMAKKTPPKRERKPSGGSSRONSPRTPBAE  GGSTSTLRAAASKLEQGKKWSMSPAARKRIHURJENSUSSESDISSE  ESDIDSEASSAFPMAKKTPFKRERKPSGGSSRONSPRTPBAE  GGSTSTLRAAASKLEQGKWSMSPAARKRIHUTDTQCSLSGKST  POPPSKTTPNSGDVQVTEDAVRTLTTKRPMTTKOLLKKFOTKK  TGLSSSCTVANLAQLIKLENBERKMIDTOMHTOLLKKFOTKK  TGLSSSCTVANLAQLIKLENBERKMIDTOMHTOLLKKFOTKK  TGLSSSCTVANLAQLIKLENBERKMIDTOMHTOLLKVRPHUTWSTAKAKFE  HICKKTPIAVRTSTAVAGSGSGADTVRDRRFAVKFYTEGORNDL  VGNNTHFFTIAURTSTAVAGSGSGADTVRDRRFAVKFYTEGORNDL  VGNNTHFFTIAURTSTAVAGSGSGADTVRDRRFAVKFYTEGORNDL  VGNNTHFFTIAURTSTAVAGSGSGADTVRDRRFAVKFYTEGORNDL  GSRCHLCENTIAGLKOAGTIFTOKAGAGAGATVYTVANLNE  EQRKLCENTIAGLKUNGTTFATTHOLTKVSKRAWFE  EQRKLCENTIAGLKUNGTTFATTHOLTKVSKRAWFE  GAPEQOPSALEHSIQVSGEVRRRNTANDDNVTQVARFYVINNE  EQRKLCENTIAGLKUNGTTFATTHOLTKVSKRAWTH  GSSCDAGGGSGKHITVFKTTISTROMGROMAGGGABNTYNNE  GSSCDAGGGSGKHITVFKTTTSTYPDTVLSILL  LFSUBELMNNTELVUSTKRQGTATAVGGRGGADAGG  GGSGAGGGGGGGAGGTATUGGSGAGGGTGGAGGAGTAGVGE  TGSSCDAGGGSGKHITVFKTTTSTYGGLTAWA				
1428	6581	228	476	RVFLKDLSSTPMASNNTASIAQARKLVEQLKMEANIDRIKVSKA
OHPLIFWTLWYPERILDENSIDLITEREKNOSQUPLSISLIS ODSKLYVI JOLLANDINILHOPPEPPLVYSMPNSEKKSILJSEE ODSKLYVI JOLLANDINILHOPPEPPLVYSMPNSEKKSILJSEE OQETSTIVETIRQSIQHNNVLKPINLLSQQMKPGMKRQRSLYRE ILPLSLVSLGRENIDIEAFDNEYGIAYNSLSSEILBRIQKIDA PSASUWMCKPCGAPLI  RIFPMTSGRLEWRCTWRPATALWSASIRLGTSSMHFSPRSISLP RSPSPLGRLQVLPRSPLHWHTHINSGKEVLGLQVQRSRSGTGPAC SQAGSGAVQGOMCIF RSPSPLGRLQVLPRSPLHWHTHINSGKEVLGLQVQRSRSGTGPAC SQAGSGAVQGOMCIF VULKEFREDOPHILENVNGKSGRKFKGIKKGVTEENTSYTITT CPDGAPEAFPVHWWYNFTFLARHRTLTAREAELEWBERNKYVGN FSIMQORRIKCHOODODDEDEEKKRKGRKKKKKGSDEAFPEDS DDGDFGQGEVTYMBIGGSSSOGBPESKKKKGRSDEAFPEDS DDGDFGQGEVTYMBIGGSSSOGBPESKKKGRNEHENTSCHELHDLEDDLEMS SDASDASGEEGGRVYRAKKKAPLLAKGGRKKKKKKGSDEAFPEDS DDGDFGQGEVTYMBIGGSSSOGBPESKKKGRKKERLHDTGDDLEMS SDASDASGEEGGRVYRAKKKAPLLAKGGRKKKKKKGSDEAFPEDS DDSSESSEEHKPPEEDKEEEEKKRGRTAREHDTGPGSLSGKST POPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTDLLKKFFOTKK TGLSSSCTVNVLAQILKKRUPPERMINDMFSKE SDASDASGAGEGGRVVNLAGKGRKSBMPARKARLHDTGPGSLSGKST POPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTDLLKKFFOTKK TGLSSSCTVNVLAQILKKRUPPERMINDMFSKE GFINSRIDDFVGGADPPAGKASCSVLHSKFHAMADSREDASDOMO HIKKSCRAACKADULTTCAGADPVDGKLUNTOPEGPLLVODVF TDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE HIGKKTPIAVEFSTVAGESGSADTVRDPRGFAVKFTEBGINDL VGNNTTIFTIEDITLFPSTIEDITLFTBIENGKRPFGTPLFRAATATGVPSSK TFYIQMTFNQAETFPPPDTLTKVPHKDDPLFVGKLVLUNTAN PVNYFAEVEDIAFDFGARGFFFVNTHATATATATVNTANE PVNYFAEVEDIAFDFGARGFFFVNTHRAGENFOKTHONNTOVRAFTVNTANE CARRECTERIAGHLKDQIFTAVATTHENH LGPNYLHIPVNCPYRARANYQRDGPMCMONQGGAPNYYPNSE GAPEQOPSALHHSIQVSCVARFATANDONNTOVRAFTVNTANE PVNYFAEVEDIAFDFGARGFFTNATHANDNTOVRAFTVNTANE PVNYFAEVEDIAFDFGARGFFTNATHANDNTOVRAFTVNTANE CARRECTERIAGHLKNOGI FTQKKAVKNETSVHPDVGGBIGALLI DKNNARKPRNAIHTFVQSGSHLAAREXANL LGPNYLHIPVNCPYRARANYQRDGPMCMONQGGAPNYYPNSE GAPEQOPSALHHSIQVSCVARFATANDONNTOVRAFTVNTUNB CORKRICCENIGHTNOGICHTAVPTYTISPROMGENFAVIVALDE CARRECTENIGHTNOGICHTAVPTYTISPROMGHANDATALGTATAVTAVTA PVNYFAEVEDIAFDFCKFTDFVGGGAGAGGAGAGTAGVGE TGSGDQAGGGCGHILGSGSGAGGTGGAGAGGAGTAGVGE TGSGDQAGGGCHILTVFTYTISPRPRICKTSKSKNGGGGOAGA GAGAGQCGCAGAGTAGVGE TGSGDQAGGGCHILTVFTYTISPRPRAMGVOPOQ				AADLMAYCEAHAKEDPLLTPVPASENPFREKKFFCAIL
ODSKLIVIOLLAWDINILHQEPREPLYVSWRNFNSEKKSSLLSEE QQETSTLVETIRQSIQHNNVLKPINLLSQQMKFQKKRQSLYRE ILPLSLVSLGRENIDIEAPTOMEYGIAYNSLSSEILBRLQKIDAR PSASVEWCRKCPGAPLI  6583 487 41 RIFSMTSGRERWRCTWRPATALWSASLRLGTSSMHPSPRSISLD LSMMLSPLPSNTRGLSPTALWRSPDSEHATSCPELHLWRCRAPL ESPSPLGRLGULPRSPLHVHTMISGKEVLGLQVQRSRSGTGPAC SQAGSGAVQGONWCIF  6584 189 1750 PLPMAALGESSGWITEYVVRVPKNTTKKYNIMAFNAADKVNFAT WOARLERDLSNKKIYQEEEMPSGAGSSFNKKLREBARKKYG IVLKERPEDOPHILRVNGKSGRKFKGIKKGGVEEMSYYIFTO CPDAAPEAPFVHWNYFTFLARRHTLIBAEEMEKRRYKVLNH FSIMQORRLKDQDODBDEEKEKRGRKASELRIHDLBDLEMS SDADASGEGGRVPKMKKKASPLAKRGSDEAPFSY ESDIDSEASSAFPMAKKKTPFKREKKGSDDEAPFS DDGDFSGGEVPYMSDGSSSSGBPESKARAPQSEGPKGVDEQS DSEESEEREKPPEEDKEEEEKKAPTOGSKRRNGROFDSTDSAE GGSTSSTLRAAASKLEQGKVSBMPAAKRLELDTGPQSLSGKST PQPPSGKTTHNSGDVQTYBPKRFKERKPSGSSGRORRPGTTSPAE GGSTSSTLRAAASKLEQGKVSBMPAAKRLELDTGPQSLSGKST PQPPSGKTTHNSGDVQTYBPKRFKERKPSGSSGSRORRPGTPSAE GGSTSSTLRAAASKLEQGKVSBMPAAKRLELDTGPQSLSGKST PQPPSGKTTHNSGDVQTYBPKRFKERKPSGSSGSRORRPGTPSAE GGSTSSTLRAAASKLEQGKVSBMPAAKRLELDTGPQSLSGKST PQPPSGKTTHNSGDVQTYBPKRFKRKPSGSSGSRORRPGTPSAE GGSTSSTLRAAASKLEQGKVSBMPAAKRLELDTGPQSLSGKST PQPPSGKTTHNSGDVQTYBPKRFKRKPSGSSGSRORRPGTPSAE GGSTSSTLRAAASKLEQGKVSBMPAAKRLELDTGPQSLSGKST PQPSGKTLAVBSGDTVALAGAGAGAGYFSVTHDTKYSLKVFFE HIGKNTIAVFSTVAGGESGSDTVROPGFALVKFYTEGGINDL VGNNTBIFPIRDPILRPSGTIGGKRAPGTFVHDTVSKAVFFE HIGKNTIAVFSTVAGGSGSADTVROPGFAVKFYTTEGGINDL VGNNTBIFPIRDPILRPSFILGGKRAPGTHKUNANGRAVYLCK FHKKTQGIRLSVFDAARLSQEDPYGTRLIFNAIATGKYPSM TYTIQWTFNOAETFFPNPFOLTKVWPHKDYPLTVPKKLVALANGRAPYLCK FHKKTQGIRLSVFDAARLSQEDPYGTRLIFNAIATGKYPSM TYTIQWTFNOAETFFPNPFOLTKVWPHKDYPLTVPKLVILANGRAPYLVL GGNYLHIPVNCPYTRAVANVQROPPGCAPAGAGAGARAYNYNS GAPQOPSALBHSIQVSGVRFMTANDDNTOVARAFYNVLNE EQRKPLCENIAGHLKDAQIFTGAGAGAGAGAATAGVGE TGSGQAGGGGKATTTVFVSGSTABNKRKSSKLIMBLTGGGGSSSGL TGSGQAGGGGKKTTTVTRYTISPFRAKKRKSSKLIMBLTGGGGSSSGL TGSGQAGGGGKKTTTVTRYTISPFRAKTKGRASKALL DKNNAKKSVPROVMLEELSLLTNRGSKMFKLAGHTVALKFA LIPPLVEGLUKUNTELVGSTRADGTHANGTVANARARALL TYGARABLKYNSFNRTAMPYGGYEKASKRMTFOMYLA LIPPLVEGLUKUNTELVGSTRADGTHANGTVANARALLGLTSTLIPDTULSH LIPPLVEGLUKU	6582	1428	718	CFTTKTHCSPVSVPYLSPLVLRKELESLLENEGDQVIHTSSFIN
OQETSTLVETTRGS IQENNULEPINLISQQMEGMKRQRSIJYRE ILPISIUSLGERNIDIEAPDNEYGIAYNSLSSEILERLQKIDAP PSASYEMCRKCPGAPILI 6583 487 41 RIFSMTSGREWRCTWRPATALWSASLRLGTSSMHFSPRSISLE LSMMLSPLPSNTRGLSPTALPRESPDEHHATSCPRILHWRCRAPL RSPSPLGRIQVLPRSPLHVHTHINSGKEVLGLQVQRSRSGTGPAC SQAGSGAVQGOMCTF  8584 189 1750 PLPMAALGPSSQNVTEYVVRVERNTTKKNIMAPNAADKVNFAT WNQARLERDLSNKKIYQEEEMPESGAGSEFNRKLREBARRKKYG IVLKEFREEDQPHLLRVNGKSGRKFKGIKGGVTENTSYYITTG CPDGAFEAFPVHWWYNFTPLARHRITJRABAEEEWRERKYG IVLKEFREEDQPHLLRVNGKSGRKFKGIKGGVTENTSYYITTG CPDGAFEAFPVHWWYNFTPLARHRITJRABAEEEWRERKRYCHAN FSIMQORRLGNOOMBEEEKKRGRRKASLERIHDLEDDLEMS SDASDASGEEGGRVPKAKKKAPLLAKGGRKKKKKGSDDEAFFDS DLOGDFFGGGEVDYWNDGOSSSOGBPESKKRGRKKKKKGSDDEAFFDS DLOGDFFGGGEVDYWNDGOSSSOGBPESKKRGRKKKKKGSDDEAFFDS DLOGDFFGGGEVDYWNDGOSSSOGBPESKKRGRKKKKGSDDEAFFDS DSEESEBERKPPERDKEBEERKAPTPQRKKRRDSSBESDASE ESDIDSEASSAFPMAKKTPPKRERKPSGGSSRGNSRPGTPSAE GGSTSSTLRAAASKLBQGKRVSBMPAARRLELDTGPGSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTKK TGLSSSQTVNVLAQILKKRUPERMINDOMFISLK GGSTSSTLRAAASKLBQGKRVSBMPAARRLELDTGPGSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLKKFQTKK TGLSSSQTVNVLAQILKKRUPERMINDOMFISLK GGSTSSTLRAAASKLBQGRAVSBMPAARRLELDTGPGSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLKKFQTKK TGLSSSQTVNVLAQILKKRUPERMINDOMFISLK GGSTSSTLRAAASKLBGGRAVSBRPARRLELDTGPGSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRAPHTCHDLKKFQTKK UNSTRIPTSPROMPTHAAGAGAFGYFEVTHDITKYSKAKVPE HIGKKTPLAVRSTVLAGESGAADTVRDRRFSLKK VFFLYNTAMATSKARDERVCKK FHYKTDGGIKKLSVEDAARLSGGADTVRDRRGPLLVODVYF TDEMAHFDRERIPERVURAKGAGAFGYFEVTHDITKYSKAKVPE PLESHQVSFLESDRGIPDGHRHMMGVGSHTFKLUNARGAVYCK FHYKTDGGIKKLSVEDAARLSGGEDPYGTGLFAYDTTHRH LGPNYLHIPVNCPYRAVANVQRDGPMCQNGGAADTVAVNSF GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVVNULNE EQRRILCENTLAGHLKDAQIFTGVKAVKNSTENDHOVGGAADTVAVNISS GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVVNULNE EQRRILCENTLAGHLKDAQIFTGVGGLATAAGGFSKAKKRKFYENH DVFSDSSMDHFOKEDFTVGGGLGTATGGGFSKASKKREGGGSQAGG GGSAGGYGGDAGGAAGTAGVGG TGSGDQAGGBCKHITVFKTYISPERAMAVDVGCGASQF PGGYGFSBMCLAAMLPSVVQHGFKYVIGIGVAGAGAATTAGVGE TGSGDQAGGBCKHITVFKTYISPERAMAVDVGCGASQF PGGYGFSBMCLAA				QHPIIFWTLVWYFRRLDLPSNLPGLILTSEHCNEGVQLPLSSLS
TIPILSLUSLIGREN ID TEAPTINE'GI AYNSLSSEILERLQKIDAP PSASYEMCRKCFGAPLI  6583  487  41 RIFSMISGRIERRCTWEPATALWSASLRLGTSSMHPSPRSISLP LSPMISGRIERRCTWEPATALWSASLRLGTSSMHPSPRSISLP LSPMIGHTINSKE KEVIGLQVQRSRSSCTOPAC SQAGSGAVQGOMWCIF  FSPENGRIQVLPRS PILHVHTINSKE KEVIGLQVQRSRSSCTOPAC SQAGSGAVQGOMWCIF  PLPMAALGPSSQNVCIF WARDENTIKKYNIMAPNAADKVNFAT WNQARLERDLSNKKI YQEEEMPESGAGSEFNRKLREBARRKKYG IVLKEFREPEDOPHILRVNGKSGRK FKGI KKGGYTENTSY ITTO CPPDAFEAP FVHNWNYTPI PLARHRITLABSABEEWERRINKVLINH FSIMQORRIKDQDDEDEEKKRGRKEKSKI KHOLEDDLEMS SDASDASGEGGRVP KAKKAPQABEEDHENTSY YITTO CPPDAFEAP FVHNWNYTPI PLARHRITLABSABEEWERRINKVLINH FSIMQORRIKDQDDEDEEKKRGRKKKKKGSDDBAFFDS DDGDFEGOEVDYWSDGSSSSGBPESKAKAPQOBEOPKKUNDEQS DSSEESEERPPEEDKEBEEKKRAPTPQEKKRKKGSBESDSSE ESDIDSEASSAFFMAKKKTPPREBRENFOGGSSRGNSRPSTFSAB GGSTSSTLRAAASKLEGGKRVSBMPAAKRIRLDTGPGSLSKST PQPPSKKTPYNSGDVYTEDAWRATIKHTTKOLLKKFOTKK TGLSSECTVNVLAQILKRINPERKHINDKHFSLKS  6585  3 1678  GFIRNSRIDDFVGGDFRABSCSVLHSKMTYTVGDRSDADOW HWKEQRAAQKADVLITTGAGNPVGSKLNVITVGPRSPLLVQDVVF TDEMAHFDERE IPERVVHAKGAGAFGYFEVTHIDITKYSKAKVFE HIGKKTPI INVESTVAGEGSGADTVDRRGFAVKYTTEGGWDL VGNNTFIFFIRDPILFPSFTHSGKNPGTHLKDPDMVDFFSLK PESLHQVSPLFSDRSGI EDGHRIMMYGFFKLVNNANGEAVYCK PHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TYTIQWITTNOABTFFPNFPDILFWEHKLVDRAVGRAVYCK PHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TYTIQWITTNOABTFFPNFPDILFWHRINDFLYFUKGHVINN PVNYFAEVEQILATPOGGAPHYYNNSF GAPEQOPSALBHSIQYSGEVRRYNADDNVTQVARFYYNNINE EQRKILCENLAGHLKDAQTFICKKAVKNFTEVEPDYGSHIQALL DKYNAEKPKNAIHTFVQSGELRARACSKLIMBLTGGGGSSGI GAPEQORSABNINGARATGKYPSW TYSSGENGRAPTTANGKYPSW TYSSGENGRAPTTANGKYPSW TYSSGENGRAPTTANGKYPSW TYSSGRAPGYTHANGKYNFASKLIMBLTGGGGASSGL GGSGAGGGGGGHTTGVFKKYNIGGGAGAYTALKFA LIPPDLVEGULJVIN DDWKGMTUHAARKLSGLIDLLA YGAKABLPKYKSFNRTAMPYGGYEKASKRIMTFQMFKV TGSGAAGAGATTAGVGE TGSGQAGGGGHTTTYTYTYTSPERFANGVDPQOWELS ILLLA YGAKABLPKYKSFNRTAMPYGGYEKASKRIMTFQMFKV HUYGKABLPKYKSFNRTALTTY SPENGENGRAATLAGGTSTLIPPTULSH LIPPDLVEGULJVIN IDDWKGMTUHAARKLSGGTSTLIPPTULSH LIPPDLVEGULJVINTDDWKGMTUHAARKLSGGTSTLIPPTULSH LIPPDLVEGULJVINTDDWKGMTUHAARKLSGG				QDSKLVYIQLLWDNINLHQEPREPLYVSWRNFNSEKKSSLLSEE
PSASYEMCRKCRGAPLI				QQETSTLVETIRQSIQHNNVLKPINLLSQQMKPGMKRQRSLYRE
41 RIFSMTSGRLRWRCTWRPATALFRSDELALGTSSMHPS PRSISLE LSWMLSPLPSNTRGLSPTALFRSPDSEHATSCPRLHLWRCRAPL RSPSPLGRLQVLPRSPLHVHTINSGKSEVLGLQVQRSRSGTOPAC SQAGSGAVQGRWCIF  6584 189 1750 PLPMALGPSSONTEVVVRVPRNTTKKYNIMAFNADKVNFAT WNQARLERDLSNKKIYQEEMPESGAGSEFNRKLREARRKKYG IVLKEFREPDOPHILRVNGKSGRKFKGIKKGGVTENTSYIYITO CPDGAFPAEAPPVHNNYNTPILARHRITLATERAEEMERRRKYLINH FSIMQGRILKDQDDEDEEKSKRGRRASELKIHDLEDDLEMS SDASDASGEEGGRVYKAKKAPLAKGGKKKKKKKGDDEAFPDS DDGDFSGGEVDYMSDGSSSSGEPPSKARKAPQOEGGPKGVDEGS DSSEESEERKPPEDLKEEEEKKAPTPQEKKRRKOSSEESDSSS ESDIDGBASSAFFMAKKTPPKRERKGKKKKGSDEAFPDS GGSTSSTLRAAASKLEGGKRVSBMPAAKRIRLDTOPQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTKK TGLSSSCTVNVLAQILKRLWPERNINDKMHFSLKS  6585 3 1678 GPIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDÖMQ HWKEGRAAQKADVLTTAGAPPUGDKINTVGPRGFLVUODVVF TDEMAHFDRERIPERVVHAKGAGAPGYFEVTHDITKYSKAKVFE HIGKKTPIAVERSTVAGESGSADTVRDPRGFAVKYTEDGWDLL VGNNTSIPFIRDPILLPSFIHSGKNDFJHLKDPDMVHDFWSLR PESHQVSFLFSBRGIPDHRHMNGYGSHTFKLVNANGEAVYCK PHYKTDQGIKKLSVEDARLSGDEDDVGLDENDATAGKYPSW TPTIQWTFNQAETFPRNPFDLTKVWPHKDYPLIPVGKLVLNN PVNYFAEVBQIAFDFSNMPPGIBAS PDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARANAYQRODWONGOGAPHYYPNSF GAPRQOPSALEHSIQYSGEVRRPNTANDDNTQVRAFYVNULNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAKKPRAAITPVQSGSHLAAREKANL LGPNYLHIPVNCPYRARANAYQRODWONGOGAPHYYPNSF GAPRQOPSALHISIQYSGEVRRPNTANDDNTQVRAFYVNULNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAKKPRAAITPVQSGSHLAREKANL LGRYNIHIPVNCPYRARANAYQRODWONGOGAPHYYPNSF GAPRQOPSALHISIQYSGEVARRYLARGMVEKFIYENHP DVFSDSMDHFQKFLPTVQGGGTSAGGAAGGAACTAGVGE TGSGQAGGGCKHITVKYTISSPEKGRAACTAGVGE TGSGQAGGCKHITVKYTISSPEKGRAACTAGVGE TGSGQAGGCKHITVKYTISSPEKGRAACTAGVGE TGSGQAGGCKHITVKYTISSPEKGRAACTAGVGE TGSGQAGGCKHITVKYTISSPEKGRAACTAGVGE TGSGQAGGCKHITVRYTISSPEKGRGAACTAGVGE TGSGQAGGCKHITVRYTISSPEKGRGAACTAGVGE TGSGQAGGCKHITVRYTISSPEKGRGAACTAGVGE TGSGCQAGGCKHITVRYTISSPEKGRGAACTAGVGE TGSGCQAGGCKHITVRYTISSPEKGRGAACTAGVGE TGSGCQAGGCKHITVRYTISSPEKGRGAACTAGVGE TGSGCQAGGCKHITVRYTISSPEKGRGAACTAGVGE TGSGCQAGGCKHITVRYTISSPEKGRGAACTAGVGE TGSGCQAGGCKHITVRYTISSPEKGRGAACTAGVGE TG				ILFLSLVSLGRENIDIEAFDNEYGIAYNSLSSEILERLQKIDAP
41 RIFSMTSGRLRWRCTWRPATALFRSDELALGTSSMHPS PRSISLE LSWMLSPLPSNTRGLSPTALFRSPDSEHATSCPRLHLWRCRAPL RSPSPLGRLQVLPRSPLHVHTINSGKSEVLGLQVQRSRSGTOPAC SQAGSGAVQGRWCIF  6584 189 1750 PLPMALGPSSONTEVVVRVPRNTTKKYNIMAFNADKVNFAT WNQARLERDLSNKKIYQEEMPESGAGSEFNRKLREARRKKYG IVLKEFREPDOPHILRVNGKSGRKFKGIKKGGVTENTSYIYITO CPDGAFPAEAPPVHNNYNTPILARHRITLATERAEEMERRRKYLINH FSIMQGRILKDQDDEDEEKSKRGRRASELKIHDLEDDLEMS SDASDASGEEGGRVYKAKKAPLAKGGKKKKKKKGDDEAFPDS DDGDFSGGEVDYMSDGSSSSGEPPSKARKAPQOEGGPKGVDEGS DSSEESEERKPPEDLKEEEEKKAPTPQEKKRRKOSSEESDSSS ESDIDGBASSAFFMAKKTPPKRERKGKKKKGSDEAFPDS GGSTSSTLRAAASKLEGGKRVSBMPAAKRIRLDTOPQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTKK TGLSSSCTVNVLAQILKRLWPERNINDKMHFSLKS  6585 3 1678 GPIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDÖMQ HWKEGRAAQKADVLTTAGAPPUGDKINTVGPRGFLVUODVVF TDEMAHFDRERIPERVVHAKGAGAPGYFEVTHDITKYSKAKVFE HIGKKTPIAVERSTVAGESGSADTVRDPRGFAVKYTEDGWDLL VGNNTSIPFIRDPILLPSFIHSGKNDFJHLKDPDMVHDFWSLR PESHQVSFLFSBRGIPDHRHMNGYGSHTFKLVNANGEAVYCK PHYKTDQGIKKLSVEDARLSGDEDDVGLDENDATAGKYPSW TPTIQWTFNQAETFPRNPFDLTKVWPHKDYPLIPVGKLVLNN PVNYFAEVBQIAFDFSNMPPGIBAS PDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARANAYQRODWONGOGAPHYYPNSF GAPRQOPSALEHSIQYSGEVRRPNTANDDNTQVRAFYVNULNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAKKPRAAITPVQSGSHLAAREKANL LGPNYLHIPVNCPYRARANAYQRODWONGOGAPHYYPNSF GAPRQOPSALHISIQYSGEVRRPNTANDDNTQVRAFYVNULNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAKKPRAAITPVQSGSHLAREKANL LGRYNIHIPVNCPYRARANAYQRODWONGOGAPHYYPNSF GAPRQOPSALHISIQYSGEVARRYLARGMVEKFIYENHP DVFSDSMDHFQKFLPTVQGGGTSAGGAAGGAACTAGVGE TGSGQAGGGCKHITVKYTISSPEKGRAACTAGVGE TGSGQAGGCKHITVKYTISSPEKGRAACTAGVGE TGSGQAGGCKHITVKYTISSPEKGRAACTAGVGE TGSGQAGGCKHITVKYTISSPEKGRAACTAGVGE TGSGQAGGCKHITVKYTISSPEKGRAACTAGVGE TGSGQAGGCKHITVRYTISSPEKGRGAACTAGVGE TGSGQAGGCKHITVRYTISSPEKGRGAACTAGVGE TGSGQAGGCKHITVRYTISSPEKGRGAACTAGVGE TGSGCQAGGCKHITVRYTISSPEKGRGAACTAGVGE TGSGCQAGGCKHITVRYTISSPEKGRGAACTAGVGE TGSGCQAGGCKHITVRYTISSPEKGRGAACTAGVGE TGSGCQAGGCKHITVRYTISSPEKGRGAACTAGVGE TGSGCQAGGCKHITVRYTISSPEKGRGAACTAGVGE TGSGCQAGGCKHITVRYTISSPEKGRGAACTAGVGE TG	ì			PSASVEWCRKCFGAPLI
LSMMLSPLPSNTRGLS PTALPRS PIDSHATSCPRLHLWRCRAPL RSPSPLGRLQVLPRS PLINVHTHNS GKEVLGLQVQRSRSGTGPAC SQAGSGAVQGGNWCIF  189  1750  PLPMAALGPSSONVTEYVVRVPRNTKKYNIMAFNAADKVNFAT WNQARLERDLSNKKI VQGEEMPSGAGSSENRKLREBARRKKYG IVLKEFRPEDQFWLLRVNGKSGRKFKGIKKGGVTENTSYYIFTO CPDGAFEAFFVWINNYNFTPLARHRILTAEBABEBERRNRVLAN FSIMQRRIKDQDQDEBEDEBEKERGREKASELRIHDLEDDLEMS SDASDASGEEGGRVFKAKKKAPLAKGGRKKKKKKGSDDEAFEDS DLOGDFSGOVDVMSDGSSSGBEPESKAPQGEGFKVVDGG DLOGDFSGOVDVMSDGSSSGBEPESKAPQGEGFKVVDGG DSSEESEBEKPPEEDKEEEEKKAPTPQBKKRRKDSSESDSSE ESDIDSEASSAFFWAKKKTPPKREKPGGGSSRGNERGTFSAE GGSTSSTLRAAASKLEGGKVSEWBAARRILDTGPGSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRVLTKKMTTKCLLKKFGTKK TGLSSECTVAVLAQILKRINPERKNINGWHFSLKE  6585  3 1678  GPIRNSRIDDFVGGDFRAEASCSVLHSKPHAMADSRDPASDOMQ HMKEQRAAQKADVLTTGAGNPVGDKLHSKPHAMADSRDPASDOMQ HMKEQRAAQKADVLTTGAGNPVGDKLHNTVUGFRGFLLVQDVVF TDEMAHFDRERI PERVVHAKGGAGSTEFVLHSKPHAMADSRDPASDOMQ HMKEQRAAQKADVLTTGAGNPVGDKHTSLLTREFTHITKTSKAKVFE HIGKKTPIAVRFSTVAGEGGSADTVRDPRGFAVKFYTEGGNDL VGNNTSIPFIRDPILLFSPTHSCHENPILKDPDWMVPDFSLR PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLVNANGEAVYCK FHYKTDQGIKALSVEDAARLSGEDPDYGIRLDFINATATSKYPSW TYTIQVMTTROAETFPRIPPDLIKVWHKDYPELFVGKLVLNRN PVNYFAEVEDIAFDSNNPPGIEAS PDMLQGLFAYPDTHRHR LGPNYLHIPVNQPYRAEVANYQRDG PMCMQDNOGGAPHYYPINSF GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIGKKAVKNFTEVHPYGGHIQALD KYNARKFRANIHTPVGGSGHAARKASKLIMBLITGGGGSSGL MKKISVPRDVMLEELSLLTNRGS KMFKLRQMRVEKFIYENHD DVFSDSSMDHRGKFLPTVGGGGTAGGGFSYSKSNGRGGSGAGG SGSAGGYGSDQOHHLGSGSGAGGTGGPAGGAGRGAGTAGVGE TGSGDQAGGGGKHTTVKTYTSFERFANGVDPQQMKELSILDLL YGAARALPKYKS FRRTAMPYGGYEKASKRMTPGMPKV  6587  75  1117  RRVPSLGKMPECWBGHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGINHKLCTNTFFNEDMGEITKHVVCHVDAPGQOVGASOF POGGFFSMEQLAAMLPSVVQHFGFKYVIGGRGAAVVLAKFA LIFPDLVEGLULVNIN IDDRKGNU IDAARKLSGLTSTLPDTUSH LIFPDLVEGGLUVNINGKGNU IDAARKLSGLTSTLPDTUSH LFSQEBLVNNYTELVQSYRQQIGNVVNQANLQLFWMYNSRSDLD INRRGTVPNNAKTLRCPWMLVVGONAPAEDGVVECNSKLDPTTT FLKMADSGGLGPCVTTPOKKUTLGGMTAWPSASHTRLARS	6583	487	41	
RSPSPIGRLQVLPRS PLHVHTHNSGKEVLGLQVQRSRSGTGPAC SQAGSGAVQGMCIF FLPMAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFAT WNQARLERDLSNKKIYQEEBFBEGAGSEPNKLREBARRKKYG IVLKEFRPEDQPHILLRVRIGKSGRYKIKKGVGTENTSTYITFTQ CPDGAFEAFFVNNWYNFTPLARHRTLTAEBAEEEWERRNKVLNH FSIMQQRILKDQDQDEDEEEKEKRGRRKKKSGDEAFPDS DDGDFBGQEVDYMSDGSSSSGBEPESKAKAPQQEGPFKGVVEQS DSSASDASGEGGGRVFKAKKAPLEKIHUDLEDDLEMS SDASDASGEGGGRVFKAKKAPLEKRGKKKKKKGDEAFPDS DDGDFBGQEVDYMSDGSSSSGBEPESKAKAPQQEGPFKGVVEQS DSSEESEEKKPPEDKEEEEKKAPTPQEKKRKKKOSSEESDSSE ESDIDSEASSAFFMAKKTPPKRERKPSGGSSGRGRFGFFSAE GGSTSSTLRAAASKLEQGKRVSBMPAAKRLRLDTGPQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRTIRKPMTKOLLKKFOTKK TGLSSEQTVNVLAQILKRLNPERMINDKMHFSLKE 6585 3 1678 GPIRNSRIDDFVGGDFRAEASCSVLHSKFRAADSSCDPASDQMQ HMKEQRAAQKAPUTTGAGRPVCDKLNVTTVGPRGPLLVQDVVYE TDEMAHFDRERIPERVVBAKGAGAFGYFEVTBDIRKYSKAKVFE HIGKKTPIAVRFSTVAGESGADTVRDPRGFAVKFYTEDGNWDL VGNNTPIFFIRDPILFPSFHBGKRNPQTHLKDPDMWDFWSLR PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKJVRANGEAVYCK PHYKTPGGIKNLSVEDAARLSGDPDYGIRDLFNALAGGKYPSK TFY1QVMTFNQAETFPRNPFDLTKVWHHKDYPLIPVGKLVLINRN PVNYFAEVEQIAFDPSNNPPGIEASPDWLQGRLFAYPDTHRHR LGENYLHIPVNCYYBARVANQRGPMCMQDNGGAPMYYNNSF GAPEQQPSALEHSIQYSGEVRRYNTANDDNVTQVRAFFVNVLNE EQRKRLCENLAGHLKDAQIFIGKNKNTFUHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL 6586 32 804 PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMBLTGGGQGSSSGL GGSGAGYGSDQCHLLGSGSGAGTGGDAGAGAGGAGAGGAGG GGSGKHTVFKTYISPHERMAGVDGVGMELGIDLLA YGAKAELPKYKSFNRTAMPVGGYEKASKKLIMBLTGGGQGSSGL GGSAGGYGSDQCHLLGSGSGAGTGGDAGAGAGGAGAGGAG GGSAGYTLAKFYPDMLLCSGNFTYFTYPMPKY 6587 75 1117 RRVPSLGKMPECMGGHDIETFYGLLHVVTGNSPKGNRPAILTY HDVGLNHKLCPNTFYRPEDMGEITKHFVVCHVDAPGQVGASQF PQGYGFPSMEGLAAMLPSVVQHFGFKYVIGIGVGAGAVILAKFA LIFPDLVGLULVINDPRGKUTBUNAATKLSGLTSTLDTTULSH LFSQEBLVNNTELVQSYROQIGNVVNQALDGLFNMYMSRRDLD INRRGTVPNAKTILCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQDGKLTLDFNAKTHLAGGLFDTTTT FLKMADSGGLPQVTQDGKLTCAFKYFLQGMGMMPSASMTRLARS	0303	1		
SQAGSGAVGGGWCTF  PLPMAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFAT WNQARLERDLSNKKIYQEEMPESGAGSEFNRKLREBARRKKYG IVLKEFREBOPWLLRVNGKSGRKFKGIKKGGYTENTSYYIFTO CPDGAPFAPFVNNWYNFTPLARHRUTLABEAEEWERRNKVLNH FSIMQORRLKDQDDEDEEKEKKGRKASELRIHDLEDDLEMS SDASDASGEEGGRVFKAKKAPLAKGGRKKKKKKGDDEAFEDS DDGFFBGGEVDYMNSOSSSSQBEPESKAKAPQOEEGPKGVDEQS DSSEESEEKPPEDKEEEEKKAPTPQEKKRKKGSDEAFEDS DSSEESEEKPPEDKEEEEKKAPTPQEKKRKGSSEGSGSFGSTSAS GGSTSSTLRAAASKLEQGKRVSBMPAAKRIRLDTOPGSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKOLLKKFQTKK TGLSSEQTVNVLAQILKRLNPERRMINDKMHFSLKE GFINSRIDDFVGGFPRAEASCSVLHSKPHAMADSRDPASDQMQ HWKSQRAQKADVLTTGAGNPVGDKLNVTTVGFRGPLLVQDVVF TDEMAHFDRRIPERVVHAKGAGAFGYFEVTHOITKYSKAVVPE HIGKKTPIAVRSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL VGNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPMVMDFWSLR PESLHQVSFLFSBGSIPOHHRHMGYGSHTFKLWNANGEAVYCK FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TYTYQWTIFNQAETFPRMPFDLTKVMPHKDYLIPVGKLVLNRN PVNYFFAEVEQIAFPSNMPPGIBASPDKMLQGRLFAVPDTHRHR LGPNYLHIPVNCPYRARVANVQRGPMCMQDNGGAPMYYDNSF GAPGQDSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVNNTTEVHPPYGSHIQALL DKYNAKKPKNAIHTFVQSGSILAAREKANL 6586 32 804 PLPPGPAASTSTMPVSGTPANKKASKLIMBLTGGGGESSGL NLGKKISVPRDVMLEELSLLITNRGSKMFKLRGMRVEKFIYENH DVFSDSSMDHFQKFLPTVGGQLGTAGGFSYSKSNGRGSQAGG SGSAGQGSDQCHHLKDAGSGGAGTGAPAGGAGGGAAATAGVGE TGSGQAGGGGKHITVFKTYISPWERAMGVDQQWGASQF TGSGQAGGGGKHITVFKTYISPWERAMGVDQQWGASQF TGSGQAGGGGCHAHLBCSGGAGTGCPAGGAGGGAATTAGVGE TGSGQAAGGGKHITVFKTYISPWERAMGVDQQWGASQF PQGYGFDSMEDLAARLPSVVQHFGFKYVIGVGROPPALTTY HDVGLNHKLCFNTFFNPEDMQEITKHFVVCHVDAPGQQVGASQF PQGYFSNEQLAANLPSVVQHFGFKYVIGSGRGNPALLTY HDVGLNHKLCFNTFNPEDMQEITKHFVVCHVDAPGQQVGASQF PQGYGFSMEQLAANLPSVVQHFGFKYVIGSGRGNPALLTY HDVGLNHKLCFNTFNPEDMQEITKHFVVCHVDAPGQQVGASQF PQGYGFSMEQLAANLPSVVQHFGFKYVIGSGRGNDFALLTY LKFBQUEGLUVNTBLVGGYRGGIGNVVNQANLGLFPMMYNSRRDLD INRPGTVPNAKTIRELVGGNGAGTGGAAGGGAAGCAGGGF LIFFDLVCGLUVNTDLDNGKGUTDMAATKLSGLTSTLDDTVLSH LFFGUEGLUVNTBLVGGYRGGIGNVVNQANLGLFPMMYNSRRDLD INRPGTVPNAKTIRELVGCMGAMYVCCNSKLDDFTTT FLKMADSGGLPQVTQPGKLTSAFKYFLQGMGMMFSASMTRLARS				
1750   FLPMAALGPSSQNVTEYVVRUPENTTKKYNIMAFNAADKVNFAT   WNQARLERDLSNKKIYQEEMPESGAGSEFWRKLREBARKKYG   IVLKEFRPEDQPPILLRVNOKSGKFKGIKKGGVVENTSYYIFTQ   CPDGAPEAFPVHNWYMFTELARHRTLTABAEEKMERRNKYLAND   CPDGAPEAFPVHNWYMFTELARHRTLTABAEEKMERRNKYLAND   SDASDASGBEGRVPKAKKKARPLAKGGRKASELAH, HIDLEDDLEMS   SDASDASGBEGRVPKAKKKARPLAKGGRKKAKKKKGSDDEAFEDS   DDGDFSGQEVDYMSDGSSSSQBEPSKAKAPQQEEGPKQVDEQS   DSSESSEEKBYPEDEKKEEKEKKAPTQBEKKRKKKKSSBDESDSS   ESDIDSEASSAFMAKKTPPKRERKPSGSSGSGNSRFGTPSAE   GGSTSSTLRAAASKLEQGKRVSEMPAAKRLDTGPQSLSGKST   PQPPSGKTTPNSGDVQVTTEDAVRRYLTKRMTTKDLLKKRYTKK   TGLSSEQTVNVLAQILKRINPERKNINDKHIPSLKE   GFIRNSIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDOMQ   HWKEQRAAGKADVLITTGAGNPVGDKINVITTGPRGPLLVQDVVF   TDEMAHPDRERIPETVVALAGGAGAGYFEVHDITKYSKAKVFF   HIGKKTPIAVRFSTVAGEGSGADTVRDPGFAVKYYTEDGNWDL   VGNNTPIPFIRDPILFPSFTHSQKRNPQTHLKDPDMVWDFWSLR   PESLHQVSFLFSDRGITPDHRHMNOYGSHTKLVNANGEAVYCK   FHYKTDQGIKKJSVEDAARLSQEDPDYGIRDLFMAIATGKYPSW   TFYIQWHTMQASTFPPNFDLIKWPHKDYPLIPVGKLVLNRN   PVNYFAEVEQIAFDPSNMPGFBASPDMLLGGRJAVPDTHRHR   LGPNYLHIPVNCPYRARVANVQRDGPMCMQDNQGGAPNYYPNSF   GAPEQQPSALEHSIQYSGEVRRFNTANDNTQVRAFYVNVLME   EQPRKLCENIZAGHLKNDQIFIGKAVWKFTSVHPDYGSHIQALL   DKYMAEKPKNAIHTPVQSGHLAREKANL   PLPEQPAESTSTMPVSGTPAPNKKKKSKLIMBLTGGGQESSGL   NLGKKISVPROWALELSLLINGSKMFKLRQMEVEKFITENHP DVFSDSSMDHFQKFLPTVGGGJTAGQGGFYSKSNGRGGSQAGG   SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAQVGE   TGSGQQAGGGKHITVFKTYISPBERAMGVDPQXMELGIDLLA   YGAKASLPXKSFNRTAMPYGGTEXSKMFFQAMPKK   TENHP DVFSDSSMDHFQKFLPTVGGGGTSVSKSNGRGSQAGG   SGSAGQYGSDQQHHLGSGSGAGGTGGAAGATAGVGE   TGSGQQAGGGKHITVFKTYISPBERAMGVDPQXMELGIDLLA   YGAKASLPXKSFNRTAMPYGGTEXSKMFFQAMPKK   LFNDEVLGVECKHOLTVINIDNOKGKIDDAATKLSGLTSTLPDTVLSH   LFSQBLVKNSFNVINIDNOKGNIDMAATKLSGLTSTLPDTVLSH   LFSQBLVVNINIDNOKGNIDMAATKLSGLTSTLPDTVLSH   LFSQBLVVNINIDNOKGNIDMAATKLSGLTSTLPDTVLSH   LFSQBLVVNINIDNOKGNIDMAATKLSGLTSTLPDTVLSH   LFSQBLVVNINIDNOKGNIDMAATKLSGLTSTLPDTVLSH   LFSQBLVVNINIDNOKGNIDMAATKLSGLTSTLPDTVLSH   LFSQBLVVNINIDNOKGNIDMAATKLSGLTSTLPDTVLSH   LFSQBLVVNINIDNOKGNIDMAATKLSGLTSTLPDTVLSH   LFSQBLVVNINIDNOKGN		1		
WNQARLERDLSNKKIYQEEEMPESGAGSEFNRKLREBARRKKYG IVLKERRPEDQPWLLRVNOKSGRKYKGIKKGVTENTSYYIFTQ CPDGAFEAFPYHWYMYFTELAHRITLITAEBABEEWERRNKVLHH FSIMQORRLKDQDDDBEEEKBKRGRKKASELRIHDLEDDLEMS SDASDASGBEGGRVPKAKKKAPLAKGGRKKKKKSDDEAFEDS SDASDASGBEGGRVPKAKKKAPLAKGGRKKKKKSDDEAFEDS DDGDFBSGEVDYMSDGSSSSGSEPESKARAPQEEGFKGVDEGS DSSESSEBKPPBEDKEBEEKKAPTPQEKKRKNDSSESDSSB ESDIDBEASSA FMAKKAPPLAKGGRKKKKKSSDEAFPSAE GGSTSSTLRAAASKLEQKKRVSMPAAKRLDTGPQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRILTKPMTTKDLLKKFQTKK TGLSSECTVNVLAQLIKERUPBKRNINDKMIFSLKE  6585 3 1678 GPIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDQMQ HWKEQRAAQKADVLTTGAGNPVGDKLNVLTGPRGPLLVQDVVF TDEMAHFDRRRI PERVVHAKGAGAGYFEVYHDITKYSKAKVFP HIGKKTPLAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL VGNNTPIFFIRDPILPPSFIHSQKRNPQTHLKDPDMVWDFWSLK PESLHQVSFLFSDRGIPDGHRHMOYGSHTKLVNANGEAVYCK PHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TFYIQVMTFNQAETFPFNPFDLTKVW WHKDYFLIPVGKLVLNRN PVNYFAEVEQIALFDFSNMPPGILASVPHRIRALAGKYPSW TFYIQVMTFNQAETFPFNPFDLTKVW WHKDYPLIPVGKLVLNRN PVNYFAEVEQIALFDPSNMPPGILASPDHALAPLEXANL LGPNYLHIPVNCPYRARVANYQRODPMCQNQGADANYYPNSF GAPBQOPSALEHSIQVSGEWRANYQRODPMCQNQGADANYYPNSF GAPBQOPSALEHSIQVSGEWRANYGRODPMCQNQGADANYYPNSF GAPBQOPSALEHSIQVSGEWRANKSSKLIMBLTGGGGBSSGL NLGKKISVPRDVMLEELSLLTNRGSKFKKNSKLIMBLTGGGGBSSGL NLGKKISVPRDVMLEELSLLTNRGSKFKLRQMRVEKFIYENHP DVFSDSSMHFQKFLDFTVGGQLGTAGQGFSYSKSONGGSQAGG GGSAGGGGSDGHHITVFKYYISPWERAMOVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGTPARAGKAGGAAGTAGVGE TGSGDQAGGGGKHITVFKYYISPWERAMOVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGTPARAGKMTFQMPKV  6587 75 1117 RRVPSIGKMPECMGGHDIETFYGLHVVIKGSPKGNRPAILTY HDVGLNHKLCFNTFFREDMGEITKHFVVCHVDAPGQOVGASQP PQGYQFPSEQLAAMLPSVVQHGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLNNTDLVOSPNAGRIDAATKLSGLTSTLPDTVLSH LFSQBLVNNTELVQSYRQQIGNVVNQANLQLFFNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAAATKLSGLTSTLPDTVLSH LFSQBLVNNTELVQSYRQQIGNVVNQANLQLFFNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAAATKLSGLTSTLPDTVLSH LFSQBLVNNTELVQSYGQIGNVNQANALQLFFNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAAAATKLSGLTSTLPDTVLSH LFSQBLVNNTELVQSYGQIGNVNQANALGLFFNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAAAATKLSGLTSTLPDTVLSH	6504	100	1750	7
IVLKEFRPEDQPWLLRVNGKSGRKFKGIKKGGVTENTSYYIFTQ CPDGAFEAFPVHNWYNFTPLARHRTLTAEAEEBWERRNKVLAH FSTMQGRILKDQDDDEEEKEKRGRRASELRIHDLEDDLEMS SDASDASGBEGGRVPKAKKAPLAKGGRKKKKKKGSDDEAFEDS DLSGBFESGEGRVPKAKKAPLAKGGRKKKKKKGSDDEAFEDS DSSEESEEKPPEDKEEEEKKAFTPQEKKRRKDSSBESDSSE ESDIDSEASSAFFMAKKKTPPKRERKPSGGSSGNSRFGTPSAE GGSTSSTLRAASKLEQGKRVSEMPAAKRLDTGPQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLITKEPMTTKOLLKKFOTKK TGLSSEGTVNVLAQILKRINPERKHINDKMHFSLKE GFIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDQMQ HWKEQRAAQKADVLTTGAGNPVGDKINVITVGPRGPLLVQDVVF TDEMAHPDRERIPERVVHAKGAGAFGYFEVYHDITKYSKAKVPE HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL VGNNTPIFFIRDPILPFSTHEGKRNPQTHLKDPDMWDFWSLK PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLVNANSEAVYCK FHYKTQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TTYTQVMTFNQAETFPFNFPLIKWPHKDYPLTPVGKLVLNRN PVNYFASVEQIAPDFSNMPPGIBAS PDKMLGGRLFAVPDTHRRR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGAPNYYPNSF GAPEQQPSALEHSIQVSGEVRRFNTANDDNVTQVAFYYNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKHTEVHPDYGSHIQALL DKYNAKKFKNAIHTFVQSGSHLAAREKANL  6586 32 804 PLPEQPAESTSTMPVSGTPAFNKKKSSKLIMBLTGGGQBSSGL NLGKKISVPRDWALEELSLITNGS KMFKLRGMRYEKF IYENHP DVFSDSSMDHPQKFLPTVGGGLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGGAAGTAGVGE TGSGDQAGGGGKHITVFKTYISPBERAMSVDPQQKMELGIDLLA YGAKAELPKYKS FNRTAMPYGGYEKASKKMTPGMPKV  6587 75 1117 RRVPSIGMPECMGEHDIETPYGLLHVVIRGSFKGNRAILTY HDVGLNHKLCFNTFFFBEMQBITKHFVVCHVDAPGQVGASQF PQGYOFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAAYVLAKFA LIFPDLVEGLUNIDIPNGKGWIDMAATKLSGLTSTLPDTVLSH LFSQELVNNTELVGSYRQGIGNVVNQANLQLFFNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVQDNAPAEDGVVECNSKLDPTTT FLKMADSGGLPQVTQPGKUTLEAFKYFLQGMEYMFSAMTLARS	0504	103	1730	1 -
CPDGAPEAFFVHNWYNFTPLARHRTLTAEBAEEEWERRNKVLNH FSIMQORRIKOQDOBDEEEKBKKGRKASELKIHDLEDDLEMS SDASDASGEEGGRVPKAKKKASDLAEKKKGSDDEAFFEDS DDGDFEGGBVDYMSDGSSSQBPESKAKAPQOEEGPKGVDEQS DSSEESEERKPPEDENKEEEEKKAPTPQEKKRRKDSSEESDSSE ESDIDSEASSAFFMAKKKTPPKRERKPSGGSKRONSRPGTPSAE GGSTSSTLRAAASKLEGGKRVSMPAAKRLLDTGPQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKPQTKK TGLSSECTVNVLAQILKRLMPERKMINDNHFSLKE GFIRNSRIDDFVGGDPRAEASCSVLHAKPPAKKKASDLEAKGAP HKEGRAAQKADVLTTGAGNPVGDKLNVITVGPRGPLLVQDVVF TDEMAHPDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE HIGKKTPIAVRFSTVAGESGSADTVRDRGFAVKFYTEDGNMDL VGNNTPIFFIRDPILPSPFHSQKRNPQTHLKDPDMWDPFWSLR PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKUNANGEAVYCK FHYKTDQGINLSVEDAARLSQEDPDVGIRDLFNAIATGKYPSW TFYTQVMTFNOAETFPRNPFDLTKVWPHKDYPLTPVGKUNNN PVNYFAEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRH LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNOGGAPNYYPNSF GAPBQOPSALEHSIQVSGVRFNTANDDMVTQVAFFYWNVLNE EQRKRLCENIAGHLKDAQIFIQKAVNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGHLAAREKANL FLEPGPAESTSTHPVSGTTPAPNKKRKSSKLIMBLTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIVENHP DVFSDSSMCHIGKFLTVGGGLGTAGQGFSYSKSNGRGSQAGG GGSAGQYGSDQQHHLGSGSGAGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGEKHITVFKTYISPHERAMGUDPQQKWELGIDLLA YGAKAELPKYKSPNTAMPYGGYEKASKRMTFQMPKV  6587 75 1117 RRVPSIGKMPECWBGEBEIETPYGLLHVVTRGSFKCNRFAILTY HDVGLNHKLCFNTFTNFEDMGEITKHFVVCHVDAPGQOVGASOP PQGYGFPSMEQLAAMLPSVVQHFGKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVUNIDDNIGKWIDMAATKLSGLTSTLPDTVLSH LFSGBELVNNTELVOSVRQQIGNVNQANLQLFMNMNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAERGGVVCNSLDPTTTT FLKMADSGGLPQVTQPGKUTTAFKYFLQGMGYMPSSAMTKLARS				1 -
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SDASDASGEEGGRVFKAKKAPLAKGGRKKKKKKGSDDEAFEDS DDGDFEGQEVDYMBDGSSSSQEBPSKARAPQQEEGFKGVDEQS DSSESSEBEKPEPEKKEREBEKKAPTQGEKKRKDKOSSESDSDSSE ESDIDSEASSAFFMAKKKTPPKRERKPSGGSSGNSRPGTPSAE GGSTSSTLRAAASKLEQGKRVSEMPAAKRLRLDTGFQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTKGLLKKFOTKK TGLSSEQTVNVLAQILKRLNPERKMINDKMHFSLKE G58S 3 1678 GPIRNSRIDDFVGGDFRAEASCSVLHSKPHAMADSRDPASDOMQ HWKEQRAAQKADVLTTGAGNPVGDKLNVITVGPRGPLLVQDVVF TDEMAHPDRRRIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNNDL VGNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVMDFWSLR PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLVNANGEAVYCK FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNALATGKYPSW TFYIQVMTFNQAETFPFNPFDLTKWPHKDYPLIFVGKLVLNRN PVNYFASVEGLTAFPSNNPPGIEASFDKMLQGRLFAYVDTHRRR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRFHTANDDNVTQVRAFYVNVLNE EQRRALCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL 6586 32 804 PLPEPPAESTSTMPVSGTPAPNKKRKSSKLIMBLTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSMGRGSQAGG SGSAGQYGSDQOHHLGSGSGAGGTGPAGQAGRGAAGTAGVGE TGSGDQAGGGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYXSFNRTAMPYGGYBKASKMTTQMFKV 6587 75 1117 RRVPSLGMPECWDGBHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNIKLCFNTFFNFEDMGSITHFFVVCHDAPGQQVGASGF PQGYGFFSMEGLAAMLPSVVOHFGFKYVIGIGYGAGAYVLAKFA LIFPDLVEGLUVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSGBLVNNTELVQSYRQQIGNVVNQAALQLFWMYNGSRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS	ł			
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LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL  6586 32 804 PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMBLTGGGQBSSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGGQFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGAAGTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV  6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQBBLVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPCTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS				
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EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL  6586  32  804  PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMBLTGGGQBSSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGEGKHITVFKTYISPMERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYBKASKRMTFQMPKV  6587  75  1117  RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEBLVNNTELVQSYRQQIGNVVNQANLQLFWMYNSRRDLD INRPCTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS	}			
DKYNAEKPKNAIHTFVQSGSHLAAREKANL  6586  32  804  PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMBLTGGGQBSSGL  NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP  DVFSDSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG  SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE  TGSGDQAGGGGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA  YGAKAELPKYKS FNRTAMPYGGYBKASKRMTFQMPKV  6587  75  1117  RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY  HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF  PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVAGAYVLAKFA  LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH  LFSQBBLVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD  INRPCTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT  FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS	1			GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE
6586  32  804  PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMELTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFGKFLPTVGGQLGTAGGGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTAGGAGGAAGTAGVGE TGSGDQAGGGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYBKASKRMTFQMPKV  6587  75  1117  RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGYGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEBLVNNTELVQSYRQQIGNVVNQANLQLFWMYNSRRDLD INRPCTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS	1		1	EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL
NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV  6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEBLVNNTELVQSYRQQIGNVNRQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS				DKYNAEKPKNAIHTFVQSGSHLAAREKANL
NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP  DVF5DSSMDHFGKFLPTVGGQLGTAGGGFSYSKSNGRGGSQAGG  SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRAGAGTAGVGE  TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA  YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFGMPKV  6587  75  1117  RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY  HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF  PQGYGFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA  LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH  LFSQEKLVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD  INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT  FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS	6586	32	804	PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMBLTGGGQBSSGL
SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFGMPKV  6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVVLSH LFSQBBLVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPCTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS		1		NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP
SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFGMPKV  6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVVLSH LFSQBBLVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPCTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS		1		DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG
TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV  6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEBLVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPCTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS				
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RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGYGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEBLVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPCTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS				
HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEBLVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS	6587	75	1117	
PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEBLVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS	330,	"		
LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEBLVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS			1	
LFSQEKLVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS				
INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS	1			
FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS	1			
			1	
RTASLTSASSVDGSRPQACTHSESSEGLGQVNHTMEVSC			1	
		J	<u> </u>	RTASLTSASSVDGSRPQACTHSESSEGLGQVNHTMEVSC

SEQ Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence se	c Acid, E= E=Glycine, ne, gine, e, wn, *=Stop
NO: nucleotide location corresponding to first amino acid residue of amino acid amino acid amino acid sequence sequence location corresponding to first amino acid residue of amino acid sequence location corresponding to first amino acid p=Proline, Q=Glutamine, R=Arginin S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unkno Codon, /=possible nucleotide dele \possible nucleotide insertion)	=Glycine, .ne, .gine, .e, .wn, *=Stop
location corresponding to first amino acid residue of amino acid	ne, gine, e, wn, *=Stop
corresponding to first amino acid residue of amino acid amino acid amino acid amino acid amino acid sequence codon, /=possible nucleotide insertion)  L=Leucine, M=Methionine, N=Aspara P=Proline, Q=Glutamine, R=Arginin S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unkno Codon, /=possible nucleotide dele	gine, e, wn, *=Stop
to first amino acid residue of amino acid residue of amino acid amino acid amino acid amino acid sequence sequence to first amino acid sequence _=possible nucleotide insertion)	wn, *=Stop
amino acid residue of residue of residue of amino acid sequence S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unkno Codon, /=possible nucleotide dele \=possible nucleotide insertion)	wn, *=Stop
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6588   137   501   LGLQAQLLELRINNYQLSDELRKNGVELTSLRQ	
AQKALSKSKKAQEVEVLLSENEMLQAKLHSQEE	DFRLQNSTLMA
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6589 2 1405 RPWGSAMATFSRQEFFQQLLQGCLLPTAQQGLD	OIWLLLAICLA
CRLLWRLGLPSYLKHASTVAGGFFSLYHFFOLH	
YLVLFLCRHSSHRGVFLSVTILIYLLMGEMHMV	
QMIVAMKAVSLGFDLDRGEVGTVPSPVEFMGYL	
ISFHSYLQAVQGRPLSCRWLQKVARSLALALLC	LVLSTCVGPYL
FPYFIPLNGDRLLRNKKRKARGTMVRWLRAYES	AVSFHFSNYFV
GFLSEATATLAGAGFTEEKDHLEWDLTVSKPLN	VELPRSMVEVV
TSWNLPMSYWLNNYVFKNALRLGTFSAVLVTYA	ASALLHGESEH
LAAVLLSLAFITYVEHVLRKRLARILSACVLSK	
LGLGVRALNLLFGALAIFHLAYLGSLFDVDVDD	TIREOGRAMMA
TVHKWSELSWASHWVTFGCWIFYRLIG	
6590 2177 656 VRAYEHVLSLLENVFTPMFCHRDEYFRQLLRGA	ESPTRNSKLNR
GSLSLDDFRNTQKRGESFGISRIGSKIKGVFKS	TIMEGAMLPNY
GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPR	NLAAWKISIPY
VDFFEDPSSERKEKKERI PVFCIDVERNDRRAV:	•
RYLEFYVLRSKLTEFHGAFPDAQLPSKRIIGPK	
FQEYLQKLLQHPELSNSQLLADFLSPNGGETQF	
KIIKSVPGKLMKEKGQHLEPFIMNFINSCESPK	
SPTSENNKKLFNDLFKNNANRAENTERKQNQNY	
DYLMYVGRVVFQVPDWLHHLLMGTRILFKNTLE	MYTDYYLQCKL
EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDK	QKGAKQTFEEM
MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVL	
VIQELFPELNKVQKEVTSVTSWM	
6591 2177 656 VRAYEHVLSLLENVFTPMFCHRDEYFRQLLRGAI	ECHTENCYT NO
GSLSLDDFRNTQKRGESFGISRIGSKIKGVFKS	
GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRI	
VDFFEDPSSERKEKKERIPVFCIDVERNDRRAVG	GHEPBHWSVYR
RYLEFYVLESKLTEFHGAFPDAQLPSKRIIGPKI	NYEFLKSKREE
FQBYLQKLLQHPELSNSQLLADFLSPNGGBTQF1	LDKILPDVNLG
KIIKSVPGKLMKEKGOHLEPFIMNFINSCESPK	PKPSRPELTIL
SPTSENNKKLFNDLFKNNANRAENTERKONONY	
DYLMYVGRVVFQVPDWLHHLLMGTRILFKNTLE	
EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDK(	
MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVL	NKOLTYVLLDI
VIQBLFPELNKVQKEVTSVTSWM	
6592 3 1861 APEPLGSTISSGSMIDANLKLLQBAEQRLKATVA	AEKFALATKEG
DLPQVERFFKIFPLLGLHEEGLRKFSEYLCKQVA	
LGTDMSDRRAAVIFADTLTLLFEGIARIVETHO	i i
LYTLIKYLQVECDRQVEKVVDKFIKQRDYHQQFE	
TTEKIEPRELDPILTEVTLMNARSELYLRFLKKI	
MASEEVKQEHQKCLDKLLNNCLLSCTMQELIGLY	
TVNKAVALDTYEKGQLTSSMVDDVFYIVKKCIGH	
CAMINLATTELESDFRDVLCNKLRMGFPATTFQI	DIQRGVTSAVN
IMHSSLQQGKFDTKGIESTDEAKMSFLVTLMNVF	EVCSENISTLK
KTLESDCTKLFSQG I GGEQAQAKFDSCLSDLAAV	,
GLTELNSTAIKPOVOPWINSFFSVSHNIEEEEFN	-
QFILNLEQQMAEFKASLSPVIYDSLTGLMTSLVF	1
TFNRLGGLQFDKELRSLIAYLTTVTTWTIRDKFA	
LERVTEILDYWGPNSGPLTWRLTPAEVRQVLALF	RIDFRSEDIKR
LRL	
6593 3 1837 EAFSAGSRRRGLALQRGVLGGLGGYCPCCCRRRG	GRLLVLLLLVR
RGGEGGGGRGDKRRRQARRQRRRPEPAEARG	
RQYNIQKKEIVVKGDEVIFGEFSWPKNVKTNYVV	
RYINIYAABIVVADEVIITGEFSWFAAVAINIV	GIGREGOPK

650	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ			,
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Ì	\=possible nucleotide insertion)
			EYYTLDSILFLLNNVHLSHPVYVRRAATENIPVVRRPDRKDLLG
ļ			YLNGEASTSASIDRSAPLEIGLQRSTQVKRAADEVLAEAKKPRI
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	1		EDEECVRLDKERLAARLEGHKEGIVQTEQIRSLSEAMSVEKIAA
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		1	RVWRTRTTILQSTGKNFSKNIFAILQSVKAREEGRAPEQRPAPN
ł	1	ľ	AAPVDPTLRTKQPIPAAYNRYDQERFKGKEETEGFKIDTMGTYH
			GMTLKSVTEGASARKTOTPAAQPVPRPVSQARPPPNQKKGSRTP
i	i	1	IIIIPAATTSLITMLNAKDLLQDLKFVPSDEKKKQGCQRENETL
į.			-
			IQRRKDQMQPGGTAISVTVPYRVVDQPLKLMPQDWDRVVAVFVQ
l			GPAWQFKGWPWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVQKW
1		1	DVTVLELSYHKRHLDRPVFLRVWETLDRYMVKHKSHLRF
6594	1	1096	EFPGRRFRGSQASPLCATCGPALLRAPTRAAMTRSLFKGNFWSA
			DILSTIGYDNIIOHLNNGRKNCKEFEDFLKERAAIBERYGKDLL
-	}		NLSRKKPCGQSEINTLKRALEVFKQQVDNVAQCHIQLAQSLREE
}	}	1	
		1	ARKMEEFREKQKLQRKKTELIMDAIHKQKSLQFKKTMDAKKNYE
<b>!</b>		1	QKCRDKDEAEQAVSRSANLVNPKQQEKLFVKLATSKTAVEDSDK
Ì		ł	AYMLHIGTLDKVREEWQSEHIKACEAFEAQECERINFFRNALWL
i			HVNQLSQQCVTSDEMYEQVRKSLEMCSIQRDIEYFVNQRKTGQI
			PPAPIMYENFYSSOKNAVPAGKATGPNLARRGPLPIPKSSPDDP
i			NYSLVDDYSLLYQ
6595	57	781	PLGTMSDSDLGEDEGLLSLAGKRKRRGNLPKESVKILRDWLYLH
0595	] =/	701	
			RYNAYPSEQEKLSLSGQTNLSVLQICNWFINARRRLLPDMLRKD
			GKDPNQFTISRRGGKASDVALPRGSSPSVLAVSVPAPTNVLSLS
ł		1	VCSMPLHSGQGEKPAAPFPRGELESPKPLVTPGSTLTLLTRAEA
Į.			GSPTGGLFNTPPPTPPEQDKEDFSSFQLLVEVALQRAAEMELQK
[			OODPSLPLLHTPIPLVSENPQ
6596	2	1026	PRLPVRRYHGRRRLOGRSRGHMAEGDAGSDORONEEIBAMAAIY
0370	-	1000	GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP
	ļ		_
	1		PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD
1			VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD
	i '	1	FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV
l	1		KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA
1		-	AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN
ļ			ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH
6597	<del> </del>	1026	PRLPVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAIY
659/	2	1026	
i			GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP
			PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD
			VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD
1			FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV
			KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA
			AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN
]			i
		<u> </u>	ILVEKNYTNSPBESSKALGKNKKVRKDKKRNEH
6598	1099	419	PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL
			VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE
			LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV
1			FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITVS
1			DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD
1	1		
		<u> </u>	SKGLQS
6599	164	1593	KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR
1			MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS
1	İ		DPOKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST
1			DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE
1		}	
1	1		LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE
ł			VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN
			EAVAAVTEEEHKLYDDIDFDIEEFAKDVGAQILLHSHKKDILMH
1	1		RWRYPSLSLHGIEGAFSGSGAKTVIPRKVVGKFSIRLVPNMTPE
	1	1	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
• • • •	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	1		VVGEQVTSYLTKKFAELRSPNEFKVYMGHGGKPWVSDFSHPHYL
			AGRRAMKTVFGVEPDLTREGGSIPVTLTFQEATGKNVMLLPVGS
			ADDGAHSQNEKLNRYNYIEGTKMLAAYLYEVSQLKD
6600	2	934	PGRLFRVAAMESAGLEQLLRELLLPDTERIRRATEQLQIVLRAP
			AALSALCDLLASAADPQIRQFAAVLTRRRLNTRWRRLAAEQRES
			LKSLILTALQRETEHCVSLSLAQLSATIFRKEGLEAWPQLLQLL
			OHSTHSPHSPEREMGLLLLSVVVTSRPEAFQPHHRELLRLLNET
	i		LGEVGSPGLLFYSLRTLTTMAPYLSTEDVPLARMLVPKLIMAMQ
			TLIPIDEAKACEALEALDELLESEVPVITPYLSEVLTFCLEVAR
			NVALGNAIRIRILCCLTFLVKVKSKALLKNRLLATLAAHPFPHC
1			GC
6601	529	1420	PRAAARAPPPAVLRRDRRAATAPGAGEMTLHGPLAQRYFLNHIE
5501	1		KITTWQDPRKAMNQPLNHMNLHPAVSSTPVPQRSMAVSQPNLVM
			NHOHOOOMAPSTLSOONHPTONPPAGLMSMPNALTTOQQQQQKL
		ì	RLORIOMERERIRMRQEELMRQEAALCRQLPMEAETLAPVQAAV
1		ł	NPPTMTPDMRSITNNSSDPFLNGGPYHSREQSTDSGLGLGCYSV
	1	i	PTTPEDFLSNVDEMDTGENAGQTPMNINPQQTRFPDFLDCLPGT
			NVDLGTLESEDLIPLFNDVESALNKSEPFLTWL
6602	127	617	LLDFPALPKFVLAQSPKAGKPSTMTSMTQSLREVIKAMTKARNF
""			ERVLGKITLVSAAPGKVICEMKVEEEHTNAIGTLHGGLTATLVD
		j	NISTMALLCTERGAPGVSVDMNITYMSPAKLGEDIVITAHVLKQ
			GKTLAFTSVDLTNKATGKLIAQGRHTKHLGN
6603	79	660	PVGPSSLAARTGLGHLPFLHRLASSRGLDMDLLQFLAFLFVLLL
			SGMGATGTLRTSLDPSLEIYKKMFBVKRREQLLALKNLAQLNDI
		1	HQQYKILDVMLKGLFKVLEDSRTVLTAADVLPDGPFPQDEKLKD
}	,		AFSHVVENTAFFGDVVLRFPRIVHYYFDHNSNWNLLIRWGISFC
		İ	NCTGVFNQGPHSPILSLM
6604	3	688	TSTAOROGGERMSFRGGGRGGFNRGGGGGGFNRGGSSNHFRGGG
			GGGGGNFRGGGRGGFGRGGGRGGFNKGQDQGPPERVVLLGEFL
1		Ì	HPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDEIFGQLR
		ì	DFYFSVKLSENMKASSFKKLQKFYIDPYKLLPLQRFLPRPPGEK
1			GPPRGGGRGGRGGGRGGGRGGGFRGGRG
			GGFRGRGH
6605	7	848	SGSRRGAMRAAGVGLVDCHCHLSAPDFDRDLDDVLEKAKKANVV
1			ALVAVAEHSGEFEKIMQLSERYNGFVLPCLGVHPVQGLPPEDQR
1			SVTLKDLDVALPIIENYKDRLLAIGEVGLDFSPRFAGTGEQKEE
1		1	QRQVLIRQIQLAKRLNLPVNVHSRSAGRPTINLLQEQGAEKVLL
			HAFDGRPSVAMEGVRAGYFFSIPPSIIRSGQQKLVKQLPLTSIC
1			LETDSPALGPEKQVRNEPWNISISARYIAQVKGISVEEVIEVTT
			QNALKLFPKLRHLLQK
6606	2	1682	FVEIRPRAEVANLSAHSASPIQDAVLKRLSLLEDIVYRQLNGLS
			KSLGLIEGYGGRGKGGLPATLSPAEEEKAKGPHBKYGYNSYLSE
1			KISLDRSIPDYRPTKCKELKYSKDLPQISIIFIFVNEALSVILR
1			SVHSAVNHTPTHLLKEIILVDDNSDEBELKVPLBEYVHKRYPGL
1	1		VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAEP
1		}	VLSRIQENRKRVILPSIDNIKQDNFEVQRYENSAHGYSWELWCM
			YISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKFFGEIGLLDPG
			MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKKPYNSNI
1			GFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER
1	]	1	RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC
			LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP
1	1		DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG
1			RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK
6607	137	986	VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSRQTT
"""	1		GISFQGRGGAGPGVPTRTQVFAAMGAVMGTFSSLQTKQRRPSKD
			KIEDELEMTMVCHRPEGLEQLEAQTNFTKRELQVLYRGFKNECP
}			VIEDEDELI MACUKAEGIEĞI EVĞINLI IVVEDĞADI VQI VAECA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:		1	H=Histidine, I=Isoleucine, K=Lysine,
1	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
Ī	sequence		\=possible nucleotide insertion)
			SGVVNEDTFKQIYAQFFPHGDASTYAHYLFNAFDTTQTGSVKFE
	į.	ł	DFVTALSILLRGTVHEKLRWTFNLYDINKDGYINQEEMMDIVKA
1	1	1	IYDMMGKYTYPVLKEDTPRQHVDVFFQKMDKNKDGIVTLDEFLE
			SCOEDDNIMRSLOLFONVM
6608	224	1140	RPCFSSPTGLCPRLSYPMILLOHAVLPPPKQPSPSPPMSVATRS
0000	223	1110	TGTLQLPPQKPFGQEASLPLAGEEELSKGGEQDCALEELCKPLY
ļ			CKLCNVTLNSAOOAOAHYQGKNHGKKLRNYYAANSCPPPARMSN
1			VVEPAATPVVPVPPQMGSFKPGGRVILATENDYCKLCDASFSSP
	1		
	l .	1	AVAQAHYQGKNHAKRLRLAEAQSNSFSESSELGQRRARKEGNEF
	•	1	KMMPNRRNMYTVQNNSGPYFNPRSRQRIPRDLAMCVTPSGQFYC
			SMCNVGAGEEMEFRQHLESKQHKSKVSEQRYRNEMENLGYV
6609	1	. 443	FRLRCRRFRVAGGRLAGAGLRESRVPAPEQRLSALTLLSWSAVT
		,	PAAEPGNFQLSPAEPRGPLASPVRAAPRAPCPAAEMSELNTKTS
l	1		PATNQAAGQEEKGKAGNVKKAEEEEEIDIDLTAPETEKAALAIQ
ĺ	1	1	GKFRRFQKRKKDPSS
6610	319	881	GRKSLCNLHIFIRFPLTYPDMYMGMMCTAKKCGIRFQPPAIILI
1 0010	313		YESEIKGKIRQRIMPVRNFSKFSDCTRAAEQLKNNPRHKSYLEQ
1			VSLRQLEKLFSFLRGYLSGQSLAETMEQIQRETTIDPEEDLNKL
1		ł	DDKELAKRKSIMDELFEKNQKKKDDPNFVYDIEVEFPQDDQLQS
	†	İ	CGWDTESADEF
6611	978	212	PGCSGAGSRVWWLPALRHLAMGSTBSSEGRRVSFGVDEBERVRV
1		1	LQGVRLSENVVNRMKEPSSPPPAPTSSTFGLQDGNLRAPHKEST
J		}	LPRSGSSGGQQPSGMKEGVKRYEQEHAAIQDKLFQVAKREREAA
ì			TKHSKASLPTGEGSISHBEQKSVRLARELESREAELRRRDTFYK
			EQLERIERKNAEMYKLSSEQFHEAASKMESTIKPRRVEPVCSGL
			QAQILHCYRDRPHEVLLCSDLVKAYQRCVSAAHKG
6612	1724	992	VSTHASALSRTQGQPQRQPRAAASGAGAGTAGGGGSGGAEGSKM
			STEAQRVDDSPSTSGGSSDGDQRESVQQEPEREQVQPKKKEGKI
			SSKTAAKLSTSAKRIQKELAEITLDPPPNCSAGPKGDNIYEWRS
			TILGPPGSVYEGGVFFLDITFSPDYPFKPPKVTFRTRIYHCNIN
ì			SQGVICLDILKDNWSPALTISKVLLSICSLLTDCNPADPLVGSI
1	ì		ATOYMTNRAEHDRMARQWTKRYAT
	130	748	ELELSSNMPEOSNDYRVAVFGAGGVGKSSLVLRFVKGTFRESYI
6613	130	/40	PTVEDTYROVISCDKSICTLQITDTTGSHQFPAMQRLSISKGHA
1			
1	i	1	FILVYSITSRQSLEELKPIYEQICEIKGDVESIPIMLVGNKCDE
1	1		SPSREVQSSEARALARTWKCAFMETSAKLNHNVKELFQELLNLE
			KRRTVSLQIDGKKSKQQKRKEKLKGKCVIM
6614	3	1191	SSAAEAMRVLVRRCWGPPLAHGARRGRPSPQWRALARLGWEDCR
			DSRVREKPPWRVLFFGTDQFAREALRALHAARENKEEELIDKLE
1			VVTMPSPSPKGLPVKQYAVQSQLPVYEWPDVGSGEYDVGVVASF
i		1	GRLLNEALILKFPYGILNVHPSCLPRWRGPAPVIHTVLHGDTVT
			GVTIMQIRPKRFDVGPILKQETVPVPPKSTAKELEAVLSRLGAN
			MLISVLKNLPESLSNGRQQPMEGATYAPKISAGTSCIKWEEQTS
1			EQIFRLYRAIGNIIPLQTLWMANTIKLLDLVEVNSSVLADPKLT
1	1		GQALIPGSVIYHKQSQILLVYCKDGWIGVRSVMLKKSLTATDFY
1			NGYLHPWYQKNSQAQPSQCRFQTLRLPTKKKQKKTVAMQQCIE
-	1	<del>                                     </del>	GRVGAGASAMSELPGDVRAFLREHPSLRLQTDARKVRCILTGHE
6615	832	35	
ļ			LPCRLPELQVYTRGKKYQRLVRASPAFDYAEFEPHIVPSTKNPH
	1		QLFCKLTLRHINKCPEHVLRHTQGRRYQRALCKYBECQKQGVEY
			VPACLVHRRRREDQMDGDGPRPREAFWEPTSSDEGGAASDDSM
1			TDLYPPELFTRKDLGSTEDGDGTDDFLTDKEDEKAKPPREKATD
			EGRRETTVYRGLVQKRGKKQLGSLKKKPKSHHRKPKSFSSCKQS
1			G
6616	347	1886	LLPPCQGARPLSSPPHASEDNLFLFWNCILCAFPHPSPQPLQYP
			VWPLLLVITQIPAPRHLRNRPFSFSRGGLDSFSGSLSTPSICRS
L	_!		

		Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	sequence	\=possible nucleotide insertion)
	Bequence	<del>                                     </del>	PAWVKMAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSP
,			PPOPHPCHTCRGLVDSFNKGLERTIRDNFGGGNTAWEEENLSKY
			KDSETRLVEVLEGVÇSKSDFECHRLLBLSEBLVESWWFHKQQEA
			PDLFOWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEG
			EGTRGGSGHCDCQAGYGGEACGQCGLGYFEAERNASHLVCSACF
			GPCARCSGPEESNCLQCKKGWALHHLKCVDIDECGTEGANCGAD
			QFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKC
1			LDVDECETEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQ
			IPESAGFFSEMTEDELVVLQQMFFGIIICALATLAAKGDLVFTA
			IFIGAVAAMTGYWLSERSDRVLEGFIKGR
6617	118	673	VWMAWQVSLLELEDRLQCPICLEVFKESLMLQCGHSYCKGCLVS
331,			LSYHLDTKVRCPMCWQAVDGSSSLPNVSLAWVIEALRLPGDPEP
			KVCVHHRNPLSLFCEKDQELICGLCGLLGSHQHHPVTPISTVCS
			RMKEELAALFSELKQEQKKVDELIAKLVKNRTRIDGSAPSLCPC
	1		LGPATFTFL
6618	548	136	DGKVARRAPNSPAFQNDIYPLVSAPRATTAESPWSKVLQNTQCR
1 3323			NVPKMTSERSRIPCLSAAAAEGTGKKQQEGRAMATLDRKVPSPE
i			AFLGKPWSSWIDAAKLHCSDNVDLEEAGKEGGKSREVMRLNKEA
			WKYGT
6619	246	842	PASSEVLTAAVMFLLLNCIVAVSQNMGIGKNGDLPRPPLRNEFR
0025			YFQRMTTTSSVEGKQNLVIMGRKTWFSIPEKNRPLKDRINLVLS
1			RELKEPPQGAHFLARSLDDALKLTERPELANKVDMIWIVGGSSV
			YKEAMNHLGHLKLFVTRIMQDFESDTFFSEIDLEKYKLLPEYPG
			ILSDVQEGKHIKYKFEVCEKDD
6620	3	1879	NSRVDDFVARARMAAENEASQESALGAYSPVDYMSITSFPRLPE
			DEPAPAAPLRGRKDEDAFLGDPDTDPDSFLKSARLQRLPSSSSE
			MGSQDGSPLRETRKDPFSAAAAECSCRQDGLTVIVTACLTFATG
1			VTVALVMQIYFGDPQIFQQGAVVTDAARCTSLGIEVLSKQGSSV
İ			DAAVAAALCLGIVAPHSSGLGGGGVMLVHDIRRNESHLIDFRES
ļ	}		APGALREETLQRSWETKPGLLVGVPGMVKGLHEAHQLYGRLPWS
1			QVLAFAAAVAQDGFNVTHDLARALAEQLPPNMSERFRETFLPSG
]	1		RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ
ĺ			HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPPPHTGPALI
			SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGDPVYD
1	1.		STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT
	1		AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS
	1		WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA
			LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV
			SIPHAANMG     VOGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP
6621	1	662	VQGITSYQQRLQALRKEKSKDAAKSKRGKENFEFIEDAKDDPDF
		1	AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT
	1		SVKVIGAQRRRSPSALAIEVFEAHLGSHILQSLDGYVFALNQEG
			KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK
L			LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCFPPASDQFLL
6622	2	319	GRASGAQEETEAGGPERARAMEANMPKRKEPGRSLRIKVISMGN
1			AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN
L			1FDMAGHPFFYEVRKPF
6623	1886	189	KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA
1			LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF
1	1	1	VSIYGLTCLYTLYWLFYRSLREYSFEYVRQETGFDDIPDVKNDF
1		1	AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL
ì		i i	
			RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM
			RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD
			RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLEELYLVGSLSHDISRNVTLESLRDLKSLKI
			RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD

			Table 13
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, B=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	Codon, /=possible nucleotide deletion,
Ì	amino acid	sequence	
	sequence		\=possible nucleotide insertion)
			HLRKLTVLKLWHNSITYIPEHIKKLTSLERLSFSHNKIEVLPSH
			LFLCNKIRYLDLSYNDIRFIPPEIGVLQSLQYFSITCNKVESLP
		-	DELYFCKKLKTLKIGKNSLSVLSPKIGNLLFLSYLDGKGNHFEI
			LPPELGDCRALKRAGLVVEDALFETLPSDVREQMKTE
6624	218	1786	GSRRGGGSRIPAVSTHVAPGRSVLRPPASGALRLRSLVKALGGC
İ		1	RGRPSGLAHLSQETSHWRAKRSGRACLGDFPGEILRSFIMKCTA
1			REWLRVTTVLFMARAIPAMVVPNATLLEKLLEKYMDEDGEWWIA
l			KQRGKRAITDNDMQSILDLHNKLRSQVYPTASNMEYMTWDVELE
ŀ			RSAESWAESCLWEHGPASLLPSIGQNLGAHWGRYRPPTFHVQSW
1		ļ	YDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIGC
			AINLCHNMNIWGQIWPKAVYLVCNYSPKGNWWGHAPYKHGRPCS
1	1		ACPPSFGGGCRENLCYKEGSDRYYPPREEETNEIERQQSQVHDT
		1	HVRTRSDDSSRNEVISAQQMSQIVSCEVRLRDQCKGTTCNRYEC
1			PAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITR
			QGRKHYFIKSNRNGIQTIGKYQSANSFTVSKVTVQAVTCETTVE
			QLCPFHKPASHCPRVYCPRKLYASKSTLCSCNWNSSLF
6625	1124	543	PGPRGGGGSLLSTKALGRSRGLGMHPGPSSGGTEGGVPTALRPP
			GPLVPSTSDDNLLKNIELFDKLALRFHGRLLFLKDVLGDEICCW
j			SFYGQGRKIAEVCCTSIVYATEKKQTKVEFPEARIFEETLNILI
			YETPRGPDPALLEATGGAAGAGGAGRGEDEENREHRVRRIHVRR
			HITHDERPHGQQIVFKD
6626	3	1498	SAVEFVYTDRFHLILGISVEFLCSLRSDATMESITACLHALQAL
		ļ	LDVPWPRSKIGSDQDSGIELLNVLHRVILTRESPSIQLASLEVV
1			RQIICAAQEHVKEKRRSAEVDDGAAEKETLPEFGEGKDTGGLVP
1			GKSLVFATLELCVCILVRQLPELNPKLTGSPGVKATKPQILLED
l l			GSRLVSAALVILSELPAVCSPEGSISILPTILYLTIGVLRETAV
1			KLPGGQLSSTVAASLQALKGILSSPMARABKSRTAWTDLLRSAL
			TTILDCWDPVDETHQELDEVSLLTAITVFILSTSPEVTTIPCLQ
-			KRCIDKFKATLEIKDPVVQIKTYQLLHSIFQYPNPAVSYPYIYS
İ	1		LASCIMEKLQEIDKRKPENTAELEIFQEGIKVLETLVTVAEEHH
			RAQLVACLLPILISFLLDENSLGSATSIMRNLHDFALQNLMQIG
1	İ	j	PQYSSVFKSLVASSPALKARLEAAIKGNQESVKVKIPTSKYTKS
-		1	PGKNSSIQLKTSFL
6627	1	697	GIPHLSSRDMTGTPGAVATRDGEAPERSPPCSPSYDLTGKVMLL
			GDTGVGKTCFLIQFKDGAFLSGTFIATVGIDFRNKVVTVDGVRV
1		1	KLQIWDTAGQERFRSVTHAYYRDAQALLLLYDITNKSSFDNIRA
			WLTEIHEYAQRDVVIMLLGNKADMSSERVIRSEDGETLAREYGV
	1		PFLETSAKTGMNVELAFLAIAKELKYRAGHQADEPSFQIRDYVE
			SQKKRSSCCSFM
6628	1	1861	QCAEFGGGSGGGGGGGGGGGGGGGEENKENERPSAGS KAN
	1		KEFGDSLSLEILQIIKESQQQHGLRHGDFQRYRGYCSRRQRRLR
		1	KTLNFKMGNRHKFTGKKVTEELLTDNRYLLLVLMDAERAWSYAM
		1	QLKQEANTEPRKRFHLLSRLRKAVKHAEELERLCESNRVDAKTK
			LEAQAYTAYLSGMLRFEHQEWKAAIEAFNKCKTIYEKLASAFTE
1			EQAVLYNQRVEEISPNIRYCAYNIGDQSAINBLMQMRLRSGGTE
1		1	GLLAEKLEALITQTRAKQAATMSEVEWRGRTVPVKIDKVRIFLL
1			GLADNEAAIVQAESEETKERLFESMLSECRDAIQVVREELKPDQ
1			KQRDYILEGEPGKVSNLQYLHSYLTYIKLSTAIKRNENMAKGLQ
			RALLQQQPEDDSKRSPRPQDLIRLYDIILQNLVELLQLPGLEED
1			KAFQKEIGLKTLVFKAYRCFFIAQSYVLVKKWSEALVLYDRVLK
			YANEVNSDAGAFKNSLKDLPDVQELITQVRSEKCSLQAAAILDA
			NDAHQTETSSSQVKDNKPLVERFETFCLDPSLVTKQANLVHFPP
		}	GFQPIPCKPLFFDLALNHVAFPPLEDKLEQKTKSGLTGYIKGIF
			GFRS
6629	5653	4549	GATPLGSVGGRTGKMDAATLTYDTLRFAEFEDFPETSEPVWILG
3023	]		RKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGWGC
	· <del></del>		

C CEO	Dan 24 - h - J	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	(	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
}	location	corresponding	
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
J	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sedneuce	Codon, /=possible nucleotide deletion,
	sequence		\-possible nucleotide insertion)
Ì			MLRCGQMIFAQALVCRHLGRDWRWTQRKRQPDSYFSVLNAFIDR
		1	KDSYYSIHQIAQMGVGEGKSIGQWYGPNTVAQVLKKLAVFDTWS
}	l	}	SLAVHIAMDNTVVMEEIRRLCRTSVPCAGATAFPADSDRHCNGF
ľ			PAGAEVTNRPSPWRPLVLLIPLRLGLTDINEAYVETLKHCFMMP
			QSLGVIGGKPNSAHYFIGYVGEELIYLDPHTTQPAVEPTDGCFI
			PDESFHCQHPPCRMSIAELDPSIAVVRGGHLSTQAFGAECCLGM
			TRKTFGFLRFFFSMLG
6630	2	423	LVQCGGTRRRSAWGAMPGRHVSRVRALYKRVLQLHRVLPPDLKS
ļ	Ì		LGDQYVKDEFRRHKTVGSDEAQRFLQEWEVYATALLQQANENRQ
İ			NSTGKACFGTFLPEEKLNDFRDEQIGQLQELMQEATKPNRQFSI
			SBSMKPKF
6631	2	423	LVQCGGIRRRSAWGAMPGRHVSRVRALYKRVLQLHRVLPPDLKS
1	1		LGDQYVKDEFRRHKTVGSDEAQRFLQEWEVYATALLQQANENRQ
			NSTGKACFGTFLPEEKLNDFRDEQIGQLQELMQEATKPNRQFSI
	<u> </u>		SESMKPKF
6632	1273	588	WNSRGRTQRGAAPLAPAAAMKAVVQRVTRASVTVGGEQISAIGR
			GICVLLGISLEDTQKELEHMVRKILNLRVFEDESGKHWSKSVMD
1			KQYEILCVSQFTLQCVLKGNKPDFHLAMPTEQAEGFYNSFLEQL
			RKTYRPELIKDGKFGAYMQVHIQNDGPVTIELESPAPGTATSDP
			KQLSKLEKQQQRKEKTRAKGPSESSKERNTPRKEDRSASSGAEG
L			DVSSEREP
6633	1145	617	ATGRHEGVPTLEGIIQQLVNGIITPATIPSLGPWGVLHSNPMDY
			AWGANGLDAIITQLLNQFENTGPPPADKEKIQALPTVPVTEEHV
1			GSGLECPVCKDDYALGERVRQLPCNHLFHDGCIVPWLEQHDSCP
			VCRKSLTGQNTATNPPGLTGVSFSSSSSSSSSSSSSSSNENATSNS
6634	1	1134	CGGIPRKGSGPRRRLPMARLRDCLPRLMLTLRSLLFWSLVYCYC
	1		GLCASIHLLKLLWSLGKGPAQTFRRPAREHPPACLSDPSLGTHC
İ		1	YVRIKDSGLRFHYVAAGERGKPLMLLLHGFPEFWYSWRYQLREF
	1	ļ	KSEYRVVALDLRGYGETDAPIHRQNYKLDCLITDIKDILDSLGY
	İ		SKCVLIGHDWGGMIAWLIAICYPEMVMKLIVINFPHPNVFTEYI
			LRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHSTG
1			IGRKGCQLTTEDLEAYIYVFSQPGALSGPINHYRNIFSCLPLKH
	1		HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEASH
-6605	1	422	WLQQDQPDIVNKLIWTFLKEETRKKD
6635	1420	470	EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAPSSSSG
	1		GRGGAEPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK ILAQOTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG
			LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS
	1		HFATYVAAMRAINIADELPRSRARKLADEOLSSVIODMAVROHL
1	1		LTNLVEVDGRFVWRVNLDALTOHLDKILAFPOROESYLGPTLFL
			LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI
	1	İ	AAIRGFLV
6636	1514	1801	SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE
5555	1 -343	1	OPIVROCLORPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD
			DGGDGVF
6637	2	1501	CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI
000,		1301	KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT
		]	VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD
			LVRRRVLPMOVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG
			DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS
			CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW
1			FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR
1	1		DDDRDEKTIOSLQISAIILHPNYDPILLDADIAILKLLDKARIS
			TRVOPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL
			RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC
			TAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAF
L	1	L	

CRA	Dradicted	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide		H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	b=beucine, m=methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			TKVLPFKDWIERNMK
6638	1391	224	GGIPQAGGKMAAPWWRAALCECRRWRGFSTSAVLGRRTPPLGPM
6638	1391		PNSDIDLSNLERLEKYRSFDRYRRRAEQEAQAPHWWRTYREYFG
			EKTDPKEKIDIGLPPPKVSRTQQLLERKQAIQELRANVEEERAA
			RLRTASVPLDAVRAEWERTCGPYHKQRLAEYYGLYRDLFHGATF
		}	VPRVPLHVAYAVGEDDLMPVYCGNEVTPTEAAQAPEVTYEAEEG
	1		VPKVPLHVAYAVGEDDINIPVICONEVITIENTENTENTENTENTENTENTENTENTENTENTENTENTE
	1	ì	SLWTLLLTSLDGHLLEPDAEYLHWLLTNIPGNRVAEGQVTCPYL
}	1	1	PPFPARGSGIHRLAFLLFKQDQPIDFSEDARPSPCYQLAQRTFR
			TFDFYKKHQETMTPAGLSFFQCRWDDSVTYIFHQLLDMREPVFE
		1	FVRPPPYHPKQKRFPHRQPLRYLDRYRDSHEPTYGIY
6639	2046	1268	IGCFIMDGGDDGNLIIKKRFVSEAELDERRKRRQEEWEKVRKPE
""	7.77		DPBECPEEVYDPRSLYERLQEQKDRKQQEYEEQFKFKNMVRGLD
	1		EDETNFLDEVSRQQELIEKQRREEELKELKEYRNNLKKVGISQE
	i	1	NKKEVEKKLTVKPIETKNKFSQAKLLAGAVKHKSSESGNSVKRL
}			KPDPEPDDKNQEPSSCKSLGNTSLSGPSIHCPSAAVCIGILPGL
l	li e	ļ	GAYSGSSDSESSSDSEGTINATGKIVSSIFRTNTFLEAP
		<u> </u>	VLEPPDVSMAESEDRSLRIVLVGKTGSGKSATANTILGEEIFDS
6640	117	1043	VLEPPDVSMAESEDRSDRIVDVGRIGSGRAATAVIIIGEEIPDS
		ļ	RIAAQAVTKNCQKASREWQGRDLLVVDTPGLFDTKESLDTTCKE
1			ISRCIISSCPGPHAIVLVLLLGRYTEEEQKTVALIKAVFGKSAM
		l .	KHMVILFTRKEELEGQSFHDFIADADVGLKSIVKECGNRCCAFS
1			NSKKTSKAEKESQVQELVELIEKMVQCNEGAYFSDDIYKDTEER
	l	1	LKQREEVLRKIYTDQLNEEIKLVEEDKHKSEEKKEKEIKLLKLK
i			YDBKIKNIREEAERNIFKDVFNRIWKMLSEIWHRFLSKCKFYSS
6641	<del> </del>	894	SAAVGRRSEVRGCAPRPRLRRSARRMDPVPGTDSAPLAGLAWSS
9047	_		ASAPPPRGFSAISCTVEGAPASFGKSFAQKSGYFLCLSSLGSLE
1	l .		NPQENVVADIQIVVDKSPLPLGFSPVCDPMDSKASVSKKKRMCV
		Į.	KLLPLGATDTAVFDVRLSGKTKTVPGYLRIGDMGGFAIWCKKAK
	3		APRPVPKPRGLSRDMQGLSLDAASQPSKGGLLERTASRLGSRAS
!	1		TLRRNDSIYEASSLYGISAMDGVPFTLHPRFEGKSCSPLAFSAF
]	j.	ì	GDLTIKSLADIEEEYNYGFVVEKTAAARLPPSVS
1			PLEERMATKMDPNDQAQRDIIFELRRIAFDAESDPSNAPGSGTE
6642	22	1296	PLEEKWALKWDANDOWOKDI I FERKITALDWESDESWARGSGIE
		ı	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV
			HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP
		l	NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN
			KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER
ļ		ļ	MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG
}	i	J.	NRRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEKIPV
	1		ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF
1			IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL
			LDLENIQIPEAPPPIPKEPSSYDFVYHYG
1	<del></del>	3365	SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI
6643	3049	2265	
1		1	DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG
1	1		HDRTMQDIVYKLVPGLQBAEMRKQREFYHKLGMEVPGDIKGETC
			SAKOHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI
1	1		CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL
1			DILCNEEILGKDHTLKFVVVTRWRFKKAPLLLHYRPKMDLL
6644	1489	290	FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR
1	.====	1	LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR
1	l l	1	TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL
1			LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ
1			LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT
1			EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL
1			KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF
			LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY
1	1		LARLMGGMEIKKPSGPEPGFRUNDFTTDEBBBQAABIRPEBBSI
ı			
ł		Ì	EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM DEL

			In the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of th
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
!	to first	amino acid	S=Serine, T=Threonine, V=Valine,
j	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	Codon, /=possible nucleotide deletion,
	amino acid	sequence	Codon, /=possible nucleotide defection,
l	sequence		\=possible nucleotide insertion)
6645	6530	4646	FVEGLAGYVYKAASEGKVLTLAALLLNRSESDIRYLLGYVSQQG
			GQRSTPLIIAARNGHAKVVRLLLEHYRVQTQQTGTVRFDGYVID
			GATALWCAAGAGHFEVVKLLVSHGANVNHTTVTNSTPLRAACFD
ļ			GRLDIVKYLVENNANISIANKYDNTCLMIAAYKGHTDVVRYLLE
ì			QRADPNAKAHCGATALHFAAEAGHIDIVKELIKWRAAIVVNGHG
ļ			MTPLKVAAESCKADVVELLLSHADCDRRSRIEALELLGASFAND
		1	RENYDIIKTYHYLYLAMLERPQDGDNILEKEVLPPIHAYGNRTE
			CRNPQELESIRQDRDALHMEGLIVRERILGADNIDVSHPIIYRG
		1	AVYADNMEFEQCIKLWLHALHLRQKGNRNTHKDLLRFAQVFSQM
1			IHLNETVKAPDIECVLRCSVLEIEQSMNRVKNISDADVHNAMDN
	1	1	YECNLYTFLYLVCISTKTQCSBEDQCKINKQIYNLIHLDPRTRE
1		1	GFTLLHLAVNSNTPVDDFHTNDVCSFPNALVTKLLLDCGAEVNA
			VDNEGNSALHIIVQYNRPISDFLTLHSIIISLVEAGAHTDMTNK
			QNKTPLDKSTTGVSEILLKTQMKMSLKCLAARAVRANDINYQDQ
			IPRTLEEFVGFH
6646	176	890	PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY
			EGREKKGISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGIENTL
1			EKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL
			TTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWPLD
		Ì	FKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFYSPPESEA
			GSEEAEEKQDSEKPLLEL
6647	176	890	PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY
			EGREKKGISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGIENTL
1		İ	EKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL
			TTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLD
1			FKVLPQEAREENRLLIVQDASERAALIPGGLSDGQFYSPPESEA
			GSEEAEEKQDSEKPLLEL
6648	413	897	RNCWNCFTKYFNSPPEDIDHKDSYLITRSIMAEPDYIEDDNPEL
	1		IRPQKLINPVKTSRNHQDLHRELLMNQKRGLAPQNKPBLQKVME
1			KRKRDQVIKQKEEEAQKKKSDLEIELLKRQQKLEQLELEKQKLQ
1			EEQENAPEFVKVKGNLRRTGQEVAQAQES
6649	1357	832	WIPRAAGIRHEVKWDVKEIMSQHNIYVDALLKEFEQFNRRLNEV
			SKRVRIPLPVSNILWEHCIRLANRTIVEGYANVKKCSNEGRALM
			QLDFQQFLMKLEKLTDIRPIPDKEFVETYIKAYYLTENDMERWI
1			KEHREYSTKQLTNLVNVCLGSHINKKARQKLLAAIDDIDRPKR
6650	32	765	LVPLVFSLLVQSCKQVYRSIAMKFVPCLLLVTLSCLGTLGQAPR
			QKQGSTGEEFHFQTGGRDSCTMRPSSLGQGAGEVWLRVDCRNTD
			QTYWCEYRGQPSMCQAFAADPKSYWNQALQELRRLHHACQGAPV
			LRPSVCREAGPQAHMQQVTSSLKGSPEPNQQPEAGTPSLRPKAT
			VKLTEATQLGKDSMEELGKAKPTTRPTAKPTQPGPRPGGNEEAK
			KKAWEHCWKPFQALCAFLISFFRG
6651	3425	1353	AKELLKVGDFSLCAGPYQNTADTMENLSKEPLASFVSESFDISA
1			CGIATEHVKIDNSGEGLTAEAGSETLSRDGEVGVNSDMHYELSG
1		1	DSDLDLLGDCRNPRLDLEDSYTLRGSYTRKKDVPTDGYESSLNF
İ	ļ	1	HNNNQEDWGCSSWVPGMETSLPPGHWTAAVKKEEKCVPPYVQIR
	1	1	DLHGILRTYANFSITKELKDTMRTSHGLRRHPSFSANCGLPSSW
1	1	1	TSTWQVADDLTQNTLDLEYLRFAHKLKQTIKNGDSQHSASSANV
	1	1	FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSPLLVTVVESDP
	1	1	RPQGQPRRGYTASSLDSSSSWRERCSHNRDLRNSQRNHTVSFHL
			NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNQFIFQDKELN
			DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA
1			CKSTFLFYLVETEDKSFFVRTKNLLRKGGHTEIEPQHFCQAFHR
[		1	ENDTLIIIIRNEDISSHLHQIPSLLKLKHFPSVIFAGVDSPGDV
	}		LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG
			RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFQSANIIELLH
			YHQCDSRSSTKAEILKCLLNLQIQHIDARFAVLLTDKPTIPREV

SEQ Predicted	Predicted end	Amino acid segment containing signal peptide
ID beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO: nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
amino acid	residue of	S=Serine, T=Threonine, V=Valine,
residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
amino acid	sequence	Codon, /=possible nucleotide deletion,
sequence	sequence	\=possible nucleotide insertion)
sequence		FENNGILVTDVNNFIENIEKIAAPFRSSYW
	1343	IPGSTISCSCHSRRLRGGSPAPRLSLGAASPRPRPPSLPLPLPL
6652 2	1343	
		PFPLFLPTRPAERAWIRSRRASEWVGKMEVPRLDHALNSPTSPC
		EEVIKNLSLEAIQLCDRDGNKSQDSGIAEMEELPVPHNIKISNI
1		TCDSFKISWEMDSKSKDRITHYFIDLNKKENKNSNKFKHKDVPT
		KLVAKAVPLPMTVRGHWFLSPRTEYTVAVQTASKQVDGDYVVSE
		WSEIIEFCTADYSKVHLTQLLEKAEVIAGRMLKFSVFYRNQHKE
		YFDYVREHHGNAMQPSVKDNSGSHGSPISGKLEGIFFSCSTEFN
		TGKPPQDSPYGRYRFEIAAEKLFNPNTNLYFGDFYCMYTAYHYV
		ILVIAPVGSPGDEFCKQRLPQLNSKDNKFLTCTEEDGVLVYHHA
		QDVILEVIYTDPVDLSLGTVAEITGHQLMSLSTANAKKDPSCKT
1		CNISVGR
6653 170	1910	FFLEPRLRPFPASRARFVPARTRPSPLHPCCFCFEGGGSMLSPQ
F I		RVAAAASRGADDAMESSKPGPVQVVLVQKDQHSFELDEKALASI
		LLQDHIRDLDVVVVSVAGAFRKGKSFILDFMLRYLYSQKESGHS
		NWLGDPEEPLTGFSWRGGSDPETTGIQIWSEVFTVEKPGGKKVA
1	ŀ	VVLMDTQGAFDSQSTVKDCATIFALSTMTSSVQIYNLSQNIQED
j	Į.	DLQQLQLFTEYGRLAMDEIFQKPFQTLMPLVRDWSFPYEYSYGL
		QGGMAFLDKRLQVKEHQHEEIQNVRNHIHSCFSDVTCFLLPHPG
		LQVATSPDFDGKLKDIAGEFKEQLQALIPYVLNPSKLMEKEING
		SKVTCRGLLEYFKAYIKIYQGEDLPHPKSMLQATAEAYNLAAAA
1		SAKDIYYNNMEEVCGGEKPYLSPDILEEKHCEFKQLALDHFKKT
		KKMGGKDFSFRYQQBLEEEIKELYENFCKHNGSKNVFSTFRTPA
1		VLFTGIVALYIASGLTGFIGLEVVAQLFNCMVGLLLIALLTWGY
		IRYSGQYRELGGAIDFGAAYVLEQASSHIGNSTQATVRDAVVGR
		PSMDKKAQ
6654 1	705	RTSLSPSQCSSFNLAMASAGMQILGVVLTLLGWVNGLVSCALPM
		WKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQMQCKVYDSLLAL
		PQDLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARL
		VLTSGIVFVISGVLTLIPVCWTAHAVIRDFYNPLVAEAQKRELG
		ASLYLGWAASGLLLLGGGLLCCTCPSGGSQGPSHYMARYSTSAP
		AISRGPSEYPTKNYV
6655 341	16	KDAYMFKKGLLALALVFSLPVFAAEHWIDVRVPEQYQQEHVQGA
		INIPLKEVKERIATAVPDKNDTVKVYCNAGRQSGQAKEILSEMG
		YTHVENAGGLKDIAMPKVKG
6656 2	1212	TELPPRPANLAIQPPLSPLRALAPLPEKPGAVPPPQKRMAKVAK
1		DLNPGVKKMSLGQLQSARGVACLGCKGTCSGFEPHSWRKICKSC
		KCSOEDHCLTSDLEDDRKIGRLLMDSKYSTLTARVKGGDGIRIY
		KRNRMIMTNPIATGKDPTFDTITYEWAPPGVTQKLGLQYMELIP
		KEKQPVTGTEGAFYRRRQLMHQLPIYDQDPSRCRGLLENELKLM
		EEFVKQYKSEALGVGEVALPGQGGLPKEBGKQQEKPEGAETTAA
1	1	TINGSLSDPSKEVEYVCELCKGAAPPDSPVVYSDRAGYNKQWHP
		TCFVCAKCSEPLVDLIYFWKDGAPWCGRHYCESLRPRCSGCDEI
		IFAEDYQRVEDLAWHRKHFVCEGCEQLLSGRAYIVTKGQLLCPT
		CSKSKRS
6653	2120	LLTCQERAGDCLLSASTMKEVVYWSPKKVADWLLENAMPEYCEP
6657 830	2120	1
		LEHFTGODLINLTQEDFKKPPLCRVSSDNGQRLLDMIETLKMEH
		HLEAHKNGHANGHLNIGVDIPTPDGSFSIKIKPNGMPNGYRKEM
		IKIPMPELERSQYPMEWGKTFLAFLYALSCFVLTTVMISVVHER
1	1	VPPKEVQPPLPDTFFDHFNRVQWAFSICEINGMILVGLWLIQWL
		LLKYKSIISRRFFCIVGTLYLYRCITMYVTTLPVPGMHFNCSPK
		LFGDWEAQLRRIMKLIAGGGLSITGSHNMCGDYLYSGHTVMLTL
		TYLFIKEYSPRRLWWYHWICWLLSVVGIFCILLAHDHYTVDVVV
1	I .	AYYITTRLFWWYHTMANOOVLKEASQMNLLARVWWYRPFQYFEK
1		
6658 35	855	NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT HCCALGAPGSPYRGLYFSSAAPCTAPRKAKHQSTLEGLTKRMLM

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ĺ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
]	amino acid	sequence	Codor, /=possible nucleotide deletion,
ì	sequence	_	\=possible nucleotide insertion)
	· · · · · ·		FDPVPVKQEAMDPVSVSYPSNYMESMKPNKYGVIYSTPLPEKFF
			OTPEGLSHGIOMBPVDLTVNKRSSPPSAGNSPSSLKFPSSHRRA
<b>,</b>			SPGLSMPSSSPPIKKYSPPSPGVQPFGVPLSMPPVMAAALSRHG
			IRSPGILPVIQPVVVQPVPFMYTSHLQQPLMVSLSEEMENSSSS
			MOVPVIESYEKPISOKKIKIEPGIEPORTDYYPEEMSPPLMNSV
		j	SPPOALLOE
			EPORGDCETWFONCSLPKFVCFFCWGFWLWRAHSMSNLHSLPGL
6659	18	523	1 7
			RGLTSISRNQLQCTNAMRVINNYQRRWKNQNTFLLATFANVVNV
1			CGNPTITCPHNRTLNNCHHSGVQVPLMYCNLTTPSPQNISNCRY
1			AQTPANMFYIVACDNRDQRRDPPQYPVVPVHLHTII
6660	514	1707	CAASLDCRHHLCEPDMKLVWPSAKLLQAAAGASARACDSVTSNV
1			LPLLLEQFHKHSQSSQRRTILEMLLGFLKLQQKWSYEDKDQRPL
1	ĺ		NGFKDQLCSLVFMALTDPSTQLQLVGIRTLTVLGAQPDLLSYED
į			LELAVGHLYRLSFLKEDSQSCRVAALEASGTLAALYPVAFSSHL
:			VPKLAEELRVGESNLTNGDEPTQCSRHLCCLQALSAVSTHPSIV
			KETLPLLLQHLWQVNRGNMVAQSSDVIAVCQSLRQMAEKCQQDP
			ESCWYFHQTAIPCLLALAVQASMPEKEPSVLRKVLLEDEVLAAM
			VSVIGTATTHLSPELAAQSVTHIVPLFLDGNVSFLPENSFPSRF
			QPFQDGSSGQRRLIALLMAFVCSLPRNVSEHIWEVLLFNLDKVT
i			PG
6661	179	430	GVHAASGTLSATWLAEAKMFDSLAKAGKYLGQAAKLMIGMPDYD
. 5001	1//	1 230	NYVEHMRVNHPDQTPMTYEEFFRERQDARYGGKGGARCC
6662	185	423	RSLPKPAPAOPASIHCARFSGVTPPTAKTAMSDGNTAFNALMYC
0002	103	423	GPKADDGNIFSACAPASSAVKASVSVAQPGQAVIP
-	<u> </u>	1005	RPVLSSRVDDFVPPLPETSGRRKKLERMYSVDRVSDDIPIRTWF
6663	3	1005	PKENLFSFOTASTTMQAISNFRKHLRMVGSRRVKAQTFAERRER
ì			
			SFSRSWSDPTPMKADTSHDSRDSSDLQSSHCTLDEAFEDLDWDT
			EKGLEAVACDTEGFVPPKVMLISSKVPKAEYIPTIIRRDDPSII
			PILYDHEHATFEDILEEIERKLNVYHKGAKIWKMLIFCQGGPGH
1			LYLLKNKVATFAKVEKEEDMIHFWKRLSRLMSKVNPEPNVIHIM
	1		GCYILGNPNGEKLFQNLRTLMTPYRVTFESPLELSAQGKQMIET
			YFDFRLYRLWKSRQHSKLLDFDDVL
6664	58	968	PRLLRLPRSVVVMDSPWDELALAFSRTSMFPFFDIAHYLVSVMA
1			VKROPGAAALAWKNPISSWFTAMLHCFGGGILSCLLLAEPPLKF
		1	LANHTNILLASSIWYITFFCPHDLVSQGYSYLPVQLLASGMKEV
			TRTWKIVGGVTHANSYYKNGWIVMIAIGWARGAGGTIITNFERL
			VKGDWKPEGDEWLKMSYPAKVTLLGSVIFTFQHTQHLAISKHNL
1			MFLYTIFIVATKITMMTTQTSTMTFAPFEDTLSWMLFGWQQPFS
			SCEKKSEAKSPSNGVGSLASKPVDVASDNVKKKHTKKNE
6665	171	1278	DERRLACROVVTQQRSELYPGFQKRQRFLPKAGEEAAAQGGRHL
	]		PGRWLGPGCTQNPCSVHTATGPEPRKLPLLPPDSPNSGYPKEPA
			ALCPGIPSPCRMTHODLSITAKLINGGVAGLVGVTCVFPIDLAK
1	1		TRLONOHGKAMYKGMIDCLMKTARAEGFFGMYRGAAVNLTLVTP
			EKAIKLAANDFFRRLLMEDGMQRNLKMEMLAGCGAGMCQVVVTC
	1		PMEMLKIQLQDAGRLAVHHQGSASAPSTSRSYTTGSASTHRRPS
1	1	1	ATLIAWELLRTQGLAGLYRGLGATLLRDIPFSIIYFPLFANLNN
		}	LGFNELAGKASFAHSFVSGCVAGSIAAVAVTPLDVLKTRIQTLK
			KGLGEDMYSGITDCAR
6666	498	2868	MTTFLPVPQMMAGFSFGTFGNPPMESPSAWQTIHQPFIVSCLTL
	1		WSPGCWPQPIQKEGVGLWDIRKPQSSLLRYGGNLSLQSAMSVRF
			NSNGTQLLALRRRLPPVLYDIHSRLPVFQFDNQVYFNSCTMKSC
]	1		CFAGDRDQYILSGSDDFNLYMWRIPADPEAGGIGRVVNGAFMVL
		1	KGHRSIVNQVRFNPHTYMICSSGVBKIIKIWSPYKQPGCTGDLD
		1	GRIEDDSRCLYTHEEYISLVLNSGSGLSHDYANQSVQEDPRMMA
1	1		FFDSLVRREIEGWSSDSDSDLSESTILQLHAGVSERSGYTDSES
			SASLPRSPPPTVDESADNAFHLGPLRVTTTNTVASTPPTPTCED
L			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
MO.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
		sequence	\=possible nucleotide insertion)
	sequence		AASRQQRLSALRRYQDKRLLALSNESDSEENVCEVELDTDLFPR
			PRSPSPEDESSSSSSSSSSEDEELNERRASTWORNAMRRROKT
			TREDKPSAPIKPTNTYIGEDNYDYPQIKVDDLSSSPTSSPERST
			STLEIQPSRASPTSDIESVERKIYKAYKWLRYSYISYSNNKDGE
			TSLVTGEADEGRAGTSHKDNPAPSSSKEACLNIAMAQRNQDLPP
			EGCSKDTFKEETPRTPSNGPGHEHSSHAWAEVPEGTSQDTGNSG
			SVEHPFETKKLNGKALSSRAEEPPSPPVPKASGSTLNSGSGNCP
			RTQSDDSEERSLETICANHNNGRLHPRPPHPHNNGQNLGELEVV
			AYSSPGHSDTDRDNSSLTGTLLHKDCCGSEMACETPNAGTREDP
			TDTPATDSSRAVHGHSGLKRQRIELEDTDSENSSSEKKLKT
6667	171	1310	ABEVERLAAMRSDSLVPGTHTPPIRRRSKFANLGRIFKPWKWRK
			KKSEKFKHTSAALERKISMRQSREELIKRGVLKEIYDKDGELSI
	1		SNEEDSLENGQSLSSSQLSLPALSEMEPVPMPRDPCSYEVLQPS
			DIMDGPDPGAPVKLPCLPVKLSPPLPPKKVMICMPVGGPDLSLV
		1	SYTAQKSGQQGVAQHHHTVLPSQIQHQLQYGSHGQHLPSTTGSL
			PMHPSGCRMIDELNKTLAMTMQRLESSEQRVPCSTSYHSSGLHS
	j	ļ	GDGVTKAGPMGLPEIRQVPTVVIECDDNKENVPHESDYEDSSCL
			YTREEEEEEBDEDDDSSLYTSSLAMKVCRKDSLAIKPSNRPSKR
			ELEEKNILPRQTDEERLELRQQIGTKL
6668	714	358	TLAVATGPALTLECHVCTSSSNCKHSVVCPASSRFCKTTNTVEP
	1		LRGNLVKKDCAESCTPSYTLQGQVSSGTSSTQCCQEDLCNEKLH
			NAAPTRTALAHSALSLGLALSLLAVILAPSL
6669	459	1207	KDEETRKDYDYMLDHPEEYYSHYYHYYSRRLAPKVDVRVVILVS
	ì		VCAISVFQFFSWWNSYNKAISYLATVPKYRIQATEIAKQQGLLK
			KAKEKGKNKKSKEEIRDEEENIIKNIIKSKIDIKGGYQKPQICD
			LLLFQIILAPFHLCSYIVWYCRWIYNFNIKGKEYGEEERLYIIR
			KSMKMSKSQFDSLEDHQKETFLKRELWIKENYEVYKQEQEEELK
			KKLANDPRWKRYRRWMKNEGPGRLTFVDD
6670	184	594	VARI+GEAAKMSSEPPPPYPGGPTAPLLEEKSGAPPTPGRSSPA
			VMQPPPGMPLPPADIGPPPYEPPGHPMPQPGFIPPHMSADGTYM
		1	PPGFYPPPGPHPPMGYYPPGPYTPGPYPGPGGHTATVLVPSGAA
			TTVTV
6671	1	763	LPAEKPRSAPNMAGGRCGPQLTALLAAWIAAVAATAGPEEAALP
	_	1	PEQSRVQPMTASNWTLVMEGEWMLKFYAPWCPSCQQTDSEWEAF
			AKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGIFRR
		1	YRGPGIFEDLONYILEKKWQSVEPLTGWKSPASLTMSGMAGLFS
		1	ISGKIWHLHNYFTVTLGIPAWCSYVFFVIATLVFGLSMDLVL*V
i		1	ISQCNWDPPYRHVS*/RPSTNLGVHTAHTSEHLRL
6672	304	1089	APGSKPVQFMDFEGKTSFGMSVFNLSNAIMGSGILGLAYAMAHT
0012		1	GVIFFLALLCIALLSSYSIHLLLTCAGIAGIRAYEQLGQRAFG
			PAGKVVVATVICLHNVGAMSSYLFIIKSELPLVIGTFLYMDPEG
			DWFLKGNLLIIVSVLIILPLALMKHLGYLGYTSGLSLTCMLFF
			LVSVIYKKFQLGLCYRATMKQQWESEALVGTPQPRDSTAAVKAQ
			MFHS*LTGVLTQWPIMAFAFVCHPGGAGPSITELCRAFQAQD
6622	1116	1963	LQIQTHHTHHGARVTHLGSHQLLANAGTMLCRQQSSSMAPAFSQ
6673	1116	1303	SVTCGPSPCVRKQESATKCLHIGACGSDLWARGWEQG*G*GLNV
	1		WLCPCVAFHRGARPOAEEGGARWNSLVSSPWIPPNP*HSSIGAE
			Which coarpoale grands by some properties and the street was the street with the street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a street was a
	1		SFSRV/SGSKGKWILPRQLM+AS+R\TPRFVPGTQWVPITW/PL
1			ITWH*SAPTPPLKACPAPRPSDPCSSCLSCPCVTQHPRFSDTGW
			FGAGHCHSSCDFTRKGAAGGPG
6674	1	440	LEFDYMCQYDYVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSL
00,4			
00,4	ì	1	HVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSY
0074			HVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSY KCACLAGYTGQRCENLLEERNCSDPG/WPSQWVPENNRGPWAYQ PTPC*IGTRVAFFLT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Trvptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
		Bequence	\=possible nucleotide insertion)
	sequence	1678	GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD
6675	277	1678	LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSWDFGIR
			RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQBLKSLFE
	}	ł	RRSNTAURLERLRAERUNGIACANI UMABANISAQSAQBBRSDEE
		l .	KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFNEYSKFDGKGHV
	,		GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ
			YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNEPIHKF
		1	GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM
			KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH
		1	HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS
	1	l	ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ
		1	KASTKFWIKQKPISIDSDLLCAC\DLAEE
		1.000	GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD
6676	277	1678	LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSWDFGIR
			TRY THAN SULFAMENCIA SET AND TRANSPORT TO SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SULF AND THE SU
		1	RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLPE
l			KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFNEYSKFDGKGHV
ĺ			GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ
ł	1	1	YTSEGREPKLNDNVSAYCLHIABDDGEVDTDFPPLDSNEPIHKF
			GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM
			KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH
ł			HYKSFKVSMIHRLRFTTDVOL/GCALFPGVLRKRAAPVDCLRPS
1	1	1	ADTWRQEQIGCCGAACAALRS+DSHKC+EGISGDKVEIDPVTNQ
İ			KASTKFWIKQKPISIDSDLLCAC\DLAEE
		1678	GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD
6677	277	16/6	LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSWDFGIR
1			RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLFE
			KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFNEYSKFDGKGHV
1		1	GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ
			GTTATKKIDVYLPLHSSQDRLLPMIVVIHASARVQDDIGDICHQ
ĺ	1	1	YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNEPIHKF
		1	GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM
1			KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH
(		1	HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS
			ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ
1			KASTKFWIKQKPISIDSDLLCAC\DLAEE
6630	221	865	GPSNQSSGSLSLIVTGCSSYWS*INDTCTILRVLSSNFGRQ*LR
6678	""		PFPCSOLPMSOGCLWHLDCCCPWVPYIPGQQWRKGRQRMRN*QS
			LLGSDQESVGLEDLCVFVNFLLHVLLGLFP*PHELFLLPVVDLG
1			FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLEGSRN
1		1.	HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP
L			LEFARGAMPFLGQDWRSPGQNWVKTVDGWKRFLDEKSGSFVSDL
6679	2	786	PERAKGAMARIA MADA MADA (COO EBRASARY B+ONOVE) DEG
	1		SSYCNKEVYNKENLFNSLNYD/SCSQEEKEGHAE*QNQNS\DPH
1			QEKWIYVHKGSTKERHGYCTLGEAFNRLDFSTAILDSRRFNYVV
			RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR
1			ELLOTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQQLN
1	1		NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLF
6680	1498	2951	PLCTLPLMPSALPGWAGERWEKQWPLA/PGPGTWQTPVGSISEE
1 0000	***		P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP
			/NOVSPPOPM*GAEENGDORGGKERAGEELHRSSSGLTAAPGFP
			EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPLLPAS
			MORSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS
			SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPVGKV\GALGAAQD
			SGP / PAPPGPTGLKPGGGSSSGGNG " PGDP VGR V / GALGAAQD
			PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP+LPSDPAS
		Į.	TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV
		1	*LPAPLSOPEGATEPOVRACGMAPPSPGTSGRLVAWGRHPGPQV
			AOGCPPGAGCWGSOPRGSORCPRTYTHSPLGHGRAPCPRRCWH*
[		1	WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR
1			FOGGGGG
	<u></u>		FQGGGGG

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine, .
Ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	sequence	\=possible nucleotide insertion)
6681	1169	511	INYIYYNQQQRAFHELK\EKLMSAPALGLPDLTKLFTLHVSERE
9661	1169	3.1	KMTVGVLTQTVGPWSRPGAYLSKQLDGVSKGWPPCPRALAATAL
1			LAQEADELTLRONLNRKSPHA\VVTLINTKGHH*LINARLTRYQ
ł			TLLCENPHKTIEVSNT/LNPATLLLVTESPVKHNCLEVLDSVYS
			SRPNLRDHP*TSVDWELYVDGSGFANPCKVTLKKETSPAPVTPR
1			S
6682	109	1238	TVLCGAMQVSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKDVD
6682	109	1236	VRRRIELIODFEMPTVCTTIKVSKDGQYILATGTYKPRVRCYDT
			YQLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYIEFHSQSG
			FYYKTRIPKFGRDFSYHYPSCDLYFVGASSEVYRLNLEQGRYLN
			_
1		1	PLQTDAABNNVCDINSVHGLFATGTIEGRVECWDPRTRNRVGLL D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAVGTTTGQVLLY
1		1	DLRSDKPLLVKDHOYGLPIKSVHFODSLDLILSADSRIVKMWNK
		1	DERSDRPELVEDHQYGEPIKSVHFQDSEDEIESADSKIVKMWNK   NSGKIFTSLEPEHDLNDVCLYPNSGMLLTANETPKMGIYYIPVL
1		1	GPAPRWCSFLDNLTEELEENPESNE
(602	100	1220	TVLCGAMQVSSINEVKIYSLSCGKSLPEWLSDRKKRALQKKDVD
6683	109	1238	VRRRIELIQDFEMPTVCTTIKVSKDGQYILATGTYKPRVRCYDT
1			YOLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYIBFHSOSG
1			FYYKTRIPKFGRDFSYHYPSCDLYFVGASSEVYRLNLEQGRYLN
			PLOTDAAENNVCDINSVHGLFATGTIEGRVECWDPRTRNRVGLL
1		ļ	D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAVGTTTGQVLLY
1			DLRSDKPLLVKDHQYGLPIKSVHFQDSLDLILSADSRIVKMWNK
			NSGKIFTSLEPEHDLNDVCLYPNSGMLLTANETPKMGIYYIPVL
1		1	GPAPRWCSFLDNLTEELEENPESNE
6684	111	527	GLRGGTSRGRAGREPEFAAGVLCVVAGFCQSPCPPGGRGREAPA
0004	+++	127	PP\SGRRHA*RPA*WLGGPGGDSGGREEGGS/GELQRAMESKMG
			ELPLDINIQEPRWDOSTFLGRARHFFTVTDPRNLLLSGAQLEAS
			RNIVONYR
6685	258	1473	KLLGDNFEGFCNKFELSDSENGSNS*QSPL\FDRLFDPDPQKVL
0005	250	1	QGVIDMKNAVIGNNKQKANLIVIGAVPRLLYLLQQETSSTELKT
1			ECAVVLGSLAMGTENNVKSLLDCHIIPALLQGLLSPDLKFIEAC
1			LRCLRTIFTSPVTPEELLYTDATVIPHLMALLSRSRYTQEYICQ
[			IFSHCCKGPDHQTILFNHGAVQNIAHLLTSLSYKVRMQALKCFS
	· .		VLAFENPQVSMTLVNVLVDGELLPQIFVKMLQRDKPIEMQLTSA
1	İ	1	KCLTYMCRAGAIRTDDNCIVLKTLPCLVRMCSKERLLEERVEGA
		1	ETLAYLIEPDVELORIASITDHLIAMLADYFKYPSSVSAITDIK
			RLDHDLKHAHELRQAAFKLYASIGANDEDIRKKVSLGEGRPPVL
			TASRQGVTST
6686	310	927	DSVTFDDLAVDFTPKEWTLLDPTQRNLYRDVMLENYKNLATVGY
			OLFKPSLISWLEGEESRTVORGDFOASEWKVOLKTKELALOODV
1			LGEPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN
-			SENTFECYLYGVDFLTLHKKTSTGEQRSVFSHVWKKPSSLNPDV
	1	1	VCQKNRCTRKKKAF*LQLTLGKSFH*SIHT
6687	181	915	EAMLEAPYKKEEDEOORKEVKKDYPSNTTSSTSNSGNETSGSST
			IGETSNRSRDRDRYRRRNSRSRSPGRQCRHRSRSWDRRHGSESR
			SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMOLAAR
			IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV
		1	PLAIGLTGQRLLGVPIIVQASQAEKNRLAAMANNLQKGNGGPMR
		[	LYVGSLHFNITEDMLRGIFEPFGKV
6688	1025	1	AEVPNYPRVFHKCPDSCWRFKFOPIQLQPYILLSFSSEKPPISF
0000	1025	1 *	SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD
		1	LPSDGGTGFFSLAGDSSSTRLSSLAFISFSLSSVSVGSSAGTTS
	1	1	STSVGSVVAAFTSSSSSSTNRDVAGLDFSTVITSVSGSLVPSRE
		}	VAVICGSKGAGASGSASCSSRAGKTTBATAASSMPSGTSSFSTC
		ľ	TMSELEELFSLPSPAPLLSKLFTSSGSIAICCQDSGPSDTGRLS
			VCQLWLADSDTGKLSDCQEVVTVGDSGGLTCPELSLGRM*MSLL
1	L	1	A CANIMAMON LOVINONCOM A L AGNOGGRIT CERTOROWIT-MOTH

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
<b>l</b> }	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	2042000-	\=possible nucleotide insertion)
I	Bequence		SSAVIPGYSSSSDSRLNTVPTVDLLCPFQTKSST
-	640	1299	SSSASYATSATSISDTAFSGSLKLKHGLLSALDSSSRTS*STSS
6689	640	1233	AEDSTFRICSPSVSDTSSDSSGSKDNVLILFSKVSI*SCFSLSS
			FFSDSISFCFSSSSFCKR*FVSSKVSQNALLSSRLSNGPGGSSK
1 1			ORNSLTAROLAMSL*ATKF*RNACNPNCLSSKKSAL*LSLNQRF
1			GGSASRKPGNISFNSQKCSALSYCCNFVIKPREVSVSSENYPAF
ĹI			
6690	1	442	GTRGKMAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGP
			QQVGAGQTFEYLKREHSLSKPYQGVGTGSSSLWNLMGNAMVMTQ
	•		YIRLTPDMQSKQGALWNRVPCFLRDWELQVHFKIHGQGKKNL\H
			GDGLAIWYTKDRMQP
6691	287	1401	LKTETSEEKARRYKDRPSQLNAVFQEQKKMIQAQESITLEDVAV
į i			DFTWEEWQLLGAAQKDLYRDVMLENYSNLVAVGYQASKPDALFK
[ [			LEQGEQLWTIEDGIHSGACSDIWKVDHVLERLQSESLVNRRKPC
			HEHDAFENIVHCSKSQFLLGQNHDIFDLRGKSLKSNLTLVNQSK
} l			GYEIKNSVEFTGNGDSFLHANHERLHTAIKFPASQKLISTKSQF
			ISPKHQKTRKLEKHHVCSECGKAFIKKSWLTDHQVMHTGEKPHR
			CSLCEKAFSRKFMLTEHQRTHTGEKPYECPECGKAFLKKSRLNI
			HQKTHTGEKPYICSECGKGFIQKGNLIVHQRIHTGEKPYICNEC
			/GKGFIQKTCLIAHQRFHTER
6692	178	939	WIKEGELSLWERFCANIIKAGPMPKHIAFIMDGNRRYAKKCQVE
			RQEGHSQGFNKLAETLRWCLNLGILEVTVYAFSIENFKRSKSEV
			DGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL
1			IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL
			DPSDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFLLWQTSH
			SCLVFQPVLWPEYTFWNLFEAILQFQMNHSVLQK
6693	178	939	WIKEGELSLWERFCANIIKAGPMPKHIAFIMDGNRRYAKKCQVE
1		, and the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second	ROEGHSOGFNKLAETLRWCLNLGILEVTVYAFSIENFKRSKSEV
1			DGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL
1			IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL
		}	DPSDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFLLWQTSH
			SCLVFQPVLWPEYTFWNLFEAILQFQMNHSVLQK
6694	292	813	SLLLHLAPPGAYTPSOPLSSVSTETASSVRRQAAESROHELPVR
6054	-32	1	EVHSLGQILPQDGLTAEAGPPEAQDPWGSPGISLPAAHIGFAAA
			LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHVV
			NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP
6695	292	813	SLLLHLAPPGAYTPSQPLSSVSTETASSVRQAAESRQHELPVR
0070	434	1 013	EVHSLGOILPODGLTAEAGPPEAQDPWGSPGISLPAAHIGFAAA
			LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHVV
		1	NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP
		700	PRVRGRVGERWAFLSVPAAMSSEMEPLLLAWSYFRRRKFQLCAD
6696	1	782	LCTOMLEKSPYDOAAWILKARALTEMVYIDEIDVDQEGIAEMML
	1		
		Ì	DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGFL
1			RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASML
1			TSPDGPFINLSRLNLTKYSQKPKLAKALIEYIFHHENDVKTALD
			LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYREAEKQIKSS
6697	3	782	PPLFLRRLNSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKDR
1		i	IPQILTKVIDTLHRHKSEFFEKHGEEGVEAEKKAISLLSKLRNE
		1	LQTDKPFIPLVEKFVDTDIWNQYLEYQQSLLNESDGKSRWFYSP
			WLLV\ECYMYRRIHEAI\IQSPPIDYFDVFKESKEQNFYGSQES
	1		IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL
			SL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK
6698	668	754	VGSCACAGSCKCKECKCTSCKKSECRAFP
1 0000		100	EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV
6699	325	492	
	325	492	LIGKRKGSVGAGSFQLPGGHLEFGETWEECAQRETWEEAALHLK NYHFASVVNSFIEKENYHYVTILMKGEVDVTHDSEPKNVEPEKN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
	bequeste		ESKRIIYNHAFFFQESKWSGGILQ
6700	1098	1392	TOCWRSSTPGMRTHFRTQP/RLECGQGFSQQENGHCMDTNECIQ
0,00	1		FPFVCPRDKPVCVNTYGSYRCRTNKKCSRGYEPNEDGTACVERT
			LLLGLCNLLGK
6701	2	1485	AAAGPRTRVRRAAAFEGQPSPSPGLGPTSDKAAAPRTPKRRRLW
8,01	-		RORO/HPAMLCYVTRPDAVLMEVEVEAKANGEDCLNQVCRRLGI
			IEVDYFGLQFTGSKGESLWLNLRNRISQQMDGLAPYRLKLRVKF
		ļ	FVEPHLILQEQTRHIFFLHIKEALLAGHLLCSPEQAVELSALLA
		1	QTKFGDYNONTAKYNYEELCAKELSSATLNSIVAKHKELEGTSQ
		1	ASAEYQVLQIVSAMENYGIEWHSVRDSEGQKLLIGVGPEGISIC
	1	1	KDDFSPINRIAYPVVQMATQSGKNVYLTVTKESGNSIVLLFKMI
			STRAASGLYRAITETHAFYRCDTVTSAVMMQYSRDLKGHLASLF
			LNENINLGKKYVFDIKRTSKEVYDHARRALYNAGVVDLVSRNNQ
			SPSHSPLKSSESSMNCSSCEGLSCQQTRVLQEKLRKLKEAMLCM
			VCCEEEINSTFCPCGHTVCCESCAAQLQVGESAAHFCLQPHLSL
			LLTGSRSQVLAR
6702	397	1971	PLAKFLKLDLVNVLCLPMEDVFLFYRTCFCSMGLGSSCHLSLPK
6702	337	1	RAEALLCSRKATVVRDLVAVRMAEEQEFTQLCKLPAQPSHPHCV
			NNTYRSAQHSQALLRGLLALRDSGILFDVVLVVEGRHIEAHRIL
			LAASCDYFKGMFAGGLKEMEQEEVLIHGVSYNAMCQILHFIYTS
			ELELSLSNVQETLVAACQLQIPEIIHFCCDFLMSWVDEENILDV
			YRLAKLFDLSRLTEQLDTYILKNFVAFSRTDKYRQLPLEKVYSL
			LSSNRLEVSCETEVYEGALLYHYSLEQVQADQISLHEPPKLLET
			VRFPLMEAEVLQRLHDKLDPSPLRDTVASALMYHRNESLQPSLQ
Į			SPOTELRSDFOCVVGFGGIHSTPS\MSSATRPKYLNPLLGEWKH
İ			FTASLAPRMSNQGIAVLNNFVYLIGGDNNVQGFRAESRCWRYDP
		ļ	RHNRWFOIOSLOOEHADLSVCVVGRYIYAVAGRDYHNDLNAVER
1			YDPATNSWAYVAPLKREVYAHAGATLEGKMYITCGRKGRIT
2500		1244	GVGPRAAAMPLELELCPGRWVGGQHPCFIIAEIGQNHQGDLDVA
6703	45	1244	KRMIRMAKECGADCAKFQKSELEFKFNRKALERPYTSKHSWGKT
		'	YGEHKRHLEFSHDQYRELQRYAEEVGIFFTASGMDEMAVEFLHE
	}		LNVPFFKVGSGDTNNFPYLEKTAK/TRGWHSVLRDVCGVQLNDE
	1		TSSWDVLGRVRTSKEKVLMVLVLDYSGRPMVISSGMQSMDTMKQ
	1		VYQIVKPLNPNFCFLQCTSAYPLQPEDVNLRVISEYQKLFPDIP
İ	ĺ		IGYSCHETGIAISVAAVALGAKVLERHITLDKTWKGSDHSASLE
			PGELAELVRSVRLVERALGSPTKQLLPCEMACNEKLGKSVVAKV
			KIPEGTILTMDMLTVKVGEPKGYPPEDIFNLVGKKVLVTVEEDD
]	1		TIMEE
)		1007	TMNTRNRVVNSGLGASPASRPTRDPQDPSGRQGELSPVEDQREG
6704	82	1007	LEAAPKGPSRESVVHAGQRRTSAYTLIAPNINRRNBIQRIAEQE
1	1		LANLEKWKEQNRAKPVHLVPRRLGGSQSETEVRQKQQLQLMQSK
1			YKOKLKREESVRIKKEAEEABLQKMKAIQREKSNKLEEKKRLQE
1			YKQKLKREESVRIKKEAEEABDQAHKAIQKEKSHKIIDIKKKIQI NLRREAFREHQQYKTAEFL/RQTEHRIARQKCLSKCCLWPTILN
			MGQKLGLQ\DSLKAEENRKLQKMKDEQHQKSELLELKRQQQEQE
			MGQKLGLQ\DSLKAEENKKLQKMKDEQRQKSEDDEDKKQQQEQE RAKIHQTEHRRVNNAFLDRLQGKSQPGGLEQSGGCWNMNSGNSW
1			· ·
			GI RLCRNSARVPCGWSASRSLGEGAGFIGPLRGPHPRAGGTGTSFT
6705	2	786	RLCRNSARVPCGWSASRSLGEGAGFIGFLRGFHPRAGGTGTSFT
			SYKRKGGIMSTIAAFYGGKSILITVATGFLGKELMEKLFRTSPD
			LKVIYILVRPKAGQTLQHRVFQILDSKLFEKVIEVRPNVHEKIR
1	1	1	AIYADLNONDFAISKEDMOELLSCTNIIFHCAATVRFDDTLRHA
1	1		VQLNVTATRQLLLMASQMPKLEAFIHISTAYSNCNLKHIDEVIY
			PCPVEPKKIIDSLEW\LDDAIIDEITPKLIRDWPNIYTYTK
6706	130	531	FTHSSSSHSQEMLGKLNMLRNDGHFCDITIRVQDKIFRAHKVVL
			AACSDFFRTKLVGQAEDENKNVLDLHHVTVTGFIPLLEYAYTAT
			LSINTENIIDVLAAASYMQMFSVASTCSEFMKSSILWNTPNSQP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
2	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
			Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence		YWSGIGYELQHFHWRKFHFEKKGPPSTCQERLYESRSRWPCIS*
6707	2233	1343	GMVVVGWTAVNGSW*GGQLRCVCVCTSHSSDSTRSSQRASKCHS
			GWAAAMCAA AGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
	1		FFILSQ*KT*SSWENWVFAKYSRIYSYGHSCSKGRGD*DFK*NV
	Į.	[	SQAR*SRFCGLCNPCGHCGLDINLRGGSSPWTDKHSCVHNNLLC
	İ	1	NRRVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEH
			TD*LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYA
			C*RCHWYFEWLLYNHCGDILVACL*RRQL*SSQ
6708	115	1729	TVGSWSRSGRSPPVGRQLLLTGRGAQAAGSPQGGMALQVELVPT
6700	1 .		GEIIRVVHPHRPCKLALGSDGVRVTMESALTARDRVGVQDFVLL
		1	ENFTSEAAFIENLRRRFRENLIYTYIGPVLVSVNPYRDLQIYSR
			QHMERYRGVSFYEEPPHLLAVADTVYRALRTERRDQAVMISVES
			GAGKTDATKRLLQLYAETCPAPQRGGAVRDRLLQSNPVLEAFGN
			AKTLRNDNSSRFGKYMDVQFDFKGAPVGGHILSYLLEKSRVVHQ
			NHGERNFHIFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAK
			VSSINDKSDWKVVRKALTVIDFTEDEVEDLLSIAASVLHLGNIH
			VSSINDKSDWKVVKKADIVIDE I GUECCEL DEN EUDEVITAVO
			FAANEESNAQVTTENQLKYLTRLLSVEGSTLREALTHRKI IAKG
		ł	EELLSPLNLEQAAYARDALAKAVYSRTFTWLVGKINRSLASKDV
	1	1	ESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQLFI
	1		ELTLKSEQEEYEAEGIAWEPVQYFNNKIICDLVEEKFKGII\SI
			LDE\ECLRPGE
6709	3	894	PPHEHLFPSGERGPFSFLVSRRGLGPGKMGKKGKKEKKGRGAEK
6703		-	TAAKMEKKVSKRSRKEEEDLEALIAHFQTLDAKRTQTVELPCPP
			PSPRLNASLSVHPEKDELILFGGEYFNGQKTFLYNELYVYNIRK
	}		DTWTKVDIPSPPPRRCAHQAVVVPQGGGQLWVFGGEFASPNGEQ
			FYHYKDLWVLHLATKTWEQVKSTGGPSGRSGHRMVAWKRQLILF
	ì		GGFHESTRDYIYYNDVYAFNLDTFTWSKLSPSGTGPTPRSGCQ\
			IPSLPRAASSVYGGYSKQRVKKDVDKGTRHSDMF
			RHKMTNYRVESSSGRARKMRLALMGPAFIAAIGYIDPGNFATN
6710	158	980	IQAGASFGYQLLWVVVWANLMAMLIQILSAKLGIATGKNLAEQI
	1		RDHYPRPVVWFYWVQABIIAMATDLAEFIGAAIGFKLIIGVSLL
			RDHYPRPVVWFYWVQAKITAMATDDAEFIGAATGFKDIDGVSDD
			QGAVLTGIATFLILMLQRRGQKPLEKVIGGLLLFVAAAYIVELI
		1	FSQPNLAQLGKGMVIPSLPTSEAVFLAAGVL\GATIMPHVI/YI
			WHSSLTQHLHGGSRQQRYSATKWDVAIAMTIAGFVNLAIMATAA
	1		SELNFYGHTGVA
6711	3	347	VTECKTMTCKMSQLERNI*TMINTLHHYSVKLGHPDTLIHGEFK
			ELVRTDLHNILMKENKNDQAI*HIMEDLDTNAHMQIIFKELIML
}			MAMLTWSYHDNMHDADYGPGQQHRPG
6712	118	578	PHGOKRTRYPOVRAPGOOPQAQLAMALCLKQVFAKDKTFRPRKR
0/12	1 110	1	FEPGTORFELYKKAQASLKSGLDLRSVVRLPPGENIDDWIAVHV
	Ĭ		VDFFNRINLIYGTMAERCS*TSCPVMAGGPRYEYRWQDERQYRR
Į.			PAKLSAPRYMALLMDWIESLI
			QARGSDSEDGEFEIQAEDDARARKLGPGRPLPTFPTSECTSDVE
6713	2485	3	DEMONSTRATION ON THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
			PDTREMVRAQNKKKKSGGFQSMGLSYPVFKGIMKKGYKVPTPI
1			QRKTIPVILDGKDVVAMARTGSGKTACFLLPMFERLKTHSAQTG
1	,		ARALILSPTRELALQTLKFTKELGKFTGLKTALILGGDRMEDQF
1			AALHENPDIIIATPGRLVHVAVEMSLKLQSVEYVVFDEADRLFE
1			MGFAEQLQEIIARLPGGHQTVLFSATLPKLLVEFARAGLTEPVL
			IRLDVDTKLNEQLKTSFFLVREDTKAAVLLHLLHNVVRPQDQTV
1			VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL
			GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA
1	İ		RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA
	}	)	GVDGMLGRVPQSVVDEEDSGLQSTLEASLELRGLARVADNAQQQ
1			YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRFEEEELQRLRL
1			VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ
	1	1	A NEW TWIND KONTILL DIMED STORES AND
l		1	COORDON CONTROL OF CORPERED ACTOURN FC
			GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEEEAGESVEDIFS EVVGRKRQRSGPNRGAKRRREEARQRDQEFYIPYRPKDFDSERG

	10	Predicted end	Amino acid segment containing signal peptide
SEQ ID	Predicted	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	beginning nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
			Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence		LSISGEGGAFEQQAAGAVLDLMGDEAQNLTRGRQQLKWDRKKKR
			FVGQSGQEDKKKIKTESGRYISSSYKRDLYQKWKQKQKID*S*L
			GRRRGILTRRRPRTEEVGEARPLAQAGCIPGPHAPRHPLQAESA
			LELKTKQQILKQRRRAQKAALSLQRWWPQAALCPQ
6714	169	1416	NNCQELLPPPPAPMAHIPSGGAPAAGAAPMGPQYCVCKVELSVS GONLLDRDVTSKSDPFCVLFTENNGRWIEYDRTETAINNLNPAF
			-
			SKKFVLDYHFEEVQKLKFALFDQDKSSMRLDEHDFLGQFSCSLG
			TIVSSKKITRPLLLLNDKPAGKGLITIAAQELSDNRVITLSLAG
			RRLDKKDLFGKSDPFLEFYKPGDDGKWMLVHRTEVIKYTLDPVW
			KPFTVPLVSLCDGDMEKPIQVMCYDYDNDGGHDFIGEFQTSVSQ
			MCEARDSVPLEFECINPKKQRKKKNYKNSGIIILRSCKINRDYS
		1	FLDYILGGCQLMFTVGIDFTASNGNPLDPSSLHYINPMGTNEYL
)	<u> </u>		SAIWAVGQIIQDYDSDKMFPALGFGAQLPPDWKVSHEFAINFNP
			TNPFCSGVDGIAQAYSACLP
6715	32	493	GPAGAESGSLHCLPATVQALAGAAHSPHGGQPPRRGPLIGSGMP
ļ			GKPKHLGVPNGRMVLAVSDGELSSTTGPQGQGEGRGSSLSIHSL
j			PSGPSSPFPTEEQPVASWALSFERLLQDPLGLAYFTEFLKKEFS
		İ	AENVTFWKACERFQQIPASDT
6716	1	176	GAGGPAPRSFGSEEPRAALERDKMSARAAAKSTAMEETAIWEQ
i			HTVTLHRVSLCCSK
6717	115	896	LFAMSGFENLNTDFYQTSYSIDDQSQQSYDYGGSGGPYSKQYAG
	į .		YDYSQQGRFVPPDMMQPQQPYTGQIYQPTQAYTPASPQPFYGNN
			FEDEPPLLEELGINFDHIWQKTLTVLHPLKVADGSIMNETDLAG
1			PMVFCLAFGATLLLAGKIQFGYVYGISAIGCLGMFCLLNLMSMT
i			GVSFGCVASVLGYCLLPMILLSSFAVIFSLQGMVGIILTAGIIG
1			WCSFSASKIFISALAMBGQQLLVAYPCALLYGVFALISVF
6718	290	599	KQSSTVPGTILPSLKWHNSGLCKFPETGGKMTTFKEGLTFKDVA
1			VIFTEEELGLLDPVQRNLYQDVMLENFRNLLSVGHHPFKHDVFL
İ			LEKEKKLDIMKTATQ
6719	1	691	PTRPEEQDREDGKCHKMEMNPISGNLNCDPIAMSQCSSDHGCET
			DLDSDDDKIEKPNNFMKDSASQDNGLSRKISRKRVCSSDSDSSL
İ			QVVKKSSKARTGLLRITRRCAATAANKIKLMSDVEDVSLENVHT
			RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP
			DPDSEGSTKVLSQALNGDSDSEDMLNSEHKHRHTNIHKIDAPSK
		1	RKSSSVTSSG
6720	3	822	HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA
			VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY
1		1	QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF
1		Ì	LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG
			IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP
	}		VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM
			SVVTLISE
6721	3	822	HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA
0/21		1	VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY
			ORLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF
		1	LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG
			IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP
1			VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM
1			SVVTLISE
(555	<del></del>	1 300	RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE
6722	1	390	LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK
1			PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW
6723	173	659	VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT
1	1	1	GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL AEIARILRPGGCLFLKEPVETAVDNNSKVKTASKLCSALTLSGL
1			

Moc   Deginning	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Note	_			
corresponding   to first   amino acid   amino acid   residue of amino acid   residue of amino acid   residue of amino acid   sequence   security   security   security   security   security   security   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   seque	- "		***	
L=Leucine, M=Methionine, N=Aeparagine, amino acid residue of amino acid residue of amino acid sequence   S=Serine, T=Threonine, V=Valine, amino acid sequence   S=Serine, T=Threonine, V=Valine, M=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typtophan, Y=Typ	1			
to first amino acid residue of amino acid residue of amino acid sequence  equence  Fermion				
amino acid   residue of amino acid   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   seque	<b>!</b>			
residue of amino acid sequence (codon, /=possible nucleotide deletion, codon, /=possible nucleotide deletion, codon, /=possible nucleotide deletion, codon, /=possible nucleotide deletion, codon, /=possible nucleotide deletion, codon, /=possible nucleotide deletion, codon, /=possible nucleotide insertion)  6724 173 659 VCQYCTARMADRISAGQFUAVWHRSSFVEALKGLVDKLQALT GNEGRUSVENIKQLIQSAHKESSFDILLGGLVPGSTTHASABIL AEIARILEGGCLUREVPERVONSKYTASKLCSALTLGGL VEVKELGREBLTPBEVQSVREHIGHESDKL VEVKELGREBLTPBEVQSVREHIGHESDKL VEVKELGREBLTPBEVQSVREHIGHESDKL VEVKELGREBELTPBEVQSVREHIGHESDKL CONSTRUCTION ASMELVPETPULATHYDDIALFYQDEVBRUCQBARDHAGESISJVD ASMELVPETPULALFYDROFFNGQLBAVEVKSVEMTLCAG ICSYEGROGOGISIBLSEPLIKGPERMICLGFPDAGHYPYIRNOG GYLYTGKQTLKKYPTPTIBGIONGKGSTTMTLNOG GYLYTGKQTLKKYPTPTBEGISTNCHKLGFPDAGHYPYIRNOG GYLYTGKQTLKYPTPTBEGISTNCHKLGFPDAGHYPYIRNOG GYLYTGKQTLKKYPTPTBEGISTNCHKLGFPDAGHYPYIRNOG GYLYTGKQTLKYPTPTBEGISTNCHKLGFPDAGHYPYIRNOG GYLYTGKQTLKYPTPTBEGISTNCHKLGFPDAGHYPYIRNOG HIMPAGNAGA GYLYTGKQTLKYPTPTBEGISTNCHKLGFPDAGHYPYIRNOG HIMPAGNAGA GYLYTGKQTLKYPTPTBEGISTNCHKLGFPDAGHYPYIRNOG HIMPAGNAGA GYLYTGKQTLKYPTPTBEGISTNCHKLGFPDAGHYPYIRNOG HIMPAGNAGA GYLYTGKQTLKYPTPTBEGISTNCHKLGFPDAGHYPYIRNOG HIMPAGNAGA GYLYTGKQTLKYPTPTBEGISTNCHKLGFPDAGHYPYIRNOG HIMPAGNAGA GYLYTGKQTLKYPTPTBEGISTNCHKLGFPDAGHYPYIRNOG HIMPAGNAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTAGA GYLYTGKGTA	i		t e	
amino acid sequence   Codon, /-possible nucleotide deletion,				1
Sequence   N=possible mucleotide insertion			1	
VEWKELGEPLITEREVGSVERHICHESDNIL	1		sequence	
173   659   VCQVCTARMADFGISAGOPVAVVADRSSPVALKGLONALKGLONALGASHESS PDILIGGLYGGSTTHISABIL AEIARILAPGGCLPIKE PVATAVDNISKYKTASKLCSALTLSGL VEVKELQREPLTPEEVQSVREHLGHESDNI.     6725   356   722   RRRTPPVILATMODDIHLALRIGGENNLGERAEDHAGESISLVD ASMELVOPTPDLQALFYQENNGYKRTASKLCSALTLSGL VEVKELQREPLTPEEVQSVREHLGHESDNI.     6726   98   714   HLQKMERKINSREKKESPELKIRAPRKDLVEVPYE     6726   98   714   HLQKMERKINSREKKESPELKIRAPRKDLVEVPYE     6727   1   631   HLQKMERKINSREKKESPEKSKINSLEDTDQGKKCSTIMILAGA     6728   1   EPGMEGDERHYLDERGGLLPFENGLAGABEFYGLKGLABEVKS     RUBENGLIPPETISLTDHINDSGGLRIPCHAGETYSILKSEN	ļ	reductice		<u> </u>
GNEGRYSVENIKQLLQSAHKESSPDILISGLYGSTTHHSAETL   AETARLIAPGCLYKEPVETANDNSKYKTASKLCSALLAGI   VEVKELQREPLTPEEVQSVERHLGHESDNIL    FRRTPPVILATMDDDIMLALRIQEEMINLQBEAEDHAQESLSLVD    ASRELVDPTPLQALFVQRNOQFFRGCLBAVEVKMSVRMTLCAG    FRRTPPVILATMDDDIMLALRIQEEMINLQBEAEDHAQESLSLVD    ASRELVDPTPLQALFVQRNOQFFRGCLBAVEVKMSVRMTLCAG    FRRTPPVILATMDDDIMLARLAGEFFGLBAVEVKMSVRMTLCAG    FRRTPPVILATMDDDIMLAGAEFFGLMGGABEVKS    REFERENCE   LAFWINDTLENGTHAGET   LAFWINDTLENGTHAGET     CYLLYITQKOTLTKYPDTFLEGIVNGKILCPPDADGHYFIDRD    LAFRIVINFLANGELLLEPGFRENDLLAGREFFGLMGIABEVKS    RWEKGLTPRETTFLEITDNIDRSQGLRIFCNAPPFISTKIKSRI    CHANGE   LAFWINDTHEEFTSISSNIL QFKYFIK    FROMGDERPHYYGKHGFPGKYDPTPKOFTYNFOCTOLICVEKIL   LAIVQFUNGGI LAMPHODPKKYITYPTORGEFGGGGGGKMSHENKY    VLVSKSRLDGFPESTISSNIL QFKYFIK    FROMGDERPHYYGKHGFPGKYDPTPKOFTYNFOCTOLICVEKOPRVLITYLAMASS    ROPETYKGFCVOFKNKWGABEVLAGDCFAALIFSALBERCE    ROHAMSIFEDYTYSTYDHISIGITAMSSLFIILLRFLAGING    ROHAMSIFEDYTYSTYDHISIGITAMSSLFIILLRFLAGING    ROHAMSIFEDYTYSTYDHISIGITAMSSLFIILLRFLAGING    ROHAMSIFEDYTYSTYDHISIGITAMSSLFIILLRFLAGING    ROHAMSIFEDYTYSTYDHISIGITAMSSLFIILLRFLAGING    ROHAMSIFEDYTYSTYDHISIGITAMSSLFIILLRFLAGING    ROHAMSIFEDYTYSTYDHISIGITAMSSLFIILLRFLAGING    ROHAMSIFEDYTYSTYDHISIGITAMSSLFIILLRFLAGING    ROHAMSIFEDYTYSTYDHISIGITAMSSLFIILLRFLAGING    ROHAMSIFEDYTYSTYDHISIGITAMSSCFTOPPGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG			450	
AEIARILAPGGCI,PILEPUTERVGOVENETASKICSALTILSGI.  VEVKEIQREPUTERVGOVENEIGHESINI.  6725 356 722 RRRTPPVILATMDDDLMLAIRIGEEMNLQEAERDHAQESLGI,VD. ASWELVDDTPDLQAIFVQFNOGFROGGRAVEVKNSVRMTLCAG. ICSTEGKIGGMESTIRSS PLIKERPRACILEVEYFVV  6726 98 714 HLQRMERKINREKEREVEGKNRSLEDTDQGKNCKSTITHING GYLYTOKQTITTKYPDTFLESIVINOKILCIPPDADGHYFIDROGI. LFRIVILNPILRIGELLIPBGFRENQLLAQEAEFFQLKGLABEVKS. RWEREQLIPBRITTELSTITNBURSQGLIFIPDADGHYFIDROGI. LFRIVILNPILRIGELLIPBGFRENQLLAQEAEFFQLKGLABEVKS. RWEREQLIPBRITTGEITINDBSQGLIFIPDADGHYFIDROGI. LFRIVILNPILRIGELLIPBGFRENQLLAQEAEFFQLKGLABEVKS. RWEREQLIPBRITTGEITINDBSQGLIFIPDADGHYFIDROGI. LFRIVILNPILRIGELLIPBGFRENQLLAQEAEFFQLKGLABEVKS. RWEREQLIPBRITTGEITINDBSQGLIFIPDADGHYFIDROGI. LFRIVILNPILRIGELLIPBGFRENQLLAQEAEFFQLKGLABEVKS. VLVSKSRRLOGFPEEFSISSNI LOFKYFIK. 40727 1 831 PROMGDERPHYVGKOMFDOKYDFYFKG. LATURVANGI LAWINGDPKVI YPDDROGEFCGQKGTNRENKP VLYFNIVKASILVLLEFQCOPPPOLOVEKCHYTLYILNABSS. RDFEYYKQFCV POFFONNGVAEVLIPDDGGGFCGGKGTNRENKP VLYFNIVKASILVLLEFQCOPPPOLOVEKCHYTLYILANGS. ROFLAMATIEDYTVSWYMDII ISLGIAMMABLIFITLLERHAGIMS. RGMITMGILVLIGY RGMITMGILVLIGY RGMITMGILVLIGY  486 935 PCSSWLRSLABSSLSWKMPLVGLTGGIASGKSVIQVFQQLGCA. VIDVDUMARHVOPGYPAHRRIVEVYGTGVLLENDGINRRVLIGD. LINPOPDRRQLUAATIHBEITREMWETFYFURSPRTSFRKK. HVPSALKEADSLMRRDT VOLTGAGSGFRAWAGPALRRWILLLIGTVTVGFLAGSV. LAGVKKPDVPCGGRDCSGGCCCYPEKGGRGQPGPVGPGCGYNOPP. GLOGFFGLGRKKKFBVGGGGRAVAGPAJROGGPGDGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	6724	173	659	
VEVKELQREPLTPERVQSVREHLGHESDNIL	ľ			
6725 356 722 RRRTPPVILATMODDIMALACIOERENIQAREDHAGESISUVD ASMELUDEPTDIQALPVOFINOCIPAVEVIKAVEVAMICAG ICSYEGKGGMCSIRLSEPLIKURPKOLVEVPFV  6726 98 714 HLGAMERKINKREKEKEVEGKHNSLEDTDQGKNCKSTIMITAVG GYLYTTQKQTITKYPDTFLEGUTNOKILCEPDADGHYFIDROGL LFRIVILIPILITRIGELLIPEGFRENQLLAGEAEFFQLKGLABEVKS RUBEKEQLTPRETTFLEITDNIDESQGLBIFEDDAGHYFIDROGL LFRIVILIPILITRIGELLIPEGFRENQLLAGEAEFFGLKGLABEVKS RUBEKEQLTPRETYFLEITDNIDESGGLBIFEDFISKIKSKI VLWSKSRILDGFPEFFSISSNIJOFKYFIK PROFISKIKSKI VLWSKSRILDGFPEFFSISSNIJOFKYFIK PROFISKIKSKI VLWSKSRILDGFPEFFSISSNIJOFKYFIK PROFISKIKSKI VLWSKSRILDGFPEFFSISSNIJOFKYFIK PROFISKIKSKI VLWSKSRILDGFPEFFSISSNIJOFKYFIK PROFISKIKSKI VLWSKSRILDGFPEFFSISSNIJOFKYFIK PROFISKIKSKI VLWSKSRILDGFPEFFSISSNIJOFKYFIK PROFISKIKSKI VLWSKSRILDGFPEFFSISSNIJOFKYFIK PROFISKIKSKI VLWSKSRILDGFPEFFSISSNIJOFKYFIK PROFISKIKSKI VLWSKSRILDGFPEFFSISSNIJOFKYFIK PROFISKIKSKI VLWSKSRILDGFPFFTGAGKTAVENKE VLSTYFIK PROFISKIKSKI VLWSKSRILDGFPFFTGAGKTAVENKE VLSTYFIK PROFISKIKSKI VLWSKSRILDGFPFTFOLGVEKCPDRVILTYLMARSS RDFFYYKGÇVOFFKNINGVARKLIDGFOLGVEKCPDRVILTYLMARSS RDFFYYKGÇVOFFKNINGVARKLIDGFOLGVEKCPDRVILTYLMARSS RDFFYYKGÇVOFFKNINGVARKLIDGFOLGVEKCPDRVILTYLMARSS RDFFYYKGÇVOFFKNINGVARKLIDGFOLGVEKCPDRVILTYLMARSS RDFFYYKGVOFFKNINGVARKLIDGFOLGVEKCPDRVILTYLMARSS RDFFYYKGVOFFKNINGVARKLIDGFOLGVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKCH VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVEKK VLDVALVALVALVALVALVEKK VLDVALVEKK VLDVALVALVALVALVALVALVALVALVALVALVALVALVALV	Į			
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6726  6726  784  714  HLORMERKINREREKEYEGKHNSLEDTDOGNNCKSTLHTLING GYLYITQKOTLTKYPDTFLEGIVNGKILCPFDADGHYFIDRGIL LFRHVINFLRRGELLIPEGFRENQLLAGEAEFFCLKGLAEBUKS RWEKEGLTPRETTFLEITDNHDRSGGLRIFCNAPDFISKIKSRI VLYSKSRIBGFPEFFSISNIJGKYFFIF  6727  1 631  FRÖMGDERPHYYGKGFDKVDPTFKSPTYNGGCTDICCVELL LAIVGVVANGTIANTHOEDREKVIYPTDSGCOKOTKNENKP YLFYFNIVKCASPLVLLEFQCPTPQICVEKCPDRYLTYLNARSS RDFFYYKGFCVPGFKNNKGVAEVLRDGOCPAVLIPSKPLARKCF PAHANKGUHVONETTYEDGHGSRNITDLVEGAKKANGVLEA RQLAMMIFEDTTVSWYMDIISLGIAMMSLLFIILLRFLAGIMG RGMIINGILVLGY  6728  6728  6729  6729  1191  VGLTGAQSGTASMGRDCAVAGFALRRWLLLGTVTVGFLAGSV LAGVKKFDVPCGGRCGCCYPEKKGRGQPGPVGGYNOPP GLOSFPGLGGKRGKGNEGAPFVTGVKGRGGNGFDGYNGPGYNOPP GLOSFPGLGGKRGKGEGAGPFVTGVKGRGGNGFGYFGADGI PGHPGOGGPRGRPGYDGCNGTGGDSGPGGSDFGGYGNGFGHVCGM GPVCAPGRGGGKGGNGGGGFTGVKGKGGNGGGPFPGHVCGM GPVCAPGRGGGFGFDGFGGKGGCGCYPEKKGRGGPGFVGGGNGGGFGHVCGM GPVCAPGRGGFGKGNGGGFGCQCYPEKKGRGGPGFVGGFGHVCGM GPVCAPGRGGFGKGNGGGRGPCYTGVKGKGGNGGGFPGHVCGM GPVCAPGRGGFGKGNGGGFGPCVGTKGGKGGNGGGFPGHVCGM GPVCAPGRGGFFGPFGFGFGKGCGNGGLGFTGVKGGKGDVGGPGN GPVCAPGRGFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	1		İ	
GYLITOKOTITKY PDTFLEGIUNGKILCPPDADGHYPIORGEL LFRHVINPIRNGELLLPEGFRENQLLAQEAEFTQLKGLAEEVKS RWEKEQLTRETTFLEITONNIDRSQGIRIFCNAPDFISKIKSRI VLVSKSRLDGFPEEFSISSNIIGKYFIK FROMGDERFHYTGKHGTPOKYDFIFKGFTYNGGCTDIICCVFLL LAIVGYVANGIIAMTHGDPRKVITYPTDSRGFCGQKGTNERKYF YLFYFHIVKCASPULLERGCOPTROITUNGAGKTOLICCVFLL LAIVGYVANGIIAMTHGDPRKVITYPTDSRGFCGQKGTNERKYF YLFYFHIVKCASPULLERGCOPTROITUNGAGKTANENKY YLFYFHIVKCASPULLERGCOPTRITYINAGSS RDFSYYKQPCVPGFKNKGVAEVLERGODCPAVLTPSKPLARCCP PAHAYKGVLMVGNETTYEDGHGSRKNITDLVEGAKKANGVLEA RQLMMIFEDTTVSWWDIISLGIAMMSLLFIILLRFLAGIMG RGMIIMGILVLGY FCSSWLFSLADSSLSWKMPLVGLTGGIASGKSVIQVFQQLGCA VIDVDVMARHVVQPGYPAHRRIVEVFGTEVLLENGDINRKVLGD LIFNQPDRAGLLNAITHPBIRKEMKETFKYFLREPTSFPGKK HVPSALKEADSLMRRDT VGLTGAGSGETASMGRQRAVAGPALRWILLGTVTVGFLAGSV LAGVKKFVDVCGGRDCSGGCCCYPEKGRGCQFGPVGPQCYMOPP GLOSFFGLGRKGDKGERGAPGVTGPKGPUGPCGYMOPP GLOSFFGLGRKGDKGERGAPGVTGPKGPUGPGCYGNPP GLOSFFGLGRKGDKGERGAPGVTGPKGPUGPGCYMOPP GLOSFFGLGRKGPROPYDCGGTCGGGSGPGPGHVGQW GPVGAPCARGFGPGPGPGTGGGSGGPGGSGFTGFDFGQG PKGGKGEPYALPKERFDRYRGEPGEPGLUGGGPPGHVGQW GPVGAPCARGFGPGPGPGTGGGSGGCCCYPEKGRGGPGHVGQGPGPHG GIPSDTLHPIIAPTGVTPHPDQYKGEKGSUGQPGPWGGGPGAPGGGGGG GFGGGGGGGGGGGGGGGGGGGGGGGG	j			ICSYEGKGGMCSIRLSEPLLKLRPRKDLVEVFFV
LFRIVINPILRNGELLLPEGFRENQLLAGEAFFOLKGLAEEVKS RWEKEQLTPRETTFLEITDHIDRSQCLRIPCNAPDFISKIKSRI VLVSKSRILGFFEEFSISSNIIQFKYFIK 6727 1 831 FROMGDERPHYYGKIGTPQKYDTFKGFIYNRGCTIICCVFLL LAIVGYVAVGIIANTHODPRKVIYTPTDSRGFFCQKGTKNENKP YLFYFNIVKCASPLVLLEFGCPTPGICVEKCPDRYLTYLINARSS RDFFYKVRGVLWYGENKGVAVELLGBCDFVLIPSKLPARCF PAIHAYKGVLWYGNETTYEDGHGSRKNITDLVEGAKKANGVLEA RQLAMRIFEDTYUSWYNDIISLGIAMANSLIFILLRFLAGIMG RGMIIMGILVLGY 6728 486 935 FCSSWLRSLADSSLSWKMFLVGLTGGIASGKSSVIQVPQQLCS LIFWQPDRRQLLINAITHPETRKEMMKETFKYFLREPRTSPRGKK HVPSALKEADSLMRRDT 6729 259 1191 VGLTGAGSGCTASMGRDQRAVAGFALRRWLLLGTVTVGFLAQSV LAGYKKFDVPCGGRGCCGGCCCYPEKGGGCQCGPVGPQCYNGPP GLQGFPGLGGRGKDKGRGAPGVTGPUGACKONGVGGAGC PGHGQGGFRGRGAPGTGRAWAGPALRRWLLLGTVTVGFLAQSV LAGYKKFDVPCGGRGCCGGGCCCYPEKGGGCQCGPVGPQCYNGPP GLQGFPGLGGRGKDKGRGAPGVTGPUGACKAGNSGESFTGPPGDG PGHGQGGFRGRGAPGTGCCOYPEKGGGCQCGPVGPQCYNGPP GLQGFPGLAGKGFVALFKERDYAGFPGGBGLVGFQCPFGADGI PGHGQGGFRGRPAYDECTYGDGAGCAGCGPGPVGPQCYNGPP GFPGQGGFRGRPAYDECTYGPGGGAGCAGGFGTAGTGFAGGG GFWGKGFPALFEKERDYAGFPGGFBLVGFQCPPGRCPGQG PKGKGGFPALFEKERDYAGFPGGFBLVGFQCPPGRCPHCQM GPVGAPGRPGPPGPPGPACQQGRRGLGFYGVKGKGKGDVQQPGN GIPSDTLHPIIAPTGVTFHPDGYKGEKGSBEBGFTGPFGPG GIM 6730 784 1015 NMVDYYEVLGLQXYASPEDIKKAYHKVALKMPDRNPENKEAE KKFKEVAEAYEVLSNDEKRDIVDKYGTGINEF 6731 1 446 GIRKRLHGAVVPRVEVGCPPETRESEGVHLERPPSFLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYBEILITEGTTAKEATY NDLQVEYGKCQLQMKERKKFFEIGTGFSLIKENGSLKKHSA LIKTARVEINRKÖBEI GRONGLAPPPSSPLUCLQFGGGSDPQOLTQLRHCLSHSFQDTPW AQRQVCYTAATTQAAAPATNCLPHSGHRPTPPSSPLKNNDEG GRGKLAPQNGSSDAPATTPPSRGRREVFSDBPPBVYGFFE PLVAKERSPVGKRTTLEFFSDSAKEBVRSAYYLRSRGRQPF PQGTEEMKTRTTILQQCHSGPPLOPFWTRFGLRSDSSES DEASSGTDLSQTISKTVRSIGABAVSEDLVTRKRRPPLAYPR YEARSVQQCKVNFSSEGETEDDQDSHSSYTTVKARSRDSDSG DKTTRSSQYIESPW YEARSVQCVCYTAATTQAAAPATSPSCGREVKFSDBPSSES DEASSGTDLSQTISKTKRDELGGARAVSEDLVTRLKRPPLAYPR YEARSVQCVCYTAATTQAAAPATSPSCGGREVKFSDBPSSES DEASSGTDLSQTISKTKRDDMASGTVKRHLKTGECERKTKKSLELSKEDLI QLISIMEGGLQARGVYHMLKTEKTKPEVLEAHYGSAPPEKVL VUHRDALIALQAESIGDEVVENTISLDLEEKKKFKESLELSKEDLL VUHRDALIALQAESIGDEVVENTISLDLEEKKKFKESULESHCBDLL LLABK	6726	98	714	HLQKMERKINRREKEKEYEGKHNSLEDTDQGKNCKSTLMTLNVG
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631   PROMODER PHYYGKHOTPOKYDTYKGPIYNRGCTDIICCVPELL LAIVGYVAVGIIAWTHODPRKVIYPTDSRGPIGYGKGTKNENKP YLFYFNIVKCASPLVLLEFQCTPGICVEKCPDRYLTYLNARSS RDFFYYKQFCVPGFKNNKGVAEVLRDGCPAVLIPSKPLARRCF PAHHAYKQHUMGNETTYEDGHGSKNATULVEGAKKANGVLEA RQLAMRIFEDYTVSWYWDIISLGIAMAMSLLFIILLRPLAGIMG RGMIIMGILVLGY   FCSSWLRSLANSSISWKMFLVGLTGGIASGKSSVIQVFQQLGCA VIDVDUMARHVVQPGYPAHRRITUEVFGTEVLLENGDINRKVLGD LIFNOPDROKLIMALTHPEIRKEMMKETFKYFLREPRTSPRGKK HVPSALKEADSLMRRDT   VGLTGAĞGGRTASMGRDQRAVAGFPALRRWLLLLGTVTVGFLAQSV LAGYKKPDVPCGGRCSGGCQCYPEKGGRGQPGPVGPQGYNGPP GLQGFPGLQGRKGDKGERGAPGTTGFKGDVGARAVSGFPGADGI PGHEGGGGFRGRPGYGCCNTCGAGSGPQPVGPPGCGYNGPP GLQGFPGLQGRKGDKGERGAPGUTGPKGDVGARAVSGFPGADGI PGHEGGGGFRGRPGYGCCNTCGAGSGPGDPVGPPGCGG PKGQKGEPYALPKEERDRYRGEPGEPGLVGFQGPPGPGCGG GPVGAPGRGPGPPGPGCGGGCQCYPEKGGRGDPGPGGGG GPVGAPGRGPGPPGPGCGGGGCQCYPEKGGRGDPGPGGGG GPVGAPGRGPGPPGPGCGGGGCQCYPEKGGRGDPGPGGGG GPVGAPGRGPGPGPGCCGGGCQCYPEKGGRGDPGPGGGG GPVGAPGRGPGPGPGCCGGGCQCYPEKGGRGDPGPGGGG GPVGAPGRGPGPPGGCGGGGCQCYPEKGGRGDPGPGGGG GPVGAPGRGPGPPGGCGGGGCQCYPEKGGCGCQPPGPGGGG GPVGAPGRGPGPPGGCGGGGCCCYPEKGGRGDPGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				RWEKEQLTPRETTFLEITDNHDRSQGLRIFCNAPDFISKIKSRI
631   PROMODER PHYYGKHOTPOKYDTYKGPIYNRGCTDIICCVPELL LAIVGYVAVGIIAWTHODPRKVIYPTDSRGPIGYGKGTKNENKP YLFYFNIVKCASPLVLLEFQCTPGICVEKCPDRYLTYLNARSS RDFFYYKQFCVPGFKNNKGVAEVLRDGCPAVLIPSKPLARRCF PAHHAYKQHUMGNETTYEDGHGSKNATULVEGAKKANGVLEA RQLAMRIFEDYTVSWYWDIISLGIAMAMSLLFIILLRPLAGIMG RGMIIMGILVLGY   FCSSWLRSLANSSISWKMFLVGLTGGIASGKSSVIQVFQQLGCA VIDVDUMARHVVQPGYPAHRRITUEVFGTEVLLENGDINRKVLGD LIFNOPDROKLIMALTHPEIRKEMMKETFKYFLREPRTSPRGKK HVPSALKEADSLMRRDT   VGLTGAĞGGRTASMGRDQRAVAGFPALRRWLLLLGTVTVGFLAQSV LAGYKKPDVPCGGRCSGGCQCYPEKGGRGQPGPVGPQGYNGPP GLQGFPGLQGRKGDKGERGAPGTTGFKGDVGARAVSGFPGADGI PGHEGGGGFRGRPGYGCCNTCGAGSGPQPVGPPGCGYNGPP GLQGFPGLQGRKGDKGERGAPGUTGPKGDVGARAVSGFPGADGI PGHEGGGGFRGRPGYGCCNTCGAGSGPGDPVGPPGCGG PKGQKGEPYALPKEERDRYRGEPGEPGLVGFQGPPGPGCGG GPVGAPGRGPGPPGPGCGGGCQCYPEKGGRGDPGPGGGG GPVGAPGRGPGPPGPGCGGGGCQCYPEKGGRGDPGPGGGG GPVGAPGRGPGPPGPGCGGGGCQCYPEKGGRGDPGPGGGG GPVGAPGRGPGPGPGCCGGGCQCYPEKGGRGDPGPGGGG GPVGAPGRGPGPGPGCCGGGCQCYPEKGGRGDPGPGGGG GPVGAPGRGPGPPGGCGGGGCQCYPEKGGRGDPGPGGGG GPVGAPGRGPGPPGGCGGGGCQCYPEKGGCGCQPPGPGGGG GPVGAPGRGPGPPGGCGGGGCCCYPEKGGRGDPGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				
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KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD	- C733	<del> </del>	<del> </del>	<u> </u>
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VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD				
LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD				
LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD	1			
6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD	1		1	
				LLEQEKAYQARKE
AQRTLYRDVMLETYSSLVSLGHCITKPEMIFKLEQGAEPWIVEE	6734	189	551	
	1_		1	AQRTLYRDVMLETYSSLVSLGHCITKPEMIFKLEQGAEPWIVEE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			TLNLRLSGGSKKQVFSGICHRSLVELQEVHLV
6735	280	558	KSRRAGVTKMSNPFLKQVFNKDKTFRPKRKFEPGTQRFELHKKA
			QASLNAGLDLRLAVQLPPGEDLNDWVAVHVVDFFNRVNLIYGTI
Ì			XDGCT
6736	195	808	MNYELNFKREMPNIKSLGLTNLNFLLKRLSSVLPLITDYVYFBN
		!	SSSNPYLIRRIEELNKTASGNVEAKVVCFYRRRDISNTLIMLAD
			KHAKEIEBESETTVBADLTDKOKHOLKHRELFLSRQYESLPATH
1			IRGKCSVALLNETESVLSYLDKEDTFFYSLVYDPSLKTLLADKG
			EIRVGPRYQADIPEMLLEGTFFCVFAVL
6737	150	1209	PVIMPLHFSPGDIVRPSCCVSSSPKLRRNAHSRLESYRPDTDLS
","			REDTGCNLOHISDRENIDDLNMEFNPSDHPRASTIFLSKSQTDV
	ļ		REKRKSLFINHHPPGQIARKYSSCSTIFLDDSTVSQPNLKYTIK
1			CVALAIYYHIKNRDPDGRMLLDIFDENLHPLSKSEVPPDYDKHN
			PEQKQIYRFVRTLFSAAQLTAECAIVTLVYLERLLTYAEIDICP
1	1 .	1	ANWKRIVLGAILLASKVWDDQAVWNVDYCQILKDITVEDMNELE
	}		ROFLELLOFNINVPSSVYAKYYFDLRSLABANNLSFPLEPLSRE
			RAHKLEAISRLCEDKYKDLRRSARKRSASADNLTLPRWSPAIIS
6738	148	653	CACAEQPARAEVGAATALPVRWASGEMAPSGSLAVPLAVLVLLL
1			WGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
1			QPEWESFABWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHC
			KDGEFRRYQGPRTKKDFINFISDKEWKSIBPVSSWF
6739	3	631	SWPDMAEEEVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQ
]	J		ANKESSSESFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF
]			VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF
1			REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ
			TAEELNASTLMNYCAEIIASHWVSEVEGVNKAL
6740	3	631	SWPDMAEEEVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQ
			ANKESSSESFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF
1			VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF
	i	i	REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ
			TAEELNASTLMNYCAEIIASHWVSEVEGVNKAL
6741	141	960	PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA
İ			HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM
1	1	}	YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI
1			WDLRSRNLOCORIFOVNAPINCVCLHPNQAELIVGDQSGAIHIW
1			DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL
		1	PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ
			LIPKTKIP
6742	141	960	PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA
0/44	141	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM
1		1	YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI
1			WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW
			The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
1			DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL
1			PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ
			LIPKTKIP
6743	1	412	MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK
1		İ	ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN
1			FAEGQETKPKYREILSELDEHTENKLDFEDFMILLLSITVMSDL
		Ì	LONIR
6744	95	1343	RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD
	1		RQKVSTVGYGMDEVEQDQHBARLKELFDSFDTTGTGSLGQBELT
1			DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILSRT
1			LSNEEHFQEPDCSLEAQPKYVRGGKRYGRRSLPEFQESVEEFPE
	1		VTVIEPLDEEARPSHIPAGDCSEHWKTQRSEEYEAEGQLRFWNP
	İ		DDLNASQSGSSPPQDWIEEKLQEVCEDLGITRDGHLNRKKLVSI
<u> </u>	.L	<u> </u>	

Deginning   nucleotide   Icoation   Cortesponding   Icoation   Cortesponding   Icoation   Cortesponding   Ico first   anino acid   residue of   anino acid   residue of   anino acid   sequence   Prolline, Gelutamine, ReArginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Rearginine, Perolline, Gelutamine, Reargini	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Note   location   corresponding   to first   maino acid   residue of   maino acid   residue of   maino acid   residue of   maino acid   residue of   maino acid   residue of   maino acid   residue of   maino acid   residue of   maino acid   residue of   maino acid   residue of   maino acid   residue of   maino   residue of   maino   residue of   maino   residue of   maino   residue of   maino   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue o	_	1		
corresponding   cofiret   amino acid   amino acid   amino acid   residue of   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   ami				
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amino acid residue of anino acid sequence  sequence  sequence  sequence  sequence  sequence  sequence  codon, /-possible nucleotide deletion, /-possible nucleotide insertion)  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion)  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion)  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion)  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible nucleotide insertion  cogorible n			1	
### Tryptoplan, Y=Tyrosine, X=Unknown, *=Stop code, anino acid sequence Coden, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide insertion)  ### Company				
amino acid sequence Codom, /-possible nucleotide deletion, /-possible nucleotide insertion) CEGYGLONVOGEMLERVENLOPOTHSVEDFEYGLERMSKEIT PENSTYPYOLKHRUSMOSFDESGRETYTSSAMTSTIGEVEYSCL DDCMGHASVERILDTWOEGGIENSQEILKOALDFGLONINLTEL TIALBANGLUVTKASIHQACI FFEOGRAGRARHULGCSMESWBRAAIAAGPGLEPSSTARQONNP AAGTSCFAAVWARGTAMGSVLSTDSGKSAFASATARALERRRDP ELPVTSPGCAVCLEVLEMPVARTGENHYCRGCLTATSLKINKWTC PYCRAYJPSSGVPATDVAKKMKSEYRNCAECOTIVCLSENRAHI RTCGKYIDKYGGLQLEBETA FTOGRAVLESSAFASHARKRESTFUTSSTLDFSQATEKSSYFQTTEI GAGGAMAESAFARHRKRESTFUTSSTLDFSQATEKSSYFQTTEI FTORTALOPENDAVOTETBELGELGLLDAGKAKINEDWHENSFENLLSWGH OPHROTHERLEEKHWMDIATQREGNSVAAGVC FTORTALOPENDAVVETEBELGLLDAGARKAKINEDWHENSFENLLSWGH OPHROTHERLEEKHWMDIATQREGNSVAAGVC TYPEKRAMTFKNOVAVYTEEBELGLIDLAGARKAKINEDWHENSFENLLSWGH OPHROTHERLEEKHWMDIATQREGNSVAAGVC TYPEKRAMTFKNOVAVYTEEBELGLIDLAGARKAKINEDWHENSFENLLSWGH OPHROTHERLEEKHWMDIATQREGNSVAAGVC TYPEKRAMTFKNOVAVYTEEBELGLIDLAGARKAKINEDWHENSFENLLSWGH OPHROTHERLEEKHWMDIATQREGNSVAAGVC TYPEKRAMTFKNOVAVYTEEBELGLIDAGARKAKINEDWHENSFENLLSWGH OPHROTHERLEEKHWMDIATQREGNSVAAGVC TYPEKRAMTFKNOVAVYTEEBELGLIDAGARKAKINEDWHENSFENLLSWGH OPHROTHERLEEKHWMDIATQREGNSVAAGVC TYPEKRAMTFKNOVAVYTEEBELGLIDAGARKAKINEDWHENSFENLLSWGH OPHROTHERLEEKHWMDIATQREGNSVAAGVC TYPEKRAMTFKOVAYTEEBELGAGARKAKINEDWHENSFENLLSWGH LSVWOOPPRODTFFFLGKKKWMMITTSORBONSGCKIOTEMST VPRAGPHEEMSCOQIWGQASDLTROGNSTRNSGFFKEDDATC TARGATARATATATATATATATATATATATATATATATAT				
Sequence   V-possible nucleotide insertion			1	
CEQYGLONVOGBMLEEVFRILDPDGTMSVEDFYGLFKONKSKI  PASSTYTROLKRILLMOSGTEDSGRETTISSANTSTIGFKYFSCL DDGMCHASVERILDTWOGEGIENSQEILKALDFGLDONINLTEL TLALLKRELLTVINGSTEDSGRETTISSANTSTIGFKYFSCL DDGMCHASVERILDTWOGEGIENSQEILKALDFGLDONINLTEL TLALLKRELLTVINGSTEDSGRETTISSANTSTIGFKYFSCL ANGTOCKAPAWARGTANGSVLSTDGGCSAPASATARALGRAPRDP ELFYSFDCAVCLEVLHQEVRITRGGVVPCRSCTATSLKKINKNITC PYCRAYLPSGVPATDVARRKSEYNCASCOTLVCLSEPRAH RTCQVYIDKYGLGLEETA  6746 110 492 GATGAMAGTANGSVLSTBGGCSAPASATARALGRAPRDP ELFYSFDCAVCLEVLHQEVRITRGGVVPCRSCTATSLKKINKNITC PYCRAYLPSGVPATDVARRKSESTANCASCOTLVCLSEPRAH RTCQVYIDKYGLGLEETA  6747 247 484 EAVTFEDVAVVTEEBLGLIDLDAGRILVRDVMLEBFRNL SUNTANALORUSKINSQARLUGSLEGRTGTAEKKLADCERMA VEGGOLGKMAVLGTLLGEVGLLOPRAGENVENLERWEN  6748 201 665 MTTFKAATY FROVAVVTEEBLGLIDLDAGRILVRDVMLEBFRNL LSVENOPHODTFHELKEKPHMUDLATGRONSVYAGVC QPHRIDTFHILKEKPHMUDLATGRONSVYAGVC QPHRIDTFHILKEKPHMUDLATGRONSVYAGVC QPHRIDTFHILKEKPHMUDLATGRONSVYAGVC QPHRIDTFHILKEKPHMUDLATGRONSVYAGVC QPHRIDTFHILKEKPHMUDLATGRONSVYAGVC QPHRIDTFHILKEKPHMUDLATGRONSVYAGVC QPHRIDTFHILKEKPHMUDLATGRONSVYAGVC QPHRIDTFHILKEKPHMUDLATGRONSVYAGVC QPHRIDTFHILKEKPHMUDLATGRONSVYAGVC QPHRIDTFHILKEKPHMUDLATGRONSVYAGVC QPHRIDTFHILKEKPHMUDLATGRONSVYAGVC QPHRIDTFHILKEKPHMUTLATGRONSVYAGVC QPHRIDTFHILKEKPHMUTLATGRONSVYAGVC QPHRIDTFHILKEKPHMUTLATGRONSVYAGVC QURACHGEBURGA SAGGPCPAALGGGPGGASCVQAFGCVGMTRALLEVREND SAGGPCPAALGGGPGGASCVQAFGCVGMTRALGVERGVAC RANGGGPGGASCVQAFGCVGMTRALGVERGVACHAGAM SAGGPCPAALGGGPGGASCVQAFGCVGMTRALGVERGVACHAGAM SAGGPCPAALGGGPGGASCVQAFGCVGMTRALGVERGVACHAGAM SAGGPCPAALGGGPGGASCVQAFGCVGMTRALGVERGVACHAGAM SAGGPCPAALGGGPGGASCVQAFGCVGMTRALGVERGVACHAGAM PATATGGASDGTITKALLSGFVCERGVACHAGAMAGAGAR PATATGGASDGTITKALLSGFVCERGVACHAGAMAGAGAR PATATGGASDGTITKALLSGFVCERGVACHAGAGAGAATANGT EPSKEPELMPKTPSKYSFNTYSVSHTSSPEDINTAGRCQAGAGAGAGAGAGAGAAAAAAAAAAAAAAAAAAAAA				
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CDCTIVIGEFQFKAHRNVLASFSEYFGAIYRSTSENNVFLDQSQ VKADGFQKLLEFIYTGTLNLDSWNVKEIHQAADYLKVEEVVTKC KIKMEDFAFIANPSSTEISSITGNIELNQOTCLLTLRDYNNREK SEVSTDLIQANPKQGALAKKSSQTKKKKKAFNSPKTGQNKTVQY PSDILENASVELFILDANKLPTPVVEQVAQINDNSELELTSVVEN TFPAQDIVHTVTVVKRKGKSQPNCALKEHSMSNIASVKSPYEAE NSGEELDQRYSKAKPMCNTCGKVFSEASSLRRHMRIHKGVKPYV CHLCGKAFTQCNQLKTHVRTHTGEKPYKCELCDKGFAQKCQLVF HSRMHHGEEKPYKCDVCNLQFATSSNLKIHARKHSGEKPYVCDR CGQRFAQASTLTYHVRRHTGEKPYVCDTCGKAFAVSSSLITHSR KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGADKTLDSSAED HTLSEQDSIQKSPLSETMDVKPSDMTLPLALPLGTEDHHMLLPV TDTQSPTSDTLLRSTVNGYSEPQLIFLQQLY  6753 2 1305 VPSLPYPPQKVVAHTEFTTSSDSETANGIAKPDPVMPGGEEKAS PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV	CEES	<del></del>	3034	
VKADGFQKLLEFIYTGTLNLDSWNVKEIHQAADYLKVEEVVTKC KIKMEDFAFIANPSSTEISSITGNIELNQQTCLLTLRDYNNREK SEVSTDLIQANPKQGALAKKSSQTKKKKKKAFNSPKTGQNKTVQY PSDLLENASVELFILDANKLPTPVVEQVAQINDNSELELTSVVEN TFPAQDIVHTVVKRKRGKSQPNCALKEHSMSNIASVKSPYEAE NSGELDQRYSKAKPMCNTGGKVFSEASSLRRHMRIHKGVRPYV CHLCGKAFTQCNQLKTHVRTHTGEKPYKCELCDKGFAQKCQLVF HSRMHHGEEKPYKCDVCNLQFATSSNLKIHARKHSGEKPYVCDR CGQRFAQASTLTYHVRRHTGEKPYVCDTCGKAFAVSSSLITHSR KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGADKTLDSSAED HTLSEQDSIQKSPLSETMDVKPSDMTLPLALPLGTEDHHMLLPV TDTQSPTSDTLLRSTVNGYSEPQLIFLQQLY  VPSLPVPPPQKVVAHTEFTTSSDSETANGIAKPDPVMPGGEEKAS PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV	0/52	24	1834	T
KIKMEDFAFIANPSSTEISSITGNIELNQQTCLLTLRDYNNREK SEVSTDLIQANPKQGALAKKSSQTKKKKKAFNSPKTGQNKTVQY PSDILENASVELFI.DANKLPTPVVEQVAQINDNSELELTSVVEN TFPAQDIVHTVTVKRKRGKSQPNCALKEHSMSNIASVKSPYEAE NSGEELDQRYSKAKPMCNTCGKVFSEASSLRRHMRIHKGVKPYV CHLCGKAFTQCNQLKHVNTHTGEKPYKCELCDKGFAQKCQLVF HSRMHHGEEKPYKCDVCNLQFATSSNLKIHARKHSGEKPYVCDR CGQRFAQASTLTYHVRRHTGEKPYVCDTCGKAFAVSSSLITHSR KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGADKTLDSSAED HTLSEQDSIQKSPLSETMDVKPSDMTLPLALPLGTEDHHMLLPV TDTQSPTSDTLLRSTVNGYSEPQLIFLQQLY  VPSLPYPPOPOVVAHTEFTTSSDSETANGIAKPDPVMPGGEEKAS PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV	1			
SEVSTDLIQANPKQGALAKKSSQTKKKKKAFNSPKTGQNKTVQY PSDILENASVELFI.DANKLPTPVVEQVAQINDNSELELTSVVEN TFPAQDIVHTVTVKRKRGKSQPNCALKEHSMSNIASVKSPYEAE NSGEELDQRYSKAKPMCNTCGKVFSEASSLRRHMRIHKGVRPYV CHLCGKAFTQCNQLKTHVRTHTGEKPYKCELCDKGFAQKCQLVF HSRMHHGEEKPYKCDVCNLQFATSSNIKIHARKHSGEKPYVCDR CGQRFAQASTLTYHVRRHTGEKPYVCDTCGKAFAVSSSLITHSR KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGADKTLDSSAED HTLSEQDSIQKSPLSETMDVKPSDMTLPLALPLGTEDHHMLLPV TDTQSPTSDTLLRSTVNGYSEPQLIFLQQLY 6753 2 1305 VPSLPYPPQKVVAHTEFTTSSDSETANGIAKPDPVMPGGEEKAS PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV				1 ~
PSDILENASVELFILDANKLPTPVVEQVAQINDNSELELTSVVEN TFPAQDIVHTVTVKRKRGKSQPNCALKEHSMSNIASVKSPYEAE NSGEELDQRYSKAKPMCNTCGKVFSEASSLRRHMRIHKGVKPYV CHLCGKAFTQCNQLKTHVRTHTGEKPYKCELCDKGFAQKCQLVF HSRMHHGEEKPYKCDVCNLQFATSSNIKHARKHSGEKPYVCDR CGQRFAQASTLTYHVRRHTGEKPYVCDTCGKAFAVSSSLITHSR KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGADKTLDSSAED HTLSEQDSIQKSPLSETMDVKPSDMTLPLALPLGTEDHHMLLPV TDTQSPTSDTLLRSTVNGYSEPQLIFLQQLY 6753 2 1305 VPSLPYPPQKVVAHTEFTTSSDSETANGIAKPDPVMPGGEEKAS PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV				
TFPAQDIVHTVTVKRKRGKSQPNCALKEHSMSNIASVKSPYEAE NSGEELDQRYSKAKPMCNTCGKVFSEASSLRRHMRIHKGVKPYV CHLCGKAFTQCNQLKTHVRTHTGEKPYKCELCDKGFAQKCQLVF HSRMHHGEEKPYKCDVCNLQFATSSNLKIHARKHSGEKPYVCDR CGQRFAQASTLTYHVRRHTGEKPYVCDTCGKAFAVSSSLITHSR KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGADKTLDSSAED HTLSEQDSIQKSPLSETMDVKPSDMTLPLALPLGTEDHHMLLPV TDTQSPTSDTLLRSTVNGYSEPQLIFLQQLY 6753 2 1305 VPSLPYPPQKVVAHTEFTTSSDSETANGIAKPDPVMPGGEEKAS PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV	1			
NSGEELDQRYSKAKPMCNTCGKVFSEASSLRRHMRIHKGVKPYV CHLCGKAFTQCNQLKTHVRTHTGEKPYKCELCDKGFAQKCQLVF HSRMHHGEEKPYKCDVCNLQFATSSNLKIHARKHSGEKPYVCDR CGQRRAQASTLTYHVRRHTGEKPYVCDTCGKAFAVSSSLITHSR KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGADKTLDSSAED HTLSEQDSIQKSPLSETMDVKPSDMTLPLALPLGTEDHHMLLPV TDTQSPTSDTLLRSTVNGYSEPQLIFLQQLY  6753 2 1305 VPSLPYPPQKVVAHTEFTTSSDSETANGIAKPDPVMPGGEEKAS PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV	1			
CHLCGKAFTQCNQLKTHVRTHTGEKPYKCELCDKGFAQKCQLVF HSRMHGEEKPYKCDVCNLQFATSSNLKIHARKHSGEKPYVCDR CGQRRAQASTLTYHVRRHTGEKPYVCDTCGKAFAVSSSLITHSR KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGAKTLDSSAED HTLSEQDSIQKSPLSETMDVKPSDMTLPLALPLGTEDHHMLLPV TDTQSPTSDTLLRSTVNGYSEPQLIFLQQLY 6753 2 1305 VPSLPYPPQKVVAHTEFTTSSDSETANGIAKPDPVMPGGEEKAS PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV				
HSRMHHGEEKPYKCDVCNLQFATSSNLKIHARKHSGEKPYVCDR CGQRFAQASTLTYHVRRHTGEKPYVCDTCGKAFAVSSSLITHSR KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGADKTLDSSAED HTLSEQDSIQKSPLSETMDVKPSDMTLPLALPLGTEDHHMLLPV TDTQSPTSDTLLRSTVNGYSEPQLIFLQQLY  6753 2 1305 VPSLPYPPQKVVAHTEFTTSSDSETANGIAKPDPVMPGGEEKAS PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV				
CGQRFAQASTLTYHVRRHTGEKPYVCDTCGKAFAVSSSLITHSR KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGADKTLDSSAED HTLSEQDSIQKSPLSETMDVKPSDMTLPLALPLGTEDHHMLLPV TDTQSPTSDTLLRSTVNGYSEPQLIFLQQLY  6753 2 1305 VPSLPYPPQKVVAHTEFTTSSDSETANGIAKPDPVMPGGEEKAS PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV				
KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGADKTLDSSAED HTLSEQDSIQKSPLSETMDVKPSDMTLPLALPLGTEDHHMLLPV TDTQSPTSDTLLRSTVNGYSEPQLIFLQQLY  6753 2 1305 VPSLPYPPQKVVAHTEFTTSSDSETANGIAKPDPVMPGGEEKAS PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV				<b>,</b>
HTLSEQDSIQKSPLSETMDVKPSDMTLPLALPLGTEDHHMLLPV TDTQSPTSDTLLRSTVNGYSEPQLIFLQQLY 6753 2 1305 VPSLPYPPQKVVAHTEFTTSSDSETANGIAKPDPVMPGGEEKAS PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV		1		
TDTQSPTSDTLLRSTVNGYSEPQLIFLQQLY  6753 2 1305 VPSLPYPPQKVVAHTEFTTSSDSETANGIAKPDPVMPGGEEKAS PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV				
6753 2 1305 VPSLPYPPQKVVAHTEFTTSSDSETANGIAKPDPVMPGGEEKAS PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV			1	
PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV	L		<u> </u>	
SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV	6753	2	1305	_
AHPGPPPASSQTPAPEHDKAANKMPLAQKPALAPKPTSQTPPAS	Ì			The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
L		<u> </u>		AHPGPPPASSQTPAPEHDKAANKMPLAQKPALAPKPTSQTPPAS

- ABA	Day 32 about	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide		H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			PLSKLSRPYLVELLSRRAGRPDPEPSEPSKEDQESSDRRPPSPP
i	ļ	İ	GPEERKGOKRDEEEEATERKPASPPLPATQQEKPSQTPEAGRKE
	į		KPMLQSRHSLDGSKLTEKVETAQPLWITLALQKQKGFREQQATR
			EERKQAREAKQAEKLSKENVSVSVQPGSSSVSRAGSLHKSTALP
			EEKRPETAVSRLERREQLKKANTLPTSVTVEISYSSPAAPLVKE
1		l .	VSKRFSSPDDAPVSSEPAWLALAKRKAKAWSDCPLIIK
			FVRRRRRLGGPEVNTMSSLHKSRIADFQDVLKEPSIALEKLRE
6754	2	413	
1	1		LSFSGIPCEGGLRCLCWKILLNYLPLERASWTSILAKQRELYAQ
		ì	FLREMIIQPGIAKANMGVSREDVTFEDHPLNPNPDSRWNTYFKD
			NEATT
6755	298	1343	PGLQLQVALEADWFLDMPGGRRGPSRQQLSRSALPSLQTLVGGG
			CGNGTGLRNRNGSAIGLPVPPITALITPGPVRHCQIPDLPVDGS
			LLFEFLFFIYLLVALFIQYINIYKTVWWYPYNHPASCTSLNFHL
Į.			IDYHLAAFITVMLARRLVWALISEATKAGAASMIHYMVLISARL
J	1	1	VLLTLCGWVLCWTLVNLFRSHSVLNLLFLGYPFGVYVPLCCFHQ
1			DSRAHLLLTDYNYVVQHEAVEESASTVGGLAKSKDFLSLLLESL
			KEOFNNATPIPTHSCPLSPDLIRNEVECLKADFNHRIKEVLFNS
1		i	LFSAYYVAFLPLCFVKVSGYLTFMCFLDLCVNYINWVFLV
	<u> </u>	254	IERALGSLPLSIPVSWGSLRTLKYQQQPLRPKVLLCQTRVQCHD
6756	180	754	LRSLQPQPPGLKQSFCLRVLGLQTGATTPGLRDLTCKELIILTE
	ļ	1	REAQKRKKRKEKESGMALTQGPLTFRDVAIEFSQEEWKSLDPVQ
1 .		1	REAUKRKKREESGMALIUGPLIFEDVALETSQLEMASHDFVQ
	ł	İ	KALYWDVMLENYRNLVFLGKDNFALEVKICPRVFLYFLCCLSWE
			PFHYLTETEALLTHK
6757	2	459	NSRVEAPEAHSRESQGSDAMRKHLSWWWLATVCMLLFSHLSAVQ
			TRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRKLDID
	1		FGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQ
			AANQGEFQKPDNKLHQQVLW
6758	<del> </del>	1008	ASGPELPGRRFRDRAPWLPARLLRGVLAVWVSLSALGPGSFCRR
1 0,30	-		RVPSLAQLGHSEAAPSPDDVRWSRVPDRCPEERDRAWPPPPPPPS
	1		LPPSFRRNMANNSPALTGNSQPQHQAAAAAAQQQQQCGGGGATK
į.	1	ļ	PAVSGKQGNVLPLWGNEKTMNLNPMILTNILSSPYFKVQLYELK
1	ì	1	TYHEVVDEIYFKVTHVEPWEKGSRKTAGQTGMCGGVRGVGTGGI
	0	1	VSTAFCLLYKLFTLKLTRKQVMGLITHTDSPYIRALGFMYIRYT
		1	OPPTDLWDWFESFLDDEEDLDVKAGGGCVMTIGEMLRSFLTKLE
1			WFSTLFPRIPVPVQKNIDQQIKTRPRKI
1			
6759	i	513	RKHNFHSLDGTSTRAFHPQTGLPLLSSPVPQRKTQSGCFDLDSS
			LLHLKSFSSRSPRPCLNIEDDPDIHEKPFLSSSAPPITSLSLLG
1		{	NFEESVLNYRFDPLGIVDGFTAEVGASGAFCPTHLTLPVEVSFY
1	,		SVSDDNAPSPYMGVITLESLGKRGYRVPPSGTIQVVCVL
6760	239	606	VLSKKKGLSAEEKRTRMMEIFSETKDVPQLKDLEKIAPKEKGIT
	1	}	AMSVKEVLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLE
1		1	VLESQLSEGSQKHASLQKSIBKAKIGRCETEERT
6761	29	1733	ERTLRGLREVAAPSDVADAAVSRRGRCCCCLHCTQTQVAQDCPS
0 /0 -	43	1 2/33	SSSSVQRCELSLFQSLHTMTSKKLVNSVAGCADDALAGLVACNP
			NLQLLQGHRVALRSDLDSLKGRVALLSGGGSGHEPAHAGFIGKG
1			MLTGVIAGAVFTSPAVGSILAAIRAVAQAGTVGTLLIVKNYTGD
i			RLNFGLAREQARAEGIPVEMVVIGDDSAFTVLKKAGRRGLCGTV
1			LIHKVAGALAEAGVGLEEIAKQVNVVTKAMGTLGVSLSSCSVPG
l	1		
1			SKPTFELSADEVELGLGIHGEAGVRRIKMATADEIVKLMLDHMT
			NTTNASHVPVQPGSSVVMMVNNLGGLSFLELGI I ADATVRSLEG
			RGVKIARALVGTFMSALEMPGISLTLLLVDEPLLKLIDAETTAA
	1	1	AWPNVAAVSITGRKRSRVAPAEPQEAPDSTAAGGSASKRMALVL
	1		BRVCSTLLGLEEHLNALDRAAGDGDCGTTHSRAARAIQEWLKEG
	}		PPPASPAQLLSKLSVLLLEKMGGSSGALYGLFLTAAAQPLKAKT
1			SLPAWSAAMDAGLEAMQKYGKAAPGDRTMLDSLWAAGQEL
L			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
- 1	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:			H-Histidine, I=Isoleucine, K-Lysine,
	location	corresponding	
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
<b>l</b>	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
į l	amino acid	sequence	Codon, /=possible nucleotide deletion,
		Bequence	\=possible nucleotide insertion)
	sequence		
6762	3	613	ASTISWRLCVAGAEARRPVPVAGERAGGGAMWFMYLLSWLSLFI
1		ł.	QVAFITLAVAAGLYYLAELIEBYTVATSRIIKYMIWFSTAVLIG
i i		1	LYVFERFPTSMIGVGLFTNLVYFGLLQTFPFIMLTSPNFILSCG
!!!			LVVVNHYLAFQFFAREYYPFSEVLAYFTFCLWIIPFAFFVSLSA
1		ł	GENVLPSTMQPGDDVVSNYFTKGKRGK
L- caca-l-	<u>2</u>	760	SGPDFPGRRFRGCCCVRPPAGAGMELGGHWDMNSAPRLVSETAE
6763	2	/60	
1 1		1	RKQEQKTGTEAEAADSGAVGARRFLLCLYLGGFLDLFGVSMVVP
			LLSLHVKSLGASPTVAGIVGSSYGILQLFSSTLVGCWSDVVGRR
ļ		1	SSLLACILLSALGYLLLGAATNVFLFVLARVPAGIFKHTLSISR
1		1	ALLSDVVPEKERPLVIGHFNTASGVGFILGPVVGGYLTELEDGF
i i		1	YLTAFICFLVFILNAGLVWFFPRREAKPGSTE
6764	80	438	LKKMDTMMLSVRNLFEQLVRRVEILSEGNEVQFIQLAKDFEDFR
0/04	δU	1 30	KKWORTDHBLGKYKDLLMKAETERSALDVKLKHARNQVDVEIKR
			RQRAEADCEKLERQIQLIREMLMCDTSGSIQ
6765	3	550	ARYSRVDHFCRRCRAVARAPRFLLQFPSGPSRHFLAACVARWL
j .		}	RGSVLVSEALSGSAMDGIVTEVAVGVKRGSDELLSGSVLSSPNS
1 1		İ	NMSSMVVTANGNDSKKFKGEDKMDGAPSRVLHIRKLPGEVTETE
		1	VIALGLPFGKVTNILMLKGKNQAFLELATEEAAITNGNYYSAVT
		1	PHLRNO
6766	1	1287	EGGSFKASLTWLWPLGEMKLHCEVEVISRHLPALGLRNRGKGVR
			AVLSLCQQTSRSQPPVRAFLLISTLKDKRGTRYELRENIEQFFT
1 1		1	KFVDEGKATVRLKEPPVDICLSKANSSSLKGFLSAMRLAHRGCN
1 1		İ	VDTPVSTLTPVKTSEFENFKTKMVITSKKDYPLSKNFPYSLEHL
1 1		ļ	QTSYCGLVRVDMRMLCLKSLRKLDLSHNHIKKLPATIGDLIHLQ
1			ELNLNDNHLESFSVALCHSTLOKSLWSLDLSKNKIKALPVQFCQ
1			LOELKNLKLDDNELIGFPCKIGQLINLRFLSAARNKLPFLPSEF
1 1	•		RNLSLEYLDLFGNTFEQPKVLPVIKLQAPLTLLESSARTILHNR
1 1			IPYGSHIIPFHLCQDLDTAKICVCGRFCLNSFIQGTTTMNLHSV
1			AHTVVLVDNLGGTEAPIISYFCSLGCYVNSSDI
6767	336	919	APMICLCSSDLQFRYKBAFLRDRGLQIGYCSVDDDPRMKHFLNV
1			GRLOSDNEYKKDFAKSRSQFHSSTDQPGLLQAKRSQQLASDVHY
1 1			ROPLPOPTCDPEQLGLRHAQKAHQLQSDVKYKSDLNLTRGVGWT
1 1			
1			PPGSYKVEMARRAAELANARGLGLQGAYRGAEAVEAGDHQSGEV
Į Į			NPDATEILHVKKKKALLL
6768	2	363	PGSTISCYLLSEGSLPLCMQVACGBEKHRAPTMKTLRARFKKTE
			LRLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDERLLQAV
] !			ENNDAPRVAALIARKGLVPTKLDPBGKSAFHL
6769	284	396	MSTPDFSTAENNQELANEVSCLKAMLTLMLQAMGQAD
	<u> </u>	397	ORNYOVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK
6770	1	/ ود	
			ITLNMGVGEAIADKKLLDNAAADLAAISGQKPLITKARKSVAGF
		l	KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS
6771	3	378	APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR
			WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM
			QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG
6772	<del>                                     </del>	1400	AAAFLOGMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA
0''4	1	1400	
			CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG
1			P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL
1 1	Ĭ	1	HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY
	Į	1	LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT
			AVPILGYPROLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT
		1	IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES
	ı	1	
		1	
			QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK
			FCLFCTVVSLLG1LVFSLHCPSVPMAGVTASYGGSLLPEGHLNL
			<u> </u>
			FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL

SEG				
No.   nucleotide   location   corresponding to first   samino acid   samino acid   samino acid   residue of   samino acid   residue of   samino acid   residue of   samino acid   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequenc	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Cortison   Corresponding   Lotist   Lotistudine, Methodine, Ne-Apparagine,   Peroline, Q-Glutanine, R-Ayginine,   caidue of   amino acid   on, /-possible nucleotide deletion,   Codon, /-possible nucleotide deletion,   Codon, /-possible nucleotide deletion,   Codon, /-possible nucleotide deletion,   Codon, /-possible nucleotide insertion)   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide insertion,   Codon, /-possible nucleotide   Codon, /-possible nucleotide   Codon, /-possible nucleotide   Codon, /-possible nucleotide   Codon, /-possible nucleotide   Codon, /-possible nucleotide   Codon, /-possible nucleotide   Codon, /-possible nucleotide   Codon, /-possible nucleotide   Codon, /-possible nucleotide   Codon, /-possible nucleotide   Codon, /-possible nucleotide   Codon, /-possible nucleoti	ID	beginning		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
to first anino acid residue of anino acid residue of anino acid residue of anino acid sequence  6773  1 630  FUNDATION OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF	NO:	nucleotide		Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence se		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
to first amino acid residue of residue of residue of amino acid amino acid amino acid sequence  6773  1 630  FWEAPKERKYABERHYOLTVORGHER X-UNKNOWN, *-Stop code, *-possible nucleotide deletion,		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
amino acid residue of anino acid sequence anino acid sequence (http://pophan.yyr/poshan.ywlnknown, *-Stop Codon, /-possible nucleotide deletion, /-possible nucleotide sequence (http://pophan.yyr/poshan.yyossible nucleotide deletion), /-possible nucleotide sequence (http://pophan.yyr/poshan.yyossible nucleotide insertion)  6774	1		amino acid	P=Proline, Q=Glutamine, R=Arginine,
residue of amino acid sequence (Codon, /-possible nucleotide deletion) equence (Codon, /-possible nucleotide deletion) requence (Codon, /-possible nucleotide deletion) requence (Codon, /-possible nucleotide deletion) requence (Codon, /-possible nucleotide deletion) requence (Codon, /-possible nucleotide deletion) requence (Codon, /-possible nucleotide deletion) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-possible nucleotide) requence (Codon, /-	ł		residue of	S=Serine, T=Threonine, V=Valine,
amino acid sequence (200n, /-possible nucleotide dicktion, /-possible nucleotide insertion)  6773 1 630 PWEAPERKYKAERHTVULTUTGEPCHFFFQYHRQLYHKCTHKG (2008)  6774 1 630 PWEAPERKYKAERHTVULTUTGEPCHFFFQYHRQLYHKCTHKG (2008)  6774 RPGGPGMCATTRPDQDGXMGYCLERKYWDLGSKISFQCWGGT (2008)  6774 1 146 389 LFELSDQYSHFFILSSWYPFFLSDWDGANYKADSFSKIISS (1008)  6775 1 104 614 TOLEGNGY LERVILHIOVSTHINSTFNOLMISO (2008)  6776 1 1 108 HERRIFREDGALFOLLERVILHIOVSTHINSTFNOLMISO (2008)  6776 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
### Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequenc				Codon, /=possible nucleotide deletion,
6773  1 630 PWRAPKERKYKAEEHTVULTVTGSPCHFFFQYHRQLYHKCHLAG RPGPGPWCATTRIPDQDRWGYCLERKYKWDGCSKISTCOKGGT CVAMPSGPHCLPGOHLTGRHGQKEKCFEPQLLRFFKNEILYHY EQAAVARCCKEPDGHCQCATTPOLGKGGCLEVEGHEL CHCPVGYTGPCDVGF*GGGASRPAPRWGGLAR 6774  146 389 LTELSDQOYFLFFLSS/WVFFFLSSWYKADGFSKIJSS GLRIGFLTGYRFQLIERVILHRYTSPOLMISO 6775 104 614 TCPSGLRVLTRKGGRRFSFGJWTLVLALIEEKKRSERILLMINS GRPETWENLBALYHTPGGEVAWFUNGGFILEEKKRGLWHET HMSSCRVLRFSSITUNVGDKWYKLIGRBWRDRIKKYSLSMKVVN QGTGKDLDPRNV-SLSKKRGGGDSSTILGRRSFRGLWHET HMSSCRVLRFSSITUNVGDKWYKLIGRBWRDRIKKYSLSMKVVN QGTGKDLDPRNV-SLSKKRGGGDSSTILGRRSFLRGS 1108 HERRERHERGLSGDALLRISTFSTILTEMUNGSSIT LNGFFNTSDAMBERCVDRWYDRISFSSTIVERUCVLOSGSL TSVAKFVERMGHWUGGLIGGHLSDRRGRRFVLRWCYLQVALVUC CAALAPTELIVEGRESTSITUNGTUSGSSTILGRRSFLRG HERRERHERGLSGDALLRISTFSTILTEMUTGSSTIL SHLLESABHLITIMDRECHGKERLSFSSTIVLEMUTGUSGSL TSVAKFVERMGHWUGGLIGAPAIRDHILGLUVSVFFVFIETI SHLLESABHLITIMDREEGLKERLARAHRSGWKNARDTUTLEIL KSTMKKELDAACKKEPLIGBRHHWPICKI SLLEPTKFANFM GITLGWCSGGIAPMILAGGRGGGTHLCFHDGOMFFFSGARKO RVSSRGRNCLGLFULOW GRSIGLIVAMDGSPLALLGSGGGTHLCFHDGOMFFFSGARKO RSSLGLAWADGSPLALLGSGGGTHLCFHDGOMFFFSGARKO RSSLGLAWADGSPLALLGSGGGTHLCFHDGOMFFFSGARKO AELLCCHLURSVCFLSPTESGGRRRGGGSISSPRFWHLECRLQLWMC GGGARLGIP**SPRARGR GGGARLGIP**SPRARGR GGGARLGIP**SPRARGR GGGARLGIP**SPRARGR 6778 311 805 1GSTDESRGSIRRNFANTRIRLNVP\EETAGDSF/ERSPEER VAADPRIRSASPRARGR GGGARLGIP**SPRARGR GGGARLGIP**SPRARGR FYRARGRAPHTRICHLNVP\LETAGDSF/ERSPEER VAADPRIRSASPRARGR TVARINEVINKESDALVLLINMPGPPRRINGDSNY TWARINEVINKESDALVLLINMPGPPRRINGDSNY TWARINEVINKESDALVLINMPGPPRRINGDSNY TWARINEVINKESDALVLINMPGPPRRINGDSNY THAY INSTITUTION SPREESTER SPRARGRESTER SPRARFSRR KRADGRAPHTUGARSSTATATSTRG PKAKPEGSSPRATESRR K K RACHTRILGSALMSTVVTMNAGSKWMSEGGSAAGSRAPGFI TVVTINSSILGUKGSOPSTIPADFRINGTSNYTHSTITTSANT SAALPTHLGSALMSTVVTMNAGSKWMSEGGSAAGSRAPGFI TVVTINSSILGUKKSOPSTIPADFRONGTSPTVISTNYTHITSANT SAALPTHLGSALMSTVVTMNAGSKWMSEGGSAAGSRAPGFI TVVTINSSILGUKKSOPSTIPADFRONGTSPTVASRIVT LVPSELISANPTTKSNHGGTASSSPMOLAGRANGTNITEN KWYGSLEKGEGGAAGGARAPSLARGSLAFTEN VPPEPPENLSSSSMOLAGKAGNAATTELS VPPEPPENLSANF	ļ	) '	boquoiie	\=possible nucleotide insertion)
RPGPQPMCATTPNPDDQRWGYCLEPKKVENDCKSKISPCQKGFT CVMPSGGHCLCPQHLTGRHCQKEKFEPGLLEFFKKNEIVYNT EQAAVARQCKSPDAHCGRLASGACRTNPCLHGGRCLEVGRHLL CHCPUCYTGPCPUCHE GGGARRAPPRWGGIAG  6774 146 389 LTELSDQYFILFSLSVWFTFLSDWDGRVIKADSFSKISS GLRIGFLTGNKLLERVILHTOVSTHESFYRQLUSSE 6775 104 614 TCPSQLRVLTARGGRRAPSPGJWTLVLALIEEKRSSERILGMRS GRPETMENLPALYTIPQGSVAMYTDVGAFIKIDSFSKYLLGMRS GRPETMENLPALYTIPQGSVAMYTDVGAFIKIDSFSKYLLGMRS GRPETMENLPALYTIPQGSVAMYTDVGAFIKIDGKOLHRT HMSSGVDKPSSITULGRRANDRIKVSLSMKVNV QGTGKDLDPRNV\SLSKRRGGDPSRITLARRSELRLS  6776 3 1108 HERRERGALSGADALRTS: FLDSIMFSFKGRRFVFFWGNGLHR LNGTFPNTSDAMMECVDGWVYDR.ISFSSITUTEMDLVCDGGSL TSVAKKVPMRGMWGGLLGGHLSDSMMFPKGRRFVFFWGNGLH- LNGTFPNTSDAMMECVDGWVYDR.ISFSSITUTEMDLVCDGGSL TSVAKKVPMRGMWGGLLGGHLSDSMMFPKGRRFVFFWGNGLH- LNGTFPNTSDAMMECVDGWVYDR.ISFSSITUTEMDLVCDGGSL TSVAKKVPMRGMWGGLLGGHLSDSMMFPKGRRFVFFWGNGLH- LNGTFPNTSDAMMECVDGWVYDR.ISFSSITUTEMDLVCDGGSL TSVAKKVPMRGMWGGLLGGHLSDSMMFPKGRRFVFFWFWGNLH- LNGTFPNTSDAMMECVDGWVYDR.ISFSSITUTEMDLVCDGGSL TSVAKKVPMRGMWGGLLGGHLSDMMFPKGRRFVFFWFWGNLH- LNGTFPNTSDAMMECVDGWVYDR.ISFSSITUTEMDLVCDGGGS GISLGMCSGCARLGHVFJCAMY GILLGCMCSGCARLGHVFJCWGCGGGAGGALGCHLFFPAGACGGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG		sequence	630	PWEAPKEHKYKAEEHTVVLTVTGEPCHFPFOYHRQLYHKCTHKG
CVMMPSGPHCLCPGHLTGNHCQKEKCFPGLLRFPHKNETHYET EQAAVARCQCKGPDHCQTLAGPACLEVBGHLL CHCPUSYTGPPCDVGG**GGAGRRPARPROGLAR  6774  146  389  LTFLESDGGYFFLISS**NUFFLGMUDGWSYLKADSYSKIISS GLRIGFLTGRKPLIERVILMIOVSTLHPSTPHQLMIGG 6775  104  614  TCRSGLRVLTRAGGRAPSPQLWTLVLALIESKORSHRILDMISG GRETMENLPALYTIFGGEVAWYDLVLALIESKORSHRILDMISG GRETMENLPALYTIFGGEVAWYDLVALIESKORSHRILDMISG GROTKOLDPHNY.SLSKKRGGGDPSRITIGRSFULLS  6776  3  1108  HERHRERBGALSGDALLRISTLDDSNNFEKCRFFHYPMQLHI LNGFFRYSDAMBEVCUGGYVDRISTSSTIYTTWHDLVCDSQSL LNGFFRYSDAMBEVCUGGYVDRISTSSTIYTTWHDLVCDSQSL TSVARFYPMAGMWVGGILGGHLSGRFFRYLRRCYLQVALVOT CAALAFFLIYLGLSLFISGIAMSLITNTHIM LAEWATHRQAM GITLGWCPSGIAFMILAGLAPAIRDWHILQLVVSVPYFYJETS SWLLESAWLINKPESGLKELRAAHSGOMRARDTITLEIL KSTHKKELBAAQKKKPFJGSRLHMPNICKRISLLPFTKFAHFMA YYGLNIHAG/LKHGSNVPLLOUTPGWYTPPGQLVTHACCSY GRSIGIAMANDDGSFLALLGGHGGGITHLCFHPDGNRFFSGAKD AELLCWDLROSCYFLWSIGSEVTTWGRIFYDDLAYGCSY GRSIGIAMANDDGSFLALLGGHGGGITHLCFHPDGNRFFSGAKD AELLCWDLROSCYFLWSIGSEVTTWGRIFYDDLAYGCSY GRSIGIAMANDDGSFLALLGGHGGGITHLCFHPDGNRFFSGAKD AELLCWDLROSCYFLWSIGSEVTTWGRIFYDLWSGT SGANSWWDTDGPGONDX PEPEVTSFPLOXCHTWSIGSLHFSLELLG HCLPVSVCFLSPTESGGRRGAGPSLSSFRRIVILLGRCLJAWG GGGARLGHEV-SPPARKGR  6779  311  805  10SITDESRGSIRRNPANTRIRLNVPLEETAGDSE / ERSPEEN VADAPRIKRSAPSPCYTSSFPFKSSPEGSBEENCYPPEKVHFHGGP KNSVARKN\KGP\SPVSSEGILDFFSMKFEWENLANGSNVRRMI TAVRINEUTVKSSPAKLULLHMPGOPPRINGGENPY KNSVARNPAPMRKKKVSJGPVSYUJUSBDGRKKFWRFKKGGG SRRBASDQARRGQGPAATATSTRGPKKAPEGSPRAKFESRY LTVIABGRGTPSLSTVKKFTVQINDINNPPHFQRSRYSPVISE KARAVWARNPAPMRKKKVSJGPVSYTJORDDGRKKFWPM KKGGG SRRBASDQARRGQGPAATATSTRGPKAKPGGSRARGFYISE  AFREVFFFLQDLSSKEPSNSTLLPHNSILLYTVSNPITTSANT SAALPTHLGSALMSTVVTMPMAGSKVMVSGGGAAAGNARPGFT TVEVINNSSIJTUMFSSSPAPHOTREPLUSSSRYSPTISERV SAALPTHLGSALMSTVVTMPMAGSSKVMVSGGGAAAGNARPGFT TVEVINNSSIJTUMFSSSPAPHOTREPLUSSSRYSSTVTSLEVSS STTWSPLLTNAPGSSFRAFSNSSKERPNSSKKRUMSGGAAAGNARPGFT TVEVINNSSIJTUMFSSPAPHOTRAPLUTSSANTIVULD SPPCTSSFVVSPREPPODARABESPFRAAGFSSPAPHTSGLSTELDSVS STWAPSILLKRARGGIASSBLAG NERTRADGGRGGFTAAAGFTSANGRIADDTLFSSG VPPSRPPPKSLAARFROKLANGFTAAAGRACHALKER VPPSRPP	6//3	1	1	PROPOPWCATTPNFDODORWGYCLEPKKVKDHCSKHSPCQKGGT
6774 146 389 LTPELSBOQYPELFPILSS/WYPTELSBOYDORYLANDSYSKIISS GLRIGFLTOPKPILSS/WYPTELSBOYDORYLANDSYSKIISS GLRIGFLTOPKPILSVIILINOSTEMPSTFOLMISO 6775 104 614 TCPSQLRVITARGGRAPSFOLWTLVLALIEEKWRSHRILRMIS GRETMENLPALYTIFOGEVAWYDYGAFIKIPOCRKGULHRI HMSSCHUKDSELTUVODGWWKLIGBENKARDRIKVSLSMKVVN QGTSKULDPNNV.SLSKKRGGOPSRITLGRRSPLRLS  6776 3 1108 HERRIERHBALGDALLIRIS IL PLDSINNFREKKERFYHPOMOLLH LINGTPRYSDAMMBCVUTGWVGNVKLIGBENKARDRIKVSLSMKVVN QGTSKULDPNNV.SLSKKRGGOPSRITLGRRSPLRLS  LINGTHYNSDAMMBCVUTGWVGNVKLIGBENKARDRIKVSLSMKVVN QGTSKULDPNNV.SLSKKRGGOPSRITLGRRSPLRLS LINGTSPYSDAMMSCVILTREVLAVATVOT CAALAPTILTVCSLEFLSGIAAMSLITNTIMLIAEWATHRYOAN GITLGWCDSGIAFMTLAGLAPALROWHICHACKVLQVALVOT CAALAPTILTVCSLEFLSGIAAMSLITNTIMLIAEWATHRYOAN GITLGWCDSGIAFMTLAGLAPALROWHICHACKVLQVALVOT CAALAPTILTVCSLEFLSGIAAMSLITNTIMLIAEWATHRYOAN GITLGWCDSGIAFMTLAGLAPALROWHICHACKVLQVALVOT CAALAPTILTVCSLEFLSGIAAMSLITNTIMLIAEWATHRYOAN GITLGWCDSGIAFMTLAGLAPALROWHICHACKVLAVALVALVALVALVALVALVALVALVALVALVALVALV				CVMMPSGPHCLCPOHLTGNHCOKEKCFEPOLLRFFHKNEIWYRT
CHCPUSTGPPCDVGE*GGGASRPAPARMOGLAR	1		Ì	EONAVAR COCKERDAH CORTASOACR TNPCLHGGR CLEVEGHRL
6774 146 389 LTELSDOYFLFILIS/WYPFICSMYDGRYIKADSFSKIISS GLRIGFLIGGRPLIGFNILINGYSTLHPSTIND(MISQ) 6775 104 614 TCPSQLRVITARGGRAPSFOLWTLVLALIEEKRSSHILISMS GRPEIMENLPALYTIFQGEWAWTDVGAFIKT DCCRGGLWHT HMSSCRVDKSPSIVUNDGWWWKLIGRBMRNDRIKVSLSMKVVN QGTGKDLDPHNV\SLSKRRGGDPSRITIGRRSPLRLS 6776 3 1108 HERHERHERGLSDALIRISIDELDSINFPEKREKERFWHFVOMCLH LNGTFPNTSDAMBPCVDGWVVDRISFSSTIVTENDLVCDSQLI TSVAKFVFMARGWVGGILGGHLSDFRRFRFVHFVOMCLH LNGTFPNTSDAMBPCVDGWVDRIFSSTIVTENDLVCDSQLI TSVAKFVEMARGWVGGILGGHLSDFRRFRFVHFVOMCLH LNGTFPNTSDAMBPCVDGWVTDRISFSSTIVTENDLVCDSQLI TSVAKFVEMARGWVGGILGGHLSDFRRFRFVHFVOMCLH LNGTFPNTSDAMBPCVDGWVTDRISFSSTIVTENDLVCDSQLI TSVAKFVEMARGWVGGILGGHLSDFRRFWHFVLGWAVLTGAL GITLGWCSSGLAFWLGGLGFHANSLITNTHMLIAEWATHRYDAM GITLGWCSSGLAFWLGGLGFHANDRICHTSTWTMLIAEWATHRYDAM GITLGWCSSGLAFWLGGLGFHANDRICHTSTWTMLIAEWATHRYDAM GITLGWCSSGLAFWLGGLGFHANDRICHTSTWTMLIAEWATHRYDAM YFGINLHG/LKHLGNNVFLLQTLFRAWNIAA YFGINLHG/LKHLGNNVFLLQTLFRAWVATHRYDAM YFGINLHG/LKHLGNNVFLLQTLFRAWYAA YFGINLHG/LKHLGNNVFLLQTLFRAWYAA YFGINLHG/LKHLGNNVFLLQTLFRAWYAA YFGINLHG/LKHLGNNVFLLQTLFRAWYAA ARUSANDTDCSPTLAKTHTANDTHLDFTQGFLVSGST SGAVSWOTTDCFSCHYBESGGRAGDSLSSFRRFVLLBCRLQLGWWC GGARLUFH**SPRARKGR GSGRAGNAGSFLWSSGSTRENDFNATELLNVP\LEFTAGDSF/EESPEE VOADPRIRSASPKCPTSSPPFKGRSPEGRGET\DPEKVHFHEDF XDKSVARKN\RGP\SPSSSCLDFFFSKGPEENLAGSSVYRMM T\AVRINEVIVKKSRDAKLULINMPGPFRRHGDENY T\AVRINEVIVKKSRDAKLULINMPGPFRRHGDENY T\AVRINEVIVKKSRDAKLULINMPGPFRRHGDENY T\AVRINEVIVKKSRDAKLULINMPGPFRRHGDENY T\AVRINEVIVKKSRDAKLULINMPGPRENGGERFXVALVEQDKO SCALGGEIVCKLHGHGHFKLQKTYENNYLLUTAALDEERSSYS LTVIAEDGFPRLAANGFFRAMSSSSSITTLPHNGITVFVTSNPITTSANT SAALPTHLQSALMSTVVTMPNAGSSKWMSSGQSAAGSNARGPFI TVPVINSSITTUNSPSSSPRANINGHPSSSTANDFRSTVULD SPPCTSSPVVSPRVSSSSSITTLPHNGITVFVTSNPITTSANT SAALPTHLQSALMSTVVTMPNAGSSKWMSSGQSAAGSNARGPFI TVPVINSSITTUNSPSSSGNRSPVSSKKKKMLKGGILLTKAC KVYTGLEKGERGVGADGETSAADFTSADFAKTPULD SPTTAGSALMSPRANGFRANSSKKLERGOGLATTARGHTVLLS KRYTGLEKGERGVGADGETSAADFTSADFAKTSCHTSCHTSATTYCLD SPTTAGSTANTSKR VPERTPFRKSCHTERDFRANTSCHTSCHTSCHTSTTTUNT VPPERLPFPKGRAGRGGGGGTTAADFTSTVGSKLI VPERTPFTKGRAFGRCGGG	ļ			CHODUCY#CD#CDUCF#GGGASPPDAPPWDGI.AR
GLRIGELTGPRPLIERVILHIOVSTHPSTROIMISG 6775 104 614 TCPSQLGVILTARGGRARAPS FOLUTIVALISE KERKSHRILDMIS GRPETMENLPALYTI POGEVAMUTDYGAFI KI POGKOGLUHRT HMSSCRVDKSSELVDVODKVWVKLIGRBMANDRIKVSLSMKVVN OGTOKOLDPNNV\SLSKRGGGDPSRITLGRRSPLRLS  6776 3 1108 HERHERBERGALSQDALLRIS FILDSMMRPEKCREVUHRVOLLH LMGTPFNTSDADMBPCVODWYDRISPSTIVTEMBLVCDSGL TSVAKFVFMAGMWIGGILAGHLSIRFGRRVLRRCVLAVIVOT CAALAFTEIN LYSLERLES LAMSLITTIMLIAEMATHRRQAM GITLGMCPSGIARMILAGLAPAR ROHHLIQUVUSVPYEVIETIS SMLLESARRLINNKPELGLELKAMAHENTIMLIAEMATHRRQAM GITLGMCPSGIARMILAGLAPAR ROHHLIQUVUSVPYEVIETIS SMLLESARRLINNKPELGLELKAMAHENTIMLIAEMATHRRQAM GITLGMCPSGIARMILAGLAPAR ROHHLIQUVUSVPYEVIETIS SMLLESARRLINNKPELGUKELKAMAHENTIMLIAEMATHRRQAM GITLGMCPSGIARMILAGLAPAR ROHHLIQUVUSVPYEVIETIS SMLLESARRLINNKPELGUKELKAMAHENTIMLIAEMATHRRQAM YFGINLHG/LHGUNNVFLLQTLFGAV/TPPGQLVHLIGHMSGS GRISGLYAMDDGSPLALLIGANGGITHLCHPDONNFFSGARK AELLCMDLROSSYPLMSLGRGGTTHLCHPDONNFFSGARK AELLCMDLROSSYPLMSLGRGGTTHLCHPDONNFFSGARK AELLCMDLROSSYPLMSLGRGGTTHLCHPDONNFFSGARK AELLCMDLROSSYPLMSLGRGGTTHLCHPDONNFFSGARK GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**SPRARKGR GGGARLCHP**GRARCHP TANGARGR GGGARLCHP**SPRARKGR GGGARLCHP**GRARCHP TANGARGR GGGARLCHP**GRAR	l		<u> </u>	CHCPVGTTGPFCDVGE GGGADAGATATAMBGILLA
6775 104 614 TCPSOLGVITARGGRRAPSPOLMTUVLALIEEKWÄSHRILRMÄN GRPETMENLPALTITIFOGEWAMTUVGAGT HEGEKRÖGUNET HMSSCRVDKPSEIVVGDWAWTULGREMKDRITKISSMKVVN QGTGKDLPNNV\SLSKRGGGDPSRITLGRRSPLKIS ERHERHERGALSQDALLRISTPLDSNMRPEKCREVHFOWOLLH LNGTFPNTSDADMEPCVDGWYYDRISFSTIVYEMDUCDGGL TSVARFVERAGMWGGILGGLAFATROMHIGLUVSVYBYFYTEMIC CAALAPTFLIYCSLRFLSGLASMSLITNTIMLIAEKATHROAM GITLGMCPSGTAPMTLAGLAFATROMHIGLUVSVYBYFYTEMIC SHLLESARWLIINNKPEBGLKELRKAHRSGMKNADDTITLELL KSTYKKELDAAQKKKPFLGBELHHPNICKRISLLPFTKFANFMA YFGINLINGI (HEHLGINVFLLGTLFGAV) TPPGGUVHHIGHNGSG RVSSRGRVNCLGLFVLQW GRISGLYAMDDGSPLALLGGRGGGTTHLCFHPDONFFSGARKO ABLLCTDLBGGSYPLWSLGREVTHORG YPDLDPTGOFLVSGST GRASCHIP*SFRARKO ABLLCTDLBGGSYPLWSLGREVTHORG YPDLDPTGOFLVSGST SGAVSVWDTDGPGNDGKPEPVLSFLPQKOCTNGVSLHPSLDLG HCLFVSVCFLSFTSSGRRGAGPSLGSPRTHVHLECRQLWHG GGGARLGH*SPRAPRAKKRVSLYLLLNAPGDPBNRGDSNYRHH TANKLMEVLYKKSPDAKULLNAPPGPBNRGDSNYRHH TANKLMEVLYKKSPDAKULLNAPPGPBNRGDSNYRHH TANKLMEVLYKKSPDAKULLNAPPGPBNRGDSNYRHH TANKLMEVLYKKSPDAKULLNAPPGPBNRGDSNYRHH TANKLMEVLYKKSPDAKULLNAPPGPBNRGDSNYRHH TANKLMEVLYKKSPDAKULLNAPPGPBNRGDSNYRHH TANKLMEVLYKKSPDAKULLNAPPGPBNRGDSNYRHH TANKLMEVLYKKSPDAKULLNAPPGPBNRGDSNYRHH TANKLMEVLYKKSPDAKULLNAPPGPBNRGDSNYRHH TANKLMEVLYKKSPDAKULLNAPPGPBNRGDSNYRHH TANKLMEVLYKKSPDAKULLNAPPGPBNRGDSNYRHH TANKLMEVLYKKSPDAKULLNAPPGPBNRGDSNYRHH TANKLMEVLYKKSPDAKULLNAPPGPBNRGDSNYRHH TANKLMEVLYKKSPDAKUSLULNAPPGPBNRGDSNYRHH TANKLMEVLYKKSPDAKULLNAPPGBPRKKKKYSIGPSYTVLVDSBGGRKKPVHFKRGP SRREASDQKAPRGQPARATASTSRGPKAKPEGSPRATNESKK V  6780 3 403 HEVMONPBININLMSGKEELSYIFEGDPDTFVALURVQDKN SCILNGEIVCKLHGHGHFKLQKTYENNYLLLNAPLDDFKRSESY LITVIAEDRGTPSLSTVHFTUNDTNONTHTYSSOLMPPSVAVOVB HEDDNIKFSSAPPTBLSTKTHYNNGSKWUSSEGSAAQSNARPOFT TPVFINSSSIIGPWBRPVSSSSISTFLPFROTTYPSTALUSSPAPPVOLD SNAPSILDSAMSSPOSSSKGRKDVALGSRGATDSLTSSO STHWSPLLINSPSGSGNRRSPVSSSKGRKDVALGSRGATPOLF TRYFINSSLIQVMKGSOPSTIPAADLTTNSGLMPPSVAVOVB HEDDNIKFSSAPVPDRALSSSPAPPLOFARGHTENSSTVISSTUTT LUPSBLISARPTYSNINGGLASSELAG KRYTGSLEKKERCHOADSTEGGGALPTSVSSIVTT LUPSBLISARPTKSNINGGLASSELAG NERTRILEBRIPGGTGGFVRVPRLPRRPVKLSSTVISSTUTT LUPSBLISARPTKSNI	6774	146	389	PARTITION AND AND AND AND AND AND AND AND AND AN
GRPETMENLPALTTIFOGEVAMTUTUGAFIKIFOGEKGGUTHAT HMSSCRVUKPSETLYDUGKVWXLIGERBKINDRIKVSLSMKVVN OCTOKOLDPINVV.SLEKKRGGODERITTGRESPLRLS  1108 HERHERHEGALSQDALLRISIFLDSNMFPEKCREFVHPOMOLDH LINGTPFINTSDADMEPCVOGWYDRISFSSTIVTEMDLVCDSQSL TSVAKRVFMAGMWYGGILGGHLSDRGRRFVLENCYLQAIVOT CAALAFTEITUCSLRFLSGLAMSLITTIMLTAEWATHRRQAM GITLGMCPSGIAFMTLAGLAFAIRDHILQLVVSVPYEVIFLS SWLLESARKLINNKPEGLEKLERKAAHRARADTITLEIL KSTMKKELEAAQKKKPFLGBELHMPHICKRISLLPFTKFANFMA YFGINLING/LHCLANVPLLQTLFGAV/TPPGQLVLHIGHMGSS RVSSRGRVNCLGLFVLQVW  6777 779 63 CFFRGFAMEDCEVEATFAKKQGGSGISCIAFSPAQPLYACGSY GRSIGLYAMDDESPLALLGORGGOTHLCFHPDONNEFFSGARK AELLCWDLRQSSYPLWSLGREVTTNORIYFDLDTTGCFVSGST SGAVSWDTDGGFOMCKPSPVLSFLCNGCUTNGSHPBLELIG HCLPVSVCPLSFTESGGRRGAGPSLGSFRHVHLECRLQLWMC GGGARLGHF*SPBAKKGR  6778 311 805 IQSITDESRGSIRRKNPANTRLRLNVP\ETAGDSE/RSSPER VQADPRIRSASPKCPTSSFPFKGRSPEGGGET/DFKWHFHGD KDKSVAEKN\KSP\SSVSSEGIKDFFSMFPERENLAQGNVRRH T\AVRINEVIVKKSRDAKLVLLNNPGFPRRNNGGEN/ NKSVAEKN\KSP\SSVSSEGIKDFFSMFPERENLAQGNVRRH T\AVRINEVIVKKSRDAKLVLLNNPGFPRRNNGGEN/ ANGANKGPREPGDARABABSBODGGHESPPKKAW ANGANKAPARNKKKKYSIGPVSVLVUSBGRKFVOTNEBLALKFP MAKCAMKGPREPGDARABABSBODGGRKFVPMFKKGPG SRREASDQKAPRGQQPAEATASTSRGRKRFVCNNEBLALKFP NACAMKGPREPGDARABABSBORGKRFVFNKRGPG SRREASDQKAPRGQQPAEATASTSRGRKRFVTNREBLAKKP VV VV VV VV VV VV VV LTV1AENGFTFSLSTVERTVUNDINTUNPPHFGRSRYEFFVISS K 6781 1 1269 APTRPVFPTLODLSSSKEPSNINLPHSNELCSSLVHPBLSEVS SNVAPSIPPMSRFVSSSISTFLPPDOTTVFVTNSPHTSANT SAALPTHLQSALMSTVVVMPNAGSKWAWSGGSAAGSNARPOFI TVFVINSSSIIQVMKGSOPSTIPAAPLTTNSGLMPPSVAVVQDL HPQNIKFSSAVVPSHPPLOVKLENDEASRAPVQNTSADQNTLBSSS STTWSPLLTNSSSIIQVMKGSOPSTIPAAPLTTNSGLMPPSVAVVQDL HPQNIKFSSAVVPSHPPHOSGSGRAGGGRGCDLATTSCSLLLDS KTPTPAPTLLMTSSFVGFTASAGFSLGGGALPTSVSSIVT LVPSSLISGARPTKSNNIGGIASESLAG KRYTGSLEKKEEROYAADSGTEGGGGLTTAAGMSTEOLSTLDS KTPTPPLASTRIKTSSFVGFTASAGFSLGGGALPTSVSSIVT LVPSSLISGARPTKSNNIGGIASESLAG KRYTGSLEKKEEROYAADSGTGGGGSTGGGGGTTATPGLHTSSTUTH VPFEREPPPFHLATHRTSSFVGFTASAGFSLGGGALPTSVSSIVT VPFEREPPPFHLATHRTSSFVGFTASAGFSLGGGALPTSVSSIVT VPFEREPPPFHLATHRTSKLPFNNYGLITABDLTVSO NRGELSCKREGOVAADSGTASSULGGETG				GLRIGFLTGPKPLTERVILHIQVSTLHPSTFRQLMISQ
HMSSCRVDKPSEIVDVODKVWKLIGREMENDRIKVSLSNKVVN OGTOKOLDDNIV\SLEKRGGGODPEILGRENDRLS 6776  3 1108 HERHERHEGALSQDALLRISIPLDSNMEPEKCREFVHPOMOLLH LINGTPENTSDALMBFCVDGWYIDLISFSSTYITVEMDLVCDSQL TSVAKEVPMAGMYNGGLIGGHLSDRFGKREFVLRGVLQVALVUT CAALAPTFLIYCSLRFLSGIAAMSLITNTIMLLBAMTHRPQAM GITLGMCSGIAFHTLAGLAPAIRUMHILQLVVSVYFYVFLTIS SWLLESARWLIINKEPEGLKELIRAAHRSGMKNARDTUTLELL KSTMKKELBAAQKKUPLGERHIMPILGLVSVYFYVFLTISS SWLLESARWLIINKEPEGLKELIRAAHRSGMKNARDTUTLELL KSTMKKELBAAQKKUPLGERHIMPILGLVSVYFYVFLTISS SWLLESARWLIJHMKPEGLKHENTUFLDFLOGPLVHLGHWGSG RVSSRGRVNCLGLEVLQVW GRSIGLYAMDDGSPLALLGGHOGGITHLCHDPGDRFFSGARUD AELLCWDHLOGSCYPLWSLGREVTTMGVILDDFTOGPLVSGST SGANSVMDTDGSGNDGKPEVLSFLPQKDCTNOVSLHPSLPLLG HCLPVSVCPLSPTESGGRRGAGPSLGSPRRHVHLECRLQLWK GGGARLQHIP*SPRAKGR GGARLQHIP*SPRAKGR GGARLQHIP*SPRAKGR VADPRIRSASSKCTSSPPPKGSPBGEGET\DPEKWHPHCPF KDKSVARKN\KOP\SPVSSEGIKDFSWKPURNLOSNVRRHH T\AVRILMVIVKKSBAKLVLLIMMPGPPRRNNDENY  6779 2 535 RALRRQPELLAANGIEPESWAISEPIKGSRKPCVNKEBLALKKP VANSAKNPAPMRKKKVSLGPVSYVLVDSBGRKKPVMPKKGPG SRREASDQKAPRGQCPARATASTSRGPKAKPEGSPRATNESKR V  6780 3 403 HEVWINNFBEININMSPGKEEISYLFEGDPIDTFVALVRVQDK SRREASDQKAPRGQCPARATASTSRGPKAKPEGSFRRATNESKR V  6781 1 1269 APTRPVFFTLQDLSSSKEPSNSINLPHSNELCSSLVHPELSEVS SNVAPSIPPWMSRPVSSSSISTPLPPNQITVFVTSNPTITSANT SAALPTHIGSALMSTVVTWPNAGSKWEGGSAAGNRAPQFI TPVFINSSIIOWMGSOPSTIPAAPLITNSGLMPPSVAVVGDK SPPCTSSEVVPSHPPVQVKELNPDEASPQVNTSADQNTLPSSQ STTMYSPLLTNSPGSSGNRRSPVSSSKGKKKVKIQILLITKAA KKYTGSLEKKEEPCYAGDETEGGALDTTAPCLMSTEGJSTELDS KYPTPAPTLLKNTSSPYGPGTASAGPSLPGALPTSVSSIVT LUPSELISAPPTKKRNGGIABSLAD KKYTTSLEKKEEPCYAGDETEGGALDTTAPCLMSTEGJSTELDS KYPTPAPTLLKNTSSPYGPGPTAAAGPSLPGALPTSVSSIVT LUPSELISAPPTKRNGGIABSLAD KKYTTSLEKKEEPCYAGDETEGGALDTTAPCLMSTEGJSTELDS KYPTPAPTLLKNTSSPYGPGTASAGPSLPGALPTSVSSIVT LUPSELISAPPTKRNGGIABSLAD KKYTTSLEKKEEPCYAGDETEGGALDTTAPCLMSTEGJSTELDS KYPTPAPTLLKNTSSPYGPGTASAGPSLPGALPTSVSSIVT LUPSELISAPPTKRNGGIABSLAD KYPTYRIPAKPGKCLHEDPGSPPPLARRFICHTSTYGKLS NNERTRALESNHHEGGTGGTVRVPPRLPRPVNGKTIPTQOCPTK VPPERPPPPKLSATRRSNKLIPTNRSSDMDLOKKGSNLATGLIS KARSQVPRNDOPVLPPRRKGHELYSKMLLIPTNGLWR	6775	104	614	TCPSQLRVLTARGGRRAPSPQLWTLVLALIEEKWRSHRILKMNS
GOTSKILDPINV\SLEKKRGGGDFSRTTIGRRSPIRGS	1			GRPETMENLPALYTIFQGEVAMVTDYGAFIKIPGCRKQGLVHRT
1108	i		}	HMSSCRVDKPSEIVDVGDKVWVKLIGREMKNDRIKVSLSMKVVN
LINGTPRYTSDADMBPCVDGWVTDRISFSSTIVTEMDLVCDSQSL TSVAKFVFMAGMOWGGLIGGHLSDR PRYLNECYLQVAIVOT CAALAPTFLIYCSLRFLSGIAAMSLITNTIMLIAEMATHRPQAM GITLGMCPSGIAFMTLAGLAFAIRDMHILQLVVSYFVFUFLTS SWLLESARMLIINNKPEGGLKELRRAAHRSGMKNARDTLTLEIL KSTMKKELEAAQKKKPFLGERLHMPNICKRISLLSFTKFANFMA YFGINLING/LKKLGNNVFLLQTLGAV/TPPGQLVLHLGHWGSG RVSSRGRVNCLGLFVLQVW  6777 779 63 CFFMGPAMRDCSVPLAFBAKKQGOSGIISCIAFSPAQPLYACGSY GRSIGLYAMDDGSSLALLGGHQGGITHLCTHPDGARFFSGARD AELLCWDLRQSGYPLWSLGREVTTNQRIYPDLDPTGQFLVSGST SGAVSWDDTDCGROBG PEPULSFLPQACTONSVSLHPSIPLIG HCLPVSVCPLSFTESGGRRGAGPSLGSPRRHVHLECRLQLWWC GGGARLQHIP*SPRAKKGR GGGARLQHIP*SPRAKKGR VOADPRIRSASFKCPTSSPFPKGRSPEGGEGT)DEKWHFHPDGP VDKSVAKEN/KQPJSVSSERILDFSKEPENNINANDVRAMH TAAVRLMEVIVKKSRDAKLULINMPGPFRNRDGDENY ARVSAKNPAPMRKKKVSLGPVSYVLVDSBDGKKPVFNKEELALKKP MAKCAMKGPREPPQDARAEAESFGGASESDQDGGHESFPKKAV AAVSAKNPAPMRKKKKVSLGPVSYVLVDSBDGKKFVVPKKGFG SRREASDQKAPRGQQFAEATASTSRGPKAKPGSRRKFVMPKKGFG SRREASDQKAPRGQQFAEATASTSRGPKAKPGSRRVEVFVSK V 6780 3 403 HEVNDNKPEININLMSPGKEEISYIFEGDFIDTFVALVEVQDKO SCLNGEIVCKLHGHGHFKLQKTYENNYLLITNATLDREKRSEYS LITVIAEDRGTPSLSTVKFFTVQINDINNNPPHFQRSRVEFVISE K 6781 1 1269 APTRPVFPTLQDLSSKREPSNSLINLPHSNELCSSLVHPELSEV SNVAPSIPPVMSRPVSSSSISTIPAPLITNSGKIMPPSVAVVGFL HPQDNIKFSSAVPPSHLSSSPANDIOTGRFLVLSSRATPVQLE SPPCTSSPVVPSHPPVQOVKELMFDEASPQVITTSANDYNTLPSSG STTMVSPLLTNNSSSISTUPARDLTTNSGKIMPPSVAVVGFL HPQDNIKFSSAVPPSHLSSSPANDIOTGRFLVLSSRATPVQLE SPPCTSSPVVPSHPPVQOVKELMFDEASPQVITTSANDYNTLPSSG STTMVSPLLTNNSSSISTUPARDLTNSGKIMPPSVAVVGFL KRYTTSSLEKGERGYGADGETEGGGLDTTAAGLMGTEQLITKAC KKYTGSLEKGERGYGADGETEGGGLDTTAAGLMGTEQLITKAC KKYTGSLEKGERGYGADGETEGGGLDTTAAGLMGTEGLITKAC KKYTGSLEKGERGYGADGETEGGGLDTTARGLMGTEGLITKAC KKYTGSLEKGERGYGADGETEGGGLDTTARGLMGTEGLITKAC KKYTGSLEKGERGYGADGETEGGGLDTTARGLMGTEGLITKAC KKYTGSLEKGERGYGADGETEGGGLDTTARGLMGTEGLITKAC KKYTGSLEKGERGYGADGETEGGGLDTTARGLMGTEGLITKAC KKYTGSLEKGERGYGADGETEGGLDTTARGLKGKLL KKYTGSLEKGERGYGADGETEGGLDTTARGLKGKLL KKYTGSLEKGERGYGADGETEGGGLDTTARGLKGKLL KKYTGSLEKGERGYGADGETEGGLDTTARGLKGKLL KKYTGSLEKGERGYGADGETEGGLDTTARGLKGKLL KKYTGSLEKGERGYGADGETEGGLDTT	ŀ			QGTGKDLDPNNV\SLSKKRGGGDPSRITLGRRSPLRLS
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ABLLCWDLRQGGYPLWSLGREVTTNQRIYFDLDPTGQFLVSGST SGAVSVWDTDGPGNDGKPEPVLSFLPQKDCTNGVSLHPSLPLLG HCLPVSVCFLSPTESGGRRGAGPSLGSPRRHVHLECRLQLWWC GGGARLQHP++SPRARKGR  1QSITDESRGSIRRKNPANTRLRLNVP\EBTAGDSE/ERSPEEE VQADPRIRSASPKCPTSSFPKGRSPEGGET\DPEKVHFHEGP KDKSVAEKN\KGP\SPVSSEGIKDFFSMKPEMENLNQSNVRRMH T\AVRLNEVIVKKSRDAKLVLLNMPGPPRINRDGENY ARACAWKGPREPPQDARAEAESPGASESDQDGGHESPPKKKAV AWSAKNPAPMRKKKVSLGPVSYVLVDSBOGRKKPVWFKKGPG SRREASDQKAPPGQPAEATASTSRGPKKKPUSKEELALKKP WAKCAWKGPREPPQDARAEAESPGASESDQDGGHESPPKKKAV AWSAKNPAPMRKKKVSLGPVSYVLVDSBOGRKKPVWFKKGPG SRREASDQKAPPGQPAEATASTSRGPKAKPEGSPRRATNESRK V  6780  3 403 HEVNDNKPBININLMSPGKEEISYIFEGDPIDTFVALURVQDKD SGLNGEIVCKLHGHGHFKLQKTYENNYLLITNATLDREKRSEYS LTV1AEDRGTPSLSTVKHFTVQINDINDMPPHFQRRYSFYLISE K  6781  1 1269 APTRPVFPTLQDLSSSKEPSNSLNLPHSNELCSSLVHPELSEVS SNAPSIPPVMSRPVSSSSISTFLPPNQITVFVTSNPITTSANT SAALPTHLQSALMSTVVTMPNAGSKVMVSEGQSAQSNARPOPI TPVFINSSSIIQVMKGSQPSTIPAPLITNISGLMPPSVAVVGPL HIPQNIKKFSAPVPPNALSSPAPNIQTGRPLVLSSRATTVQLP SPPCTSSPVVPSHPPVQQVKELNPDEASPQVNTSADQNTLPSSQ STTMVSPLLTNSPGSSGNRRSPVSSSKGKVDKVMKIQQILITKAC KKVTGSLEKGEQYGADGTEGGGLDTTAGGLMSTEDLSTELDS KTPTPPAPTLLKMTSSPVGPGTASAGPSLPGGALPTSVRSIVTT LVPSELISAVPTTKSNHGGIAESLAG KRYTTPAPTTLKMHGGIAESLAG  6782 3 1327 RKPTVIRIPAKPGKCHEDPQSPPPLPAEKPIGNTFSTVSGKLS NVERTENLESNHBQOTGGFVRVPPRLPPREVNGKTIPTQOPPTK VPPERPPPPKLSATRRSNKKLPFNRSSSMDLLQKKQSNLATGLS KAKSQVFKNQDPVLPPRFKPGFPLPLSKYMLSVPHGIANEDIVSQ NPGELSCKKGDVLVMLKQTENNYLSCYKGEDTGRVHLSOMKLIT	6777	779	63	CPCLOLVANDDOCEDLALLOCUOCCITULCEUPDCNRFFSGARKD
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NPGELSCKRGDVLVMLKQTENNYLBCQKGEDTGRVHLSQMKLIT	1	1	1	KAKSOVFKNODPVLPPRPKPGHPLYSKYMLSVPHGIANEDIVSO
PLDEHLRSRPNPFSPPKAPSHAQKPVDSGAPHAVVLHDFPAEQV				NPGELSCKRGDVLVMLKQTENNYLBCQKGEDTGRVHLSQMKLIT
				PLDEHLRSRPNPFSPPKAPSHAQKPVDSGAPHAVVLHDFPAEQV

		Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	p=proline, Q=Glutamine, R=Alginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nuclectide insertion)
	Bequence	<del></del>	DDLNLTSGELVYLLEKIDTDWYRGNCRNQIGIFPANYVKVIIDI
		1	PEGGNGKRECVSSHCVKGSRCVARFEYIGEQKDELSFSEGEIII
		l	LKEYVNEEWARGEVRGRTGIFPLNFVEPVEDYPTSGANVLSTKV
		1	PLKTKKEDSGSNSQVNSLPAEWCEALHSFTAETSDDLSFKRGDR
		1	
			I COMMITTENE DI VI KAATA
6783	3	1750	SYHHHHAQQSAAASPNLTASQKTVTTTSMITTKTLPLVLKAATA
•	ļ		TMPASVVGQRPTIAMVTAINSQKAVLSTDVQNTPVNLQTSSKVT
	}	1	GPGAEAVQIVAKNTVTLQVQATPPQPIKVPQFIPPPRLTPRPNF
		1	LPQVRPKPVAQNNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTL
		1	PTSONSIHPVRVVNGOTATIAKTFPMAQLTSIVIATPGTRLAGP
	1		QTVQLSKPSLEKQTVKSHTETDEKQTESRTITPPAAPKPKREEN
			POKLAFMVSLGLVTHDHLEEIQSKRQERKRRTTANPVYSGAVFE
		1	PERKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQS
		j	PEKKASATTI DASTRING TRANSPORTE DE DECENCIO
		1	SHPDSPENEKTETTFTFPAPVQPVSLPSPTSTDGDIHEDFCSVC
			RKSGQLLMCDTCSRVYHLDCLDPPLKTIPKGMWICPRCQDQMLK
	ı	ļ	KEEAIPWPGTLAIVHSYIAYKAAKEBEKQKLLKWSSDLKQEREQ
	}	1	LEQKVKQLSNSISKCMEMKNTILARQKEMHSSLEKVKQLIRLIH
	}	1	GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSSQSCT
			ANCNOGEETK
			SYHHHHAQQSAAASPNLTASQKTVTTTSMITTKTLPLVLKAATA
6784	3	1750	TMPASVVGQRPTIAMVTAINSQKAVLSTDVQNTPVNLQTSSKVT
		ı	GPGAEAVQIVAKNTVTLQVQATPPQPIKVPQFIPPPRLTPRPNF
ļ	ļ	L	GPGAEAVQIVAKNIVILQVQAIPPQPIKVPQPIPPEKDIIKI
ļ		1	LPQVRPKPVAQNNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTL
		ŀ	PTSQNSIHPVRVVNGQTATIAKTFPMAQLTSIVIATPGTRLAGP
	1	1	QTVQLSKPSLEKQTVKSHTETDEKQTESRTITPPAAPKPKREEN
l	i	I .	POKLAFMVSLGLVTHDHLEEIQSKRQERKRRTTANPVYSGAVFE
			DERKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQS
}	1	)	SHPDSPENEKTETTFTFPAPVQPVSLPSPTSTDGDIHEDFCSVC
1	1		RKSGQLLMCDTCSRVYHLDCLDPPLKTIPKGMWICPRCQDQMLK
ļ	1	ļ	KEEAIPWPGTLAIVHSYIAYKAAKEEEKQKLLKWSSDLKQBREQ
1			LEQKVKQLSNSISKCMEMKNTILARQKEMHSSLEKVKQLIRLIH
]		ì	LEOKVKOLSNSISKCMEMKNIIILAROKEMKSSEEKVKOETKE
1	1		GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSSQSCT
	ļ	1	ANCNQGEETK
6785	<del></del> -	528	LGNTVLHYCSMYSKPECLKLLLRSKPTVDIVNQAGETALDIAKR
0 / 0 3	_		LKATQCEDLLSQAKSGKFNPHVHVEYEWNLRQEEIDESDDDLDD
		]	KPSPVKKERSPRPOSECHSSSISPODKLALPGESTPRDKQRLSY
		}	GAFTNOIFVSTSTDSPTSPTTEAPPLPPRNAGKGPTGPPITPHR
L			RSPKVLVLAPTRELANHVSRDFKDI\TRKLTVARFYGGTSYQSQ
6786	1820	1397	INHIRNGIDILVGTPGRIKDHLQSGRLDLSKLRHVVLDEVDQML
1		1	DLGFAEQVEDIIHESYKTDSEDNPQTLLFSATCPQWVYTVA\KK
			DLGFAEQVEDIIHESYKTDSEDNPQTTLLFSATCPQWVITVAXA
1	1		YMKSRYEQVDLDGKMTQKAATTVEHLAIQCHWSQRPAVIGDVLQ
1	1		VYSGSEGRAIIFCETKKNVTEMAMNPHIKQNAQCLHGDIAQSQR
	1		EITLKGFREGSPKVLVATNVAARGLDIPEVDLVIQSSPPQDVES
1			YTHRSGRTGRAGRTGICICFYQPRERGQLRYVEQKAGITFKRVG
1			VPSTMDLVKSKSMDAIRSLASVSYAAVDFFRPSAQRLIEEKGAV
1	1	1	DALAAALAHISGASSFEPRSLITSDKGFVTMTLESLEEIQDVSC
1			AWKELNRKLSSNAVSQITRMCLLKGNMGVCFDVPTTESERLQAE
1		}	WHDSDWILSVPAKLPEIEEYYDGNTSSNSRQRSGWSSGRSGRSG
1			WHOSOWILSVPAKEPETEETTOGNISSNSKQKSGNSGKSGKSG
			RSGGRSGRSGRQSRQGSRSGSRQDGRRRSGNRNRSRSGGHKRS
		[	FD*VFYHLVDFLSDFLVDSVYLTGRQIDHLTGLTGLIDHLTSHS
1			CYNINI
	2545	2270	PSSEDKNUPLEELEEPPK*KRSGLGSLTPKSQIQNGP*PQTFFF
6787	2646	22/0	FELGSPSGVISAHCNLRLLGSSDSPAPASRVAGIIGTCHHAWLI
			LVFLVRMGFHHVGQAGLKLLTL\VIHPPWPPKVLGLQT
1	1		TALTARWGLHUAGAGUITTII ATULLUATALLIA TOTAL
6788	3 16	936	GGTVDLR\DMLAVSVLAAVRGGR/ATVRRVRESNVLHEKSKGKT REGAEDKMTSGDVLSNRKMFYLLKTAFPSVQINTEEHVD\ELDQ

000	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	location	to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding		P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	Walryptopnan, Yalyrosine, Awonkhown, "-Scop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	]	\=possible nucleotide insertion)
			EVILWGS*DS*GYPKGK*LLPKEVPSR/RVLLSGLTPLDATQE\
	ļ	Ļ	FTEDLSK\YVTTMVCVAVNGKPMLGVIHKPFSEYTAWAMVDGGS
			NVKARSSYNEKTPRIVVSRSHSGMVKQVALQTFGNQTTIIPAGG
	1		AGYKVLALLDVPDKSQEKADLYIHVTYIKKWDICAGNAILKALG
		1	GHMTTLSGEEISYTGSDGIEGGLLASIRMNHQALVRKLPDLEKT
			GHK
		678	GNGINVLKIAPESAIKFMAYEQIKRLVW**PGDS*GF/YERLVA
6789	2	676	GSLAGAIAQSSIYPMEVLKTRMALRKTGQYSGMLDCARRILARE
			GVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNSAD
ļ		ŀ	PGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVT
	1		PGVFVLDACGIMSSICGQDASIPHADVRIRAQAQASIBOATEVI
ł		ł	MSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLKI
			TLGVQSR
6790	2	4068	APPAGRRRMQAAPRAGCGAALLLWIVSSCLCRAWTAPSTSQKCD
			EPLVSGLPHVAFSSSSSISGSYSPGYAKINKRGGAGGWSPSDSD
1		1	HYQWLQVDFGNRKQISAIATQGRYSSSDWVTQYRMLYSDTGRNW
ļ.		1	KPYHQDGNIWAFPGNINSDGVVRHELQHPIIARYVRIVPLDWNG
1		Į.	EGRIGLRIEVYGCSYWADVINFDGHVVLPYRFRNKKMKTLKDVI
ł			ALNFKTSESEGVILHGEGQQGDYITLBLKKAKLVLSLNLGSNQL
ì	ĺ		GPIYGHTSVMTGSLLDDHHWHSVVIERQGRSINLTLDRSMQHFR
1	1		TNGEFDYLDLDYEITFGGIPFSGKPSSSSRKNFKGCMESINYNG
1			VNITDLARRKKLEPSNVGNLSFSCVEPYTVPVFFNATSYLEVPG
		l .	RLNQDLFSVSFQFRTWNPNGLLVFSHFADNLGNVEIDLTESKVG
			VHINITQTKMSQIDISSGSGLNDGQWHEVRFLAKENFAILTIDG
1		)	DEASAVRTNSPLQVKTGEKYFFGGFLNQMNNSSHSVLQPSFQGC
			DEASAVRINSPLOVRIGERYF FGGF ENQUINNSSHSVEQFSFQGC
1			MQLIQVDDQLVNLYEVAQRKPGSFANVSIDMCAIIDRCVPNHCE
ļ			HGGKCSQTWDSFKCTCDETGYSGATCHNSIYEPSCEAYKHLGQT
]		}	SNYYWIDPDGSGPLGPLKVYCNMTEDKVWTIVSHDLQMQTPVVG
ì	1	1	YNPEKYSVTQLVYSASMDQISAITDSAEYCEQYVSYFCKMSRLL
-	ļ.	1	NTPDGSPYTWWVGKANEKHYYWGGSGPGIQKCACGIERNCTDPK
		1	YYCNCDADYKQWRKDAGFLSYKDHLPVSQVVVGDTDRQGSEAKL
}	1		SVGPLRCQGDRNYWNAASFPNPSSYLHFSTFQGETSADISFYFK
1			TLTPWGVFLENMGKEDFIKLBLKSATEVSFSFDVGNGPVEIVVR
			SPTPLNDDQWHRVTAERNVKQASLQVDRLPQQIRKAPTEGHTRL
1			ELYSQLFVGGAGGQQGFLGCIRSLRMNGVTLDLEERAKVTSGFI
}	1		SGCSGHCTSYGTNCENGGKCLERYHGYSCDCSNTAYDGTFCNKD
1	i	ł	VGAFFEEGMWLRYNFQAPATNARDSSSRVDNAPDQQNSHPDLAQ
	Ì		EEIRFSFSTTKAPCILLYISSFTTDFLAVLVKPTGSLQIRYNLG
1			GTREPYNIDVDHRNMANGQPHSVNITRHEKTIFLKLDHYPSVSY
1 .			HLPSSSDTLFNSPKSLFLGKVIETGKIDQEIHKYNTPGFTGCLS
1			HDF555DTDFN5FA5DFDGAVIETGATDQDIRATRIFGFTGCD5
			RVQFNQIAPLKAALRQTNASAHVHIQGELVESNCGASPLTLSPM
	}		SSATDPWHLDHLDSASADFPYNPGQGQAIRNGVNRNSAIIGGVI
1			A\VVIFTPSLCTP\VLP*SR*HVSPHKGTLPIPNEAKGAGSRQK
			KPGRRPSMNNDPPTSQRPIDESKKEWPHLRGGYLAMG
6791	1801	1193	TGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPEL/PGW
","	1		SAVV*SWLTAASTKVQAILLPQPLE*LGLQIAFMASLATHFSNQ
1			NSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDV
1	}	1	EEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVW
1		[	LRMGNGALHGDHQRFSTFAGFLLFETK
		1000	VRHTNWGVDMYLFSLGSESPKGAIGHIVSTEKTILAVERNKVLL
6792	33	1073	PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFENLAAWGRCLCAV
	1	İ	PADMINKI LOMBLE DE LOCATION CONTROL DE BOYLACITATION DE LA COMPONITATION DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL
1	1		CPSPTTIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHTQAV
			TCLAASVTFSLLVSGSQDCTCILWDLDHLTHVTRLPAHREGISA
			ITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCC
			CLMEGPAWDTSQIIITGSQDGMVRVWKT/VGCEDVCSWTASRRG
}			APGSASKPKRPQVGEEPGLESRAGR*HCFDREAQQNQP\PVTAL
			AVSRNHTKLLVGDERGRIFCWSADG*EERGSRGSGTTVPG
L			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	location		L=Leucine, M=Methionine, N=Asparagine,
1	corresponding	to first	
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6793	2340	805	GRKEANY\YGSLTQAGTVSLGLDAEGQEVFVPFSAVLPMVAPND
1 1			LVFDGWDISSLNLAEAMRRAKVLDWGLQEQLWPHMEALRPRPSV
1		1	YIPEFIAANQSARADNLIPGSRAQQLEQIRRDIRDFRSSAGLDK
1 1		İ	VIVLWTANTERFCEVIPGLNDTAENLLRTIELGLEVSPSTLFAV
1			ASILEGCAFLNGSPONTLVPGALELAWOHRVFVGGDDFKSGOTK
, ,		1	VKSVLVDFLIGSGLKTMSIVSYNHLGNNDGENLSAPLQFRSKEV
			SKSNVVDDMVQSNPVLYTPGEEPDHCVVIKYVPYVGDSKRALDE
1 1		·	YTSELMLGGTNTLVLHNTCEDSLLAAPIMLDLALLTELCQRVSF
			· ·
1		]	CTDMDPEPQTFHPVLSLLSFLFKAPLVPPGSPVVNALFRQRSCI
		Ì	ENILRACVGLPPQNHMLLEHKMERPGPSLKRVGPVAATYPMLNK
1 1			KGPVPAATNGCTGDANGHLQEEPPMPTT*GPGHTVSRLFLPAAP
			HDPTLKAPTNKGRCHFSPPSTWGSWGL
6794	169	1349	DDVKRKPEASAH*EKPGPPSRPGVRGGRERAGGRGSHGARSCR\
		1	EPAPPAPAPPEDHPDEEMGFTIDIKSFLKPGEKTYTQRCRLFVG
1		!	NLPTDITEEDFKRLFERYGEPSEVFINRDRGFGFIRLESRTLAE
1 1		1	IAKAELDGTILKSRPLRIRFATHGAALTVKNLSPVVSNELLEQA
) 1			FSQFGPVEKAVVVVDDRGRATGKGFVEFAAKPPARKALERCGDG
1		1	AFLLTTTPRPVIVEPMEQFDDEDGLPEKLMQKTQQYHKEREQPP
1 1			RFAQPGTFEFEYASRWKALDEMEKQQREQVDRNIREAKEKLEAE
1 1			MEAARHEHQLMLMRQDLMRRQEELRRLEELRNQELQKRKQIQLR
			HEEEHRREBEMIRHREQEELRRQQEGFKPNYMENYVCHFLR
6795	1740	1010	GPRROTOVRDHELDSF*DWAAQETDCAQNSGERL*KGV/LENFS
0/35	1740	1010	TMSKSAVKISLDLLSNPLCEQDQDLLNMVTALDTAMKRMDAFNQ
			EKVNQIQKTVIEPLKKFGSVFPSLNMAVKRREQALQDYRRLQAK
			VEKYEEKEKTGPVLAKLHQAREELRPVREDFEAKNRQLLEEMPR
			FYGSRLDYFQPSFESLIRAQVVYYSEMHKIFGDLSHQLDQPGHS
			DEQRERENEAKLSELRALSIVADD
6796	48	683	GKEIQIPTIKLAWLLFGLE*PVGALGKGVVSF**SHVALGQLGW
1 1			LTRAVRSSWRWELCVSAQEVVSQRSA*SSPSFVGACPSLNPPET
			SVQBGRDCWQR+LPRLFSALVGQPGCWPQGAPPERCV+PGRCKW
			HLQSQVLR*ERRRCCRCLPRFA*GWRRRHQRLGLGIHPAPLGST
			SPPHPEGNSQQCRR*GWAAELRLPSSVVL*GKLGC*
6797	1620	211	TERMTPSQPTRGSSCTRPSSMLWTSTWRCLTCHWAGMRMSVVGV
1		1	TLGPMAQGLLSASGTTTEATWTRPTTHLTLIRWWLLTASRVDPP
	j		ERPPPPPSDDLTLLESSSSYKNL/DAQIPQ/DWSMSPSTSG*RP
	1		LTSRASSIMRSRTAIPSAS*SRLTTKHTVGGSPSAWRPRPTSRS
			VSTPVSSSTETTASGSCLTWWSSSPAPCPSSSAPAHSFEASCCK
	1	1	TSLWGSCGGSGDGSSACGSGWNLSMAGTSCSSPAMCSPSRAPS*
	1		RSASRPRTWRATTSAASSWAPRRCWCGWA*SAT*PSSTTTISSS
	1		PHCGWPCPASCASAAAWLSSTWATASVAGSCWGPIM*SSAHSPW
			CLSACSRSSMGTTCL*RSPP\SGASRAAAAWCGSSPSSTFTPSS
	1		ASSSTWCSASSSRSSPAPTTPSSIPAAQAQRRASCRPTSHSART
ł			APPPASSAAGAARPAAFSAAAEGTPRRSIRCW
6798	3894	1696	STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS
0/90	3034	1030	ALWGQLRGSGLGRGTTMAKEGQPGSPRLSALECVLLVPQ\PQIA
			VRLLAHKIQSPQEWEALQALTYLGDRVSEKVKTKVIELLYSWTM
	1		ALPEEAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPKNP
			VFDDEEKSKLLAKLLKSKNPDDLQEANKLIKSMVREDEARIQKV
}		1	TKRLHTLEEVNNNVRLLSEMLLHYSQEDSSDGDRELMKELFDQC
1			ENKRRTLFKLASETEDNDNSLGDILQASDNLSRVINSYKTIIEG
1		1	QVINGEVATLTLPDSEGNSQCSNQGTLIDLAELDTTNSLSSVLA
1			PAPTPPSSGIPILPPPPQASGPPRSRSSSQAEATLGPSSTSNAL
1		l.	
			SWLDEELLCLGLADPAPNVPPKESAGNSQWHLLQREQSDLDFFS
}			SWLDEELLCLGLADPAPNVPPKESAGNSQWHLLQREQSDLDFFS PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPPFPAPVVPASVP
			PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPPFPAPVVPASVP

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
Į.	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence		PLSFQSQGSPPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF
			RILFHFAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLQAAVPKS
			MKVKLQPPSGTELSPFSPIQPPAAITQVMLLANPLKEKVRLRYK
ļ	i		
_			LTFALGEQLSTEVGEVDQFPPVEQWGNL STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS
6799	3894	1696	STISWESLESWINKATNPSNRQEDWEITIGFCDQINKEDEG VS
			ALWGQLRGSGLGRGTTMAKEGQPGSPRLSALECVLLVPQ\PQIA
}			VRLLAHKIQSPQEWEALQALTYLGDRVSEKVKTKVIELLYSWTM
1	1		ALPEEAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPKNP
			VFDDEEKSKLLAKLLKSKNPDDLQEANKLIKSMVREDEARIQKV
			TKRLHTLEEVNNNVRLLSEMLLHYSQEDSSDGDRELMKELFDQC
1	Į.		ENKRRTLFKLASETEDNDNSLGDILQASDNLSRVINSYKTIIEG
		i	QVINGEVATLTLPDSEGNSQCSNQGTLIDLAELDTTNSLSSVLA
			PAPTPPSSGIPILPPPPQASGPPRSRSSQAEATLGPSSTSNAL
1			SWLDEELLCLGLADPAPNVPPKESAGNSQWHLLQREQSDLDFFS
1			PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPPFFAPVVPASVP
Į.		1	APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSALHHLDAL
1			DQLLEEAKVTSGLVKPTTSPLIPTTTPARPLLPFSTGPGSPLFQ
1		Į.	PLSFQSQGSPPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF
l .			RILFHFAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLQAAVPKS
1			MKVKLQPPSGTELSPFSPIQPPAAITQVMLLANPLKEKVRLRYK
1			LTFALGEQLSTEVGEVDQFPPVEQWGNL
6800	404	1646	RRSPSTGLSPVPQPSSPSLSDYS1PWSLLLSGT1AWATPGK*AG
1			*PQAW*LGLAPAIAFI/GLTRGRKQNKEKMAEGGSGDVDDAGDC
1			SGARYNDWSDDDDDSNESKSIVWYPPWARIGTEAGTRARARA
			RATRARRAVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILE
-{	l		AALIALGNNAAYAFNRDIIRDLGGLPIVAKILNTRDPIVKEKAL
i			IVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLAGLRLL
			TNMTVTNEYQHMLANSISDFFRLFSAGNEETKLQVLKLLLNLAE
i i			NPAMTRELLRAQVPSSLG\SLFNKKENKEVILKLLVIFENINDN
1	1		FKWEENEPTQNQFGEGSLFFFLKEFQVCADKVLGIBSHHDFLVK
		460	VKVGKFMAKLAEHMFPKSQE
6801	2	1755	SAEEFESQQASVTMHDVDAESFEVLVDYCYTGRVSLSEANVERL
ì	1		YAASDMLQLEYVREACASFLARRLDLINCTAILKFADAFGHRKL
1			RSQAQSYIAQNFKQLSHMGSIREETLADLTLAQLLAVLRLDSLD
		1	VESEQTVCHVAVQWLEAAPKERGPSAABVFKCVRWMHFTEEDQD
1		1	YLEGLLTKPIVKKYCLDVIEGALQMRYGDLLYKSLVPVPNSSSS
1		1	/R*QQQLSCICSRKSTPETGYVCQGDGDLLWTPQRSLS\RYDPY
1		Į.	SGDIYTMPSPLTSFAHTKTVTSSAVCVSPDHDIYLAAQPRKDLW
		1	VYKPAQNSWQQLADRLLCREGMDVAYLNGYIYILGGRDPITGVK
			LKEVECYSVQRNQWALVAPVPHSFYSFELIVVQNYLYAVNSKRM
			LCYDPSHNMWLNCASLKRSDFQEACVFNDEIYCICDIPVMKVYN
1	ļ		PARGEWRRISNIPLDSETHNYQIVNHDQKLLLITSTTPQWKKNR
			VTVYEYDTREDOWINIGTMLGLLQFDSGFICLCARVYPSCLEPG
1	į		QSFITEEDDARSESSTEWDLDGFSELDSESGSSSSFSDDEVWVQ
			VAPORNAODOOGSL
6802	157	1341	ETFPLFFFLLSKTPGKTASMAHFVQGTSRMIAAESSTEHKECAE
3502	1		PSTRKNLMNSLEOKIRCLEKQRKELLEVNQQWDQQFRSMKELYE
	1	1	RKVAELKTKLDAAERFLSTREKDPHQRQRKDDRQREDDRQRDLT
		1	RDRLORERKEKERLNEELHELKEENKLLKGKNTLANKEKEHYEC
			FIKRLNKALODALNIKCSFSEDCLRKSRVBFCHEEMRTEMEVLK
		1	OOVOIYEEDFKKERSDRERLNQEKEELQQINETSQSQLNRLNSQ
			IKACOMEKEKLEKOLKOMYCPPCNCGLVFHLQDPWVPTGPGAVQ
-		1	KOREHPPDYOWYALDOLPPDVOHKAN/DWCLAPPPVCCQAG/PR
			TPGLK*SSCLWLPKC*NFRFILSKESPSVEVHTNRERQQATRER
			G
- 5000	1	2203	KLSGRPYRHMGVLGTSKLYDIRKTIFTFTPQFIDQQQFYLALDN
6803		2203	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of		Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence		KMIVEMLRTDLSYLCSRWRMTGQPTITFPISHSMLDEDGTSLNS
		· ·	KMIVEMERTDESYECSKWRMTGQP111FP1SHSMEEDG13ERS
			SILAALRKMODGYFGGARVOTGKLSEFLTTSCCTHLSFMDPGPE
			GKLYSEDYDDNYDYLESGNWMNDYDSTSHARCGDEVARYLDHLL
			AHTAPHPKLAPTSQKGGLDRFQAAVQTTCDLMSLVTKAKELHVQ
	ł	1	NVHMYLPTKLFQASRPSFNLLDSPHPRQENQVPSVRVEIHLPRD
	1	1	OSGEVDFKALVLOLKETSSLQEQADILYMLYTMKGPDWNTELYN
		1	ERSATVRELLTELYGKVGEIRHWGLIRYISGILRKKVEALDEAC
		1	TDLLSHQKHLTVGLPPEPREKTISAPLPYEALTQLIDEASEGDM
		1	SISILTQEIMVYLAMYMRTQPGLFAEMFRLRIGLIIQVMATELA
		Ì	HSLRCSAEEATEGLMNLSPSAMKNLLHHILSGKEFGVERK/SVR
	}		HSLRCSAEEATEGEMNESPSAMKNEEHHILBSGREFGVERK/SVR
			PTDSNVSPAISIHEIGAVGATKTERTGIMQLKSEIKQVEFRRLS
	1		ISAESQSPGTSMTPSSGSFPSAYDQQSSKDSRQGQWQRRRRLDG
			ALNRVPVGFYQKVWKVLQKCHGLSVEGFVLPSSTTREMTPGEIK
		1	FSVHVES\VLNVLLRPEYRQLLVEAILVLTMLADIEIHSIGSII
		ļ	AVEKIVHIANDLFLQEQKTLGP\DDTMLAKDPASG\ICTLR\YD
		į.	SAPSGRFGTMTYLS\RAA\ATYVQEFLP\HSICAMQ
		951	GSPGKKEEKAKNKESLCMENSSNSSSDEDEEETKAKMTPTKKYN
6804	1	1 331	GLEEKRKSLRTTGFYSGFSEVAEKRIKLLNNSDERLQNSRAKDR
			KDVWSSIQGQWPKKTLKELFSDSDTEAAASPPHPAPEEGVAEES
l .		1	LQTVAEEESCSPSVELEKPPPVNVDSKPIEEKTVEVNDRKAEFP
			LOTVALERSCSPSVEDERPPPVMVDSKFIEDKTVDKKG DD1
1			SSGSNFSA*IPLPYLHLNRLHQSL*QKGSRQQSSVTVSEPLAPN
ì		1	QEEVRSIKSETDSTIEVDSVAGELQDLQSERE*LASRF*CQCEL
ł			KQ**SARTRTS*KSLYRSEKSERCSGRRKFIKKAEKKP*SNSGK
İ		İ	QQKEGKRHK
6805	1539	206	ROPDLKYFGKSFDVSVSESSSLLSNDLPKFADGIKARNRNQNYL
9902	1333		VPSPVLRILDHTAFSTEKSADIVICDEECDSPESVNQQTQEESP
			IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLQDQTDEEPPA
i	Ì	<b>!</b>	KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS
1		ì	DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI
l			CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY
		}	LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD
ì			KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV
		<b>\</b>	KYNNGERGQYSLESKI IFDRCKNFF VCQVCGFRSKEITKVKARI
		1	AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW
			EYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERELISHLP
1		1	VHETT
6806	272	3794	VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV
1 5000	2,2		GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI
1			DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA
1		1	SLLAOCRALTOACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR
	}		MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMHWSLLAQ
			RGQRDVSLSSLRMLIVADGANPWSISSCDAFLNVFQSRGLRPEV
			ICPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGLSYGVIRVD
1			TEEKLSVLTVQDVGQVMPGANVCVVKLEGTPYLCKTDEVGEICV
1			TREKTSATLAGDAGGAWAGAWACAAKTEGIAITEKIDEAGEICA
1	1		SSSATGTAYYGLLGITKNVFEAVPVTTGGAPIFDRPFTRTGLLG
1			FIGPDHLVFIVGKLDGLMVTGVRRHNADDVVATALAVEPMKFVY
			RGRIAVFSVTVLHDDRIVLVAEQRPDASEEDSFQWMSRVLQAID
			SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN
1			VIMCPHTCVTNLPKPROKOPEVGPASMIVGNLVAGKRIAQASGR
1		1	ELAHLEDSDOARKFLFLADVLOWRAHTTPDHPLFLLLNAKGTVT
			STATCVOLHKRAERVAAALMEKGRLSVGDHVALVYPPGVDLIAA
1		1	FYGCLYCGCVPVTVRPPHPQNLGTTLPTVKMIVEVSKSACVLTT
1			QAVTRLLRSKEAAAAVDIRTWPTILDTDDIPKKKIASVFRPPSP
1		1	DVLAYLDFSVSTTGILAGVKMSHAATSALCRSIKLQCELYPSRQ
1			DVLAYLDFSVSTTGI LAGVKMSHAATSABCKSTRIQCEDIPSKQ
1			IAICLDPYCGLGFALWCLCSVYSGHQSVLVPPLELESNVSLWLS
1	1		AVSQYKARVTFCCYSVMEMCTKGLGAQTGVLRMKGVNLSCVRTC MVVAEERP\RIALTQSFSKLFKDLGLPARAVSTTFGCRVNVAIC
	i .		LICENT TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE
1			MOVARSODIDIA CATISTISTISTISTA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA ARTITUDA

		Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
ID	beginning	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valle,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LOGTAGPDPTTVYVDMRALRHDRVRLVERGSPHSLPLMESGKIL
			PGVKVIIAHTETKGPLGDSHLGEIWVSSPHNATGYYTVYGEEAL
	I		HADHFSARLSFGDTQTIWARTGYLGFLRRTELTDASGGRHDALY
			VVGSLDETLELRGMRYHPIDIETSVIRAHRSIAECAVFTWTNLL
		}	VVVVELDGLEQDALDLVALVTNVVLEEHYLVVGVVVIVDPGVIP
			INSRGEKORMHLRDGFLADQLDPIYVAYNM
6005	7444	606	VGHDTVHAMFTCFPKCLGFSPPVNVTVSPRSEESHTTTVSGGNG
6807	1444	1	SVFQAGPQLQALANLEARRGSIGAALSSRDVSGLPVYAQSGEPR
			RLTQAQVAAFPGENALEHSSDQDTWDSLRSPGFCSPLSSGGGAE
			SLPPGGPGHAEAGHLGKVCDFHLNHQQPSPTSVLPTEVAAPPLE
			KILSVDSVAVDCAYRTVPKPGPQPGPHGSLLTEGCLRSLSGDLN
	1		RFPCGMEVHSGQRELESVVAVGEAMA\LKFPMGAMSYCLRDRSR
	1		FLFRLPMGLSCPLQVQ
6808	2063	737	GVGSGAASALARSRPLASRLSSRRRTRAPRSGAMQRLAMDLRML
	1		SRELSLYLEHQVRVGFFGSGVGLSLILGFSVAYAFYYLSSIAKK
			PQLVTGGESFSRFLQDHCPVVTETYYPTVWCWEGRGQTLLRPF\
			ITSKPPVQYRNELIKTADGGQISLDWFDNDNSTCYMDASTRPTI
			LLLPGLTGTSKESYILHMIHLSEELGYRCVVFNNRGVAGENLLT
		}	PRTYCCANTEDLETVIHHVHSLYPSAPFLAAGVSMGGMLLLNYL
			GKIGSKTPLMAAATFSVGWNTFACSESLEKPLNWLLFNYYLTTC
			LQSSVNKHRHMFVKQVDMDHVMKAKSIREFDKRFTSVMFGYQTI
		1	DDYYTDASPSPRLKSVGIPVLCLNSVDDVFSPSHAIPIETAKQN
		į	PNVALVLTSYGGHIGFLEGIWPRQSTYMDRVFKQFVQAMVEHGH
			RLS
5000	939	65	DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ
6809	939	83	TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLRQMF
		į.	GOFGKILDVEIIFNERGSKGFGFVTFETSSDADRAREKLNGTIV
Į.	1	<b>\</b>	EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFYA
		1	VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG
		1	AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP
	1		
			TRTITPSGPRRPTALEPCETFHRFLLGP
6B10	939	65	DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ
}			TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLRQMF
			GQFGKILDVBIIFNERGSKGFGFVTFETSSDADRAREKLNGTIV
Ì			EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFYA
{		Į.	VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPPIPTYG
ļ			AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP
			TRTITPSGPRRPTALEPCETFHRFLLGP
6811	1522	658	DLVTVWSFVDCRVIASTHGH\KSWVSVVAFDPYTTSVEEGDPME
1 0017	1,22		FSGSDEDFODLLHFGRDRADSTQCRLSRRNSTDSRPVSVTYRFG
Į.		1	SVGQDTQLCLWDLTEDILFPHQPLSRARTHTNVMNATSPPAGSN
	1	ì	
			GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV
			GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV
			GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK
			GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI
			GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACOEGFICTWGRPGKVVSFNP
6812	4001	1682	GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP EDAVFSLDLSTIIOGTWFLNGEELKSNEPEGQVEPGALRYRIEQ
6812	4001	1682	GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLMLVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLOHRLILHAVKHODSGALVGFSCPGVQDSAALTIQESPVHIL
6812	4001	1682	GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLMLVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPODKVSLIPTTSERVVLTCELSRVDFPATWYKDGQKVEESELL
6812	4001	1682	GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGGKVEESELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV
6812	4001	1682	GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE
6812	4001	1602	GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSKLNLVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGTTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI
6812	4001	1682	GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMCGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFFATWYKDGQKVEESELL VVKMDGRKIRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE
6812	4001	1682	GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV H1VDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE EVVESPALLIOKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT
6812	4001	1682	GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLINLVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP EDAVFSLDLSTIIQGTWFLINGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE EVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT VTYTRPPVRIIYPRDEVTLIAVTLECVVLMCELSREDAPVRWYK
6812	4001	1682	GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE EVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT VTVTEPPVRIIYPRDEVTLIAVTLECVVLMCELSREDAPVRWYK DGILFVEESEALVLERDGFRCRLVLPAAQPEDGGEFVCDAGDDSA
6812	4001	1602	GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV H1VDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE EVVESPALLIOKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT

		I D. It at all and	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	to first	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence	ļ	VWSHNGRPVQEGEGLELHAEGPRRVLCIQAAGPAHAGLYTCQSG
	Ì		AAPGAPSLSFTVQVAEPPVRVVAPEAAQTRVRSTPGGDLELVVH
	1	ì	LSGPGGPVRWYKDGERLASQGRVQLEQAGARQVLRVQGARSGDA
		1	GEYLCDAPQDSRIFLVSVEEPLLVKLVSDLTPLTVHEGDDATFR
			CEVSPPDADVTWLRNGAVVTPGPQRQSCCSYGGCRMCGQRKART
		1	CVSKWRQAEWVQRGPCAGCEVGSPCPTTLACPWPRMGTSTASSS
			MVSYWPTRAPTAARATTIAPWPGSA
			STQQRPGVPAGPRPLDGYLGVADHKPLKMHCRDCALVTSSGHL
6813	9	836	LHSRQGSQIDQTECVIRMNDAPTRGYGRDVGNRTSLRVIAHSSI
			QRILRNRHDLLNVSQGTVFIFWGPSSYMRRDGKGQVYNNLHLLS
į		}	QVLPRLKAFMITRHKMLQFDELFKQETGQ\NRKISNTWLSTGWF
	1		TMTIALELCDRINVYGMGPPDFCRDPNHPSVPYHYYEPFGPDEC
l			TMTIALELCORINVIGMGPPDFCRDPMRPSVFIRTIEFFGFDEC
		İ	TMYLSHERGRKGSHHRFITEKRVFKNWARTFNIHFFQPDWKPES
			LAINHPENKPVF
6814	3	737	KFRRQEAN/ARERNRMHGLNDALDNLRKVVPCYSKTQKLSKIET
			LRLAKNYIWALSEILRIGKRPDLLTFVQNLCKGLSQPTTNLVAG
Ì	1	1	CLQLNARSFLMGQGGEAAHHTRSPYSTFYPPYHSPELTTPPGHG
			TLDNSKSMKPYNYCSAYESFYESTSPECASPQFEGPLSPPPINY
1		Ì	NGIFSLKQEETLDYGKNYNYGMHYCAVPPRGPLGQGAMFRLPTD
1			SHFPYDLHLRSQSLTMQDELNAVFHN
6815	906	553	QGLDPASQTKVVELLKDGSGRRGDRRSSRDMAGGAGPRSESDLE
1			DVGPTAEWNGDGSGSLRRSGSFGKLRDALRRSSEMLVKKLQGGT
			PQEPPNPRMKRASSLNFLNKSVEEPTQPGG
6816	1	803	NLLKTHKF\LLGQDEDSLHSVPVAQMGNYQEYLKTLASPLREID
1	1		PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN
			SPMSSKRRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN
			LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM
1	1		TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS
	1	İ	VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF
	Ì		GRSK
6817	172	3457	LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS
			DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL
ľ			NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA
	Ì		IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI
1			LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC
1			TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE
1			ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET
1			CLNEVRDEIFISLQPQLRCTLGDMESPVFAFPLLLKLETHIEKL
1			FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHF
1			GPCNNCNSKSQIRKMVLEKVSPIFMLHFVEGLPQNDLQHYAFHF
1	1		EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH
			KKFRVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE
			KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD
			HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV
			AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ
1			VVNTNMOSVOLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ
			LKOFLTPKTEOLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ
	1		SLKENOKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS
I			VKGVNNFGGFKTKGINOKASHVSKKARKSASKPPPISKPPAGPP
			SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH
	i	1	EDLVEGOIHKLELKLEKKLKAEKKKLAALMSSPQSETVESENLE
		1	OVPODGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS
			QTHEBILAELLSPTPVSTBLSENGEGDFRYLGMGDSHIPPPVPS
			EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL
	1	1	ESPMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY
6818	2	240	RGFDKVLWT/LSGAVK\CVQFSRISPDGEEGYPGELKVWVTYTL
6818	<u></u>		

SEQ ID	Predicted	Predicted end	Amino acid segment containing signal peptide
ID		1	a contract b remette haid En
	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
			Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence	L	DGGE/LHS/ATTEHKP/VQATPVNLT\TILTSTWQARLPQI
			GIPCTEMGNFDNANVTGEIEFAIHYCFKTHSLEICIKACKNLAY
6819	1	961	GIPCTEMGNFDNANVTGETEFAIHICFKIHSDETCTKACKUMAT
	1	į.	GEEKKKKCNPYVKTYLLPDRSSQGKRKTGVQRNTVDPTFQETLK
	1	ļ	YQVAPAQLVTRQLQVSVWHLGTLARRVFLGEVIIPLATWDFEDS
	l .		TTQSFRWHPLRAKADKYEDSVPQSNGELTVRAKLVLPSRPRKLQ
			EAGEGTDQPSLHGQLCLVVLGAKNLPVRPDGTLNSFVKGCLTLP
		1	DOOKLRLKSPVLRKQACPOWKHSFVFSGVTPAQLRQSSLELTVW
	j	1	DQALFGMNDRLLGGT\RLGSKGDTAVGGDACSQSKLQWQKVLSS
			PNLWTDMTLVLH
		<del></del>	GDMVYIVGHVPPGFFEKTQNKAWFREGFNEKYLKVVRKHHRVIA
6820	1014	340	GOFFGHHHTDSFRMLYDDAGVPISAMFITPGVTPWKTTLPGVVN
			GANNPAIRVFEYDRATLSLKDMVTYFMNLSQANAQGTPRWELEY
			GANNPAIRVFEYDRATLSLEDMVTYFMINLSQANAQGIPRWELLEI
	1		QLTEAYGVPDASAHSMHTVLDRIAGDQSTLQRYYVYNSVSYSAG
	1	Į.	VCDEACSMQHVCAMRQVDIDAYTTCLYASGTTPVPQLPLLLMAL
		1	LGLCT
6821	1088	518	EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN
0021	1		RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT
		ļ	FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG
	1	1	GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI
	1	ł	GSVIEVLQRRQEGLAS
			EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN
6822	1088	518	RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT
		1	FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG
			FFAFSLIEGYI\SIVMDAEIQARFPSDEEDISSSGEDWAWARIG
		· ·	GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI
			GSVIEVLQRRQEGLAS
6823	654	221	PPKLLSRWARMGHGDBIV\LSDLNFPGLLHLPVVGPWRSVQTAC
0023			GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE
	i	Į.	YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNI
	1		ILRKGVLALNPLL
6004	858	104	LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLLTQFGFRC
6824	838	1 20.	ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWT
	1	\	NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS
	1	<b>\</b>	LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFY
	1		WYPHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS
	ı	1	WALKLIPATETM OF THE OBODEDACAOACAAAA
	ľ		AALHICHAVILLQLWLGPQPFPKSTQHSKKAH
6825	3	1173	SSGEFGLQASDIMWTISDTGWILLILCSLMEPWALGACTFVHLI
			PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ
			NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKT
		}	KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRP
			GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADI
			IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKA
			VILALOFISHDPEOLTKELOOHVKSVTAPYKYPRKIEFVLNLPI
			margy topa VI. PDKEWKMSGKAPCAVRHI.RDIHI.DSPLILSLS
			LAIGHTON (GROSSIMERREAKEGI'YI'ALGAKI'AHABU
			PEGPENDERGE GENERAL GENERAL GENERAL DE L'ATTENDE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTENDE DE L'ATTEND
6826	2304	954	LKTESFKPW/VNIALAFHILIGERASPNSFWQFIIQILPREIDII
			LYFEEDEVRYLQSTQAIHDVFSQYKNTARQYAYFYKVIQTHPH
			NKLPLKDSFTYEDYRWAVSSVMTRQNQIPTEDGSRVTLALIPL
			DMCNHTNGLITTGYNLEDDRCECVALQDFRAGEQIYIFYGTRS
			AEFVIHSGFFFDNNSHDRVKIKLGVSKSDRLYAMKAEVLARAG:
		1	PTSSVFALHFTEPPISAOLLAFLRVFCMTEEELKEHLLGDSAI
			PIETLGNSEFPVSWDNEVKLWTFLEDRASLLLKTYKTTIEBDK
			VI VALUDI CUPAKMATKI RI GEKETI RKAVKSAAVNRRYYROOM
		i	A DUTUINDO A LOUGHEST STOREST CONTROL TOPICS AND A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STOREST OF A STORES
		1	HIADI DEVERONI CLI ECCUCDODI DI VI DNI EERAGVODALN
i			EKAPLPKYEESNLGLLESSVGDSRLPLVLRNLEEEAGVQDALN
i			EKAPLPKYEESNLGLLESSVGDSRLPLVLRNLEEEAGVQDALN REAISKAKATENGLVNGENSIPNGTRSENESLNQESKRAVEDA GSSSDSTAGVKE
		954	SSGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTF PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQDDLSSYKF NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMV KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKP GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMG IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEV VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVI TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLL PFGPLALPMDGYGDSLWEEHEYKFCLALVISTKLYHVRC LKTESFKPW/VNIALAFHLLGERASPNSFWQPYIQTLPRE LYFEEDEVRYLQSTQAIHDVFSQYKNTARQYAYPYKVIQT NKLPLKDSFTYEDYRWAVSSVMTRQNQIPTEDGSRVTLAI DMCNHTNGLITTGYNLEDDRCECVALQDFRAGEQIYIFYG AEFVIHSGFFFDNNSHDRVKIKLGVSKSDRLYAMKAEVLF PTSSVFALHFTEPPISAQLLAFLRVFCMTEEELKEHLLGI RIFTLGNSEFPVSWDNEVKLWTFLEDRASLLLKTYKTTIE

ID beg NO: nuc loc co: to am. re	edicted ginning cleotide cation rresponding	Predicted end nucleotide location	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine,
NO: nucleon local to am.	cleotide cation	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=   Clutemic Acid, F=Phenylalanine, G=Glycine,
loc co: to am: re:	cation		l Clutamic Acid. FaPhenVizianine. GEGIVCIUC: I
to am	1		Gracamic Moral remaining
to am. re	rresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
to am. re		to first	L=Leucine, M=Methionine, N=Asparagine,
am: re	first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
re	ino acid	residue of	S=Serine, T=Threonine, V=Valine,
	sidue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1 4111	ino acid	sequence	Codon, /=possible nucleotide deletion,
l		Bequence	\=possible nucleotide insertion) .
	quence	779	SSVVEFGLSVLGGLFLLFVLENMLGLLRHRGLRPRCCRRKRRNL
6827	1	119	ETRNLDPENGSGMALQPLQAAPEPGAQGQREKNSQHPPALAPPG
			HQGHSHGHQGGTDITWMVLLGDGLHNLTDGLAIGAAFSDGFSSG
ļ	i		HOGHSHGHOGGIDIIWWVDDGDGHANDIDGHAIGAAIDDGIDG
			LSTTLAVFCHELPHELGDFAMLLQSGLSFRRLILLSLVSGALGL
Ì			GGAVLGVGLSLGPVPLTPWVFGVTAGVFLYVALVDMLPALFPSS
į į			GAPAYA\HVLLQGLGLLLGGCLMLAITLLEERLLPVTTEG
6828	<u>3</u>	1654	KSQHG/WILQLMHSCKEGYVKDLKGNPGLHRAMLDLDNGTRPSE
0020	-		LGHLSQTASLKRGSSFQSGRDDTWRYKTPHRVAFVEKLTKLVLS
			OLPNFWKLWISYVNGSLFSETAEKSGQIERSKNVRQRQNDFKKM
	l	i	IQEVMHSLVKLTRGALLPLSIRDGEAKQYGGWEVKCELSGQWLA
. 1			HAIQTVRLTHESLTALEIPNDLLQTIQDLILDLRVRCVMATLQH
			TAEEIKRLAEKEDWIVDNEGLTSLPCQFEQCIVCSLQSLKGVLE
			CKPGEASVFQQPKTQEEVCQLSINIMQVFIYCLEQLSTKPDADI
l			DTTHLSVDVSSPDLFGSIHEDFSLTSEQRLLIVLSNCCYLERHT
			PLNIAEHFEKHNFQGIEKITQVSMASLKELDQRLFENYIELKAD
<b>(</b>			FLN IAEHFEKHNFOGIEKITOVSFASIKEBDOKBFENTIEBKAD
			PIVGSLEPGIYAGYFDWKDCLPPTGVRNYLKEALVNIIAVHAEV
			FTISKELVPRVLSKVIEAVSEELSRLMQCVSSFSKNGALQARLE
1			ICALRDTVAVYLTPESKSSFKQALEALPQLSSGADKKLLEELLN
{			KFKSSMHLQLTCFQAASSTMMKT
6829	1	782	MRMEAGEAAPPAGAGGRAAGGWGKWVRLNVGGTVFLTTRQTLCR
0025	-	•	BQKSFLSRLCQGEELQSDRDETGAYLIDRDPTYFGPILNFLRHG
1 1			KLVLDKDMAEEGVLBEAEFYNIGPLIRIIKDRMEEKDYTVTQVP
1		İ	PKHVYRVLQCQEEELTQMVSTMSDGWRFEQLVNIGSSYNYGSED
}			QAEFLCVVSKELHSTPNGLSSESSRKTKSTEEQLEEQQQQEEEV
			EEVEVEQVQVEADAQEK/CCYKPEAPGCEAPDHLQGLGVPI
			MEPGSVENLSIVYRSRDFLVVNKHWDVRIDSKAWRETLTLQKQL
6830	1	939	RYRFPELADPDTCYGFRFCHQLDFSTSGALCVALNKAAAGSAYR
1			CFKERRVTKAYLALLRGHIQESRVTISHAIGRNSTEGRAHTMCI
			CFKERRYTKAY LALLKGHIQESKVI I BHAIGKNOI EGGAITMEI
1			EGSQGCENPKPSLTDLVVLEHGLYAGDPVSKVLLKPLTGRTHQL
1			RV\HCSALGHPVVGDLTYGEVSGREDRPFRMMLHAFYLRIPTDT
1			ECVEVCTPDPFLPSLDACWSPHTLLQSLDQLVQALRATPDPDPE
1 1			DRGPRPGSPSALLPGPGRPPPPPTKPPETEAQRGPCLQWLSEWT
1 1			LEPDS
6831	3	1087	SLFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNF
0031	<b>J</b>		NVAEKPADHSLSEVKLKTADEPRGTLVKSGDGQNVKEKSMILSN
			VEDLOOPKFISEVSREDYGKKEISGDSEEMNINSVVTSADGENL
			EIQSYSLIGEKLVMEEAKTIVPPHVTDSKRVQKPAIAPPSKWNI
1			SIFKEEPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE
1		ì	SEKPESIILPVEESKGSLIDFSEDRLKKEMONPTSLKISEEETK
1		1	LRSVSPTEKKDNLENR\SYTL\ABKKVLAEKQNSV\APLELRDS
		1	NEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG
1		1	
			SEKEKDEKKKK
6832	1809	412	MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV
			VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF
			CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG
			PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL
[ [			REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL
] [			LHCLSFEOILOIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY
1			PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME
1 1			EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT
1			AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHPQERSFCK
1			ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE
1		}	ADISKINKKI VKKI VKIQDI SUFIQOMERSINI FAGI FQQKIDD
			YEEQKKQ/TETKGKNCEIRAVVNKND
6833	1	1129	PLMTLSQCGGIPGHGHSHGGHGHGHGLPKGPRVKSTRPGSSDIN
		1	VAPGEQGPDQEETNTLVANTSNSNGLKLDPADPENPRSGDTVEV
			QVNGNLVREPDHMELEEDRAGQLNMRGVFLHVLGDALGSVIVVV

			the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
		Beducine	\=possible nucleotide insertion)
	sequence		NALVFYFSWKGCSEGDFCVNPCFPDPCKAFVEIINSTHASVYEA
		1	GPCWVLYLDPTLCVVMVCILLYTTYPLLKESALILLQTVPKQID
			IRNLIKELRNVEGVEEVHELHVWQLAGSRIIATAHIKCEDPTSY
			MEVAKTIKDVFHNHGIHATTIQPEFASVGSKSSVVPCELACRTQ
			MEVAKTIKDVFHNHGIHATITQPEFASVGSKSSVVI CHIMICKTY
	l	•	CALKQCCGTLPQAPSGKDAEKTPAVSISCLELSNNLEKKPRRTK
	Ì		AENIPA\VVIEIKN\IPNK\QPESSL
6834	78	1151	AGQERPAPIWRLLWLPTPSVSRKAEPAHIPINR*GA*E*RGGLP
6034	, ,		LCGSSASAYGWH*RLTPWSPGGS*HM*SSKAPVTQARBVLVAGP
			CSKLVLSGARGIVGTTVOVLVEAQQPLLLLFTGVWGLNLRAGEE
		Į	SPAL*LIREVTOVRDAHLGNAVVGCAQCLSQGQVGSALAKALLE
			AAAAVRDCKEVLTVSGDKQQAEVSVRL*VRDVCVEEAGCVEFGQ
ı		1	AHGRPGLALAKGRGGTNEVEEQVQVDGVQKLVLSAHECHELVAG
	ļ	1	QQDGEDQAARTRLLQAGAHSVAHGRRQGQAPCRPHQEAGVSCHE
[		· I	LOQVVGDAL*ARE*APQIIVLLLLEDVAQLRTGKKA*DLVVDVE
1	,		
ł			QLLRQL
6835	1	834	GTPAADR\EASLELIKLDISRTFPNLCIFQQGGPYHDMLHSILG
1 0000	<u> </u>		AYTCYRPDVGYVQGMSFIAAVLILNLDTADAFIAFSNLLNKPCQ
ļ		i	MAFFRVDHGLMLTYFAAFEVFFEENLPKLFAHFKKNNLTPDIYL
-	}	1	IDWIFTLYSKSLPLDLACRIWDVFCRDGEBFLFRTALGILKLFE
ł	1	1	DILTKMDFIHMAOFLTRLPEDLPAEELFASIATIQMQSRNKKWA
1	1	1	QVLTALQKDSREMREGKSVPPTLRLQREFALGTNQSPMPRPLCC
1	1		FRLTPGQPRRTDAL
			MSCGRPPPDVDGMITLKV\DNLTYRTSPDSLRRVFEKYGRVGDV
6836	1	850	YIPREEHTKAPRGFAFVRFHDRRDAQDAEAAMDGAELDGRELRV
1		1	QVARYGRRDLPRSRQGRRHAAGPEAA/RYGRRSRSYGRRSRSPR
1	1	l l	QVARYGRRDLPRSRQGRRHAAGPEAA/RIGRRSRDIGRCDVCDCDVCDCDVCDCDVCDCDVCDCDVCDCDVCDCDV
}	1		RRHRSRSRGPSCSRSRSRSRYRGSRYSRSPYSRSPYSRSRYSRS
1			PYSRSRYRESRYGGSHYSSSGYSNSRYSRYHSSRSHSKSGSSTS
l			SRSASTSKSSSARRSKSSSVSRSRSRSRSSSMTRSPPRVSKRKS
1		i	KSRSRSKRPPKSPEEEGQMSS
6837	1	1369	TDGAAVAGNPGSDYFPGGTAP/GGPRTRRP\SGTSSSGSKASGP
6837	1	1 2000	PNPPAOGDGTSLSPNYTLESTSGNDGKPVSGGGGRGRGRRKRDS
			GHVSPGTFFDKYSAAPDSGGAPGVSPGQQQASGAAVGGSSAGET
1			RGAPTPHEKALTSPSWGKGAELLLGDQPDLIGSLDGGAKSDSSS
	[	1	PNVGEFASDEVSTSYANEDEVSSSSDNPQALVKASRSPLVTGSP
İ			KLPPRGVGAGEHGPKAPPPALGLGIMSNSTSTPDSYGGGGPGH
i			PGTPGLEQVRTPTSSSGAPPPDEIHPLEILQAQIQLQRQQFSIS
		1	PGTPGLEQVRTPTSSSGAPPPDETHPLETHQAQTQHQKQQTGTS EDQPLGLKGGKKGECAVGASGAQNGDSELGSCCSEAVKSAMSTI
		ì	EDGAPGPKGCKKGECAAGASGAGNGDSFTGSCCGTGAKSGALIQIT
Į			DLDSLMAEHSAAWYMPADKALVDSADDDKTLAPWEKAKPONPNS
1			KEAHDLPANKASASQPGSHLQCLSVHCTDDVGDAKARASVPTWR
1		(	SLHSDISNRFGTFVAALT
C030	16	499	LTDTPPPKTHMIHHSISDYKATLRCWALGFYPMEITLTWQQDEE
6838	1	1	DOTEDMELVETRPAGDGTFOKWAAVVVPSGEE/Q/RYMCHVQHE
			GLPEPLTLRWEQSSQPTIPIVGIVAGLVLLGAVVTGAVVSAVMC
			RKKNSDRVSYSEAASSDHAOGSDVSLTACKV
L		1105	AAPAGGGPDPEALSAFPGRHLSGLSWPQVKRLDALLSEPIPIHG
6839	1	1195	RGNFPTLSVQPRQIRAGGPQHPGGAG\IHVHRVRLHGSAASHVL
1			RGNFPTLSVQPRQTRAGGPQAPGGAG\THYRAVLACLLDFLPAGV HPESGLGYKDLDLVFRMDLRSEASFQLTKAVVLACLLDFLPAGV
}	Į		HPESGLGIKULULYFKINDIKSEASTQUIKAYVLIAGEBUFUTAV
1	1		SRAKITPLTLKEAYVQKLVKVCTDSDRWSLISLSNKSGKNVELK
1		1	FVDSVRRQFEFSIDSFQIILDSLLLFGQCSSTPMSEAFHPTVTG
			ESLYGDFTEALEHLRHRVIATRSPEEIRGGGLLKYCHLLVRGFR
		<b>\</b>	PRPSTDVRALORYMCSRFFIDFPDLVEQRRTLERYLEAHFGGAD
		1	AARRYACLVTLHRVVNESTVCLMNHERRQTLDLIAALALQALAE
			QGPAATAALAWRPPGTDGVVPATVNYYVTPVQPLLAHAYPTWLP
1			CN
		2061	FLOGDESVPDVPKSMAWCENSICVGFKRDYYLIRVDGKGSIKEL
6840	4254	2061	FPTGKQLEPLVAPLADGKVAVGQDDLTVVLNEKGICTQKCALNW
			F. LOWODE DAVI OF DOLLARS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	Bequence		TDIPVAMEHQPPYIIAVLPRYVEIRTFEPRLLVQSIELQRPRFI
			TSGGSNIIYVASNHFVWRLIPVPMATQIQQLLQDKQFELALQLA
1	l	1	EMKDDSDSEKQQQIHHIKNLYAFNLFCQKRFDESMQVFAKLGTD
		· ·	PTHVMGLYPDLLPTDYRKQLQYPNPLPVLSGAELEKAHLALIDY
Į.			LTQKRSQLVKKLNDSDHQSSTSPLMEGTPTIKSKKKLLQIIDTT
}	1		LLKCYLHTNVALVAPLLRLENNHCHIEESEHVLKKAHKYSELII
1	1		LYEKKGLHEKALQVLVDQSKKANSPLKGHERTVQYLQHLGTENL
i			HLIFSYSVWVLRDFPEDGLKIFTEDLPEVESLPRDRVLGFLIEN
1			FKGLAIPYLEHIIHVWEETGSRFHNCLIQLYCEKVQGLMKEYLL
l			SFPAGKTPVPAGEEEGELGEYRQKLLMFLEISSYYDPGRLICDF
1			PFDGLLEERALLIGRMGKHEQALFIYVHILKDTRMAREYCHKHY
1			DRNKDGNKDVYLSLLRMYLSPPSIHCLGPIKLELLEPKANLQAA
1	1		LQVLELHHSKLDTTKALNLLPANTQINDIRIFLEKVLEENAQKK
			RFNQVLKNLLHAEFLRV\QEERILHQQVKCIITEEKVCMVCKKK
ł		_	IGNSAFARYPNGVVVHYFCS\KEVNPADT
6841	1	3206	TPSTTGTKSNTPTSSVPSAAVTPLNESLQPLGDYGVGSKNSKRA
1			REKRDSRNMEVQVTQBMRNVSIGMGSSDEWSDVQDIIDSTPELD
i			MCPETRLDRTGSSPTQGIVNKAFGINTDSLYHELSTAGSEVIGD
		1	VDEGADLLGEFSGMGKEVGNLLLENSQLLETKNALNVVKNDLIA
1		1	KVDQLSGEQEVLRGELEAAKQAKVKLENRIKELEEELKRVKSEA
			IIARREPKEEAEDVSSYLCTESDKIPMAQRRRFTRVEMARVLME
1			RNQYKERLMELQEAVRWTEMIRASREHPSVQEKKKSTIWQFFSR
		1	LFSSSSPPPAKRPYPSGNIHYKSPTTAGFSQRRNHAMCPISAG
1	i		SRPLEFFPDDDCTSSARREQKREQYRQVREHVRNDDGRLQACGW
1			SLPAKYKQLSPNGGQEDTRMKNVPVPVYCRPLVEKDPTMKLWCA
1	1		AGVNLSGWRPNEDDAGNGVKPAPGRDPLTCDREGDGEPKSAHTS
1			PEKKKAKELPEMDATSSRVWILTSTLTTSKVVIIDANQPGTVVD
1			QFTVCNAHVLCISSIPAASDSDYPPGEMFLDSDVNPEDPGADGV
1			LAGITLYGCATRCNVPRSNCSSRGDTPVLDKGQGEVATIANGKV
1	1		NPSQSTEEATEATEVPDPGPSEPETATLRPGPLTEHVFTDPAPT
			PSSGPQPGSENGPEPDSSSTRPEPEPSGDPTGAGSSAAPTMWLG
1	· f		AQNGWLYVHSAVANWKKCLHSIKLKDSVLSLVHVKGRVLVALAD
1	1		GTLAIFHRGEDGQWDLSNYHLMDLGHPHHSIRCMAVVYDRVWCG
1			YKNKVHVIQPKTMQIEKSFDAHPRRESQVRQLAWIGDGVWVSIR
1	1		LDSTLRLYHAHTHQHLQDVDIEPYVSKMLGTGKLGFSFVRITAL
į.			LVAGSRLWVGTGNGVVISIPLTETVVLHRGQ\LLG\LRANKTSP
	1	1	TSGEG\ARPGG\IIHVYG\DDSSDRAARSFIPYCSMAQAQLCFH
	1		GHRDAVKFFVSVPGNVLATLNGSVLDSPAEGPGPAAPASEVEGQ
ļ		İ	KLRNVLVLSGGEGYIDFRIGDGEDDETEEGAGDMSQVKPVLSKA
l			
L			ERSHIIVWQVSYTPE RCQQLSATILTDHQYLERTPLCAILKQKAPQQYRIRAKLRSYKP
6842	3	926	KCOOPSALITING I DEVILOOD DI LECONGALAMENTALON
	1		RRLFQSVKLHCPKCHLLQEVPHEGDLDIIFQDGATKTPDVKLQN
			TSLYDSKIWTTKNQKGRKVAVHFVKNNGILPLSNECLLLIEGGT
	1		LSEICKLSNKFNSVIPVRSGHEDLELLDLSAPFLIQGTVHHYGC
1			KQWST*RSIQNLNSLVDKTSWIPSSVAEALGIVPLQYVFVMTFT
1			LDDGTGVLEAYLMDSDKFFQIPASEVLMDDDLQKSVDMIMDMFC
	1		PPGIKIDAYPWLECFIKSYNVTNGTDNQICYQIFDTTVAEDVI
6843	2	851	NHRKVLSGAKRYECNECGKSFAYTSSLIKHRRIHTGERPYECSE
'''	}		CGRSFAENSSLIKHLRVHTGERPYECVECGKSFRRSSSLLQHQR
1			VHTRERPYECSECGKSFSLRSNLIHHQRVHTGERHECGQCGKSF
1		1	SRKSSLIIHLRVHTGERPYECSDCGKSFAENSSLIKHLRVHTGE
			RPYECIDCGKSFRHSSSFRRHQRVHTGMRPYK*SKFWKFSCPGF
1			LLLQGQRVHTGSRCYECDKWGIFFS*NASFFT*KSAPTEEVPFE
			CNECEKAFSPLSLVTTIFT
C 0 4 4	244	642	EHOLAGFELRKTOTSMSLGTTREKTDRVKSTAYLSPQELEDVFY
6844	4 ** **	1 032	The same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the same and the s
			QYDVKSEIYSFGIVLWEIATGDIPFQGCNSEKIRKLVAVKRQQE

		edicted end	Amino acid segment containing signal peptide
SEQ Predi		cleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID begin		cation	Glutamic Acid, F=Phenylalanine, G=Glycine,
		orresponding	H=Histidine, I=Isoleucine, K=Lysine,
locat		first	L=Leucine, M=Methionine, N=Asparagine,
		nino acid	P=Proline, Q=Glutamine, R=Arginine,
tofi		sidue of	S=Serine, T=Threonine, V=Valine,
			W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		nino acid	Codon, /=possible nucleotide deletion,
		dreuce	\=possible nucleotide insertion)
seque	nce		PLGEDCPSELREIIDECRAHDPSVRPSVDEILKKLSTFSK*CIK
			I I
			VAVRDECYWRHVFWDQDLWMLLFILMCHPETARARLEYRIRTLD
6845	3	1519	GALENAQNLGYQGAKFAWESADSGLEVCPEDIYGVQEVHVNGAV
		1	GLAFELYYHTTQDLQLFREAGGWDVVRAVAEFWCSRVEWSPREE
	ì		KYHLRGVMSPDEYHSGVNNSVYTNVLVQNSLRFAAALAQDLGLP
			I PSQWLAVADKI KVPFDVEQNFHPEFDGYEPGEVVKQADVVLLG
	ļ		YPVPFSLSPDVRRKNLEIYEAVTSPQGPAMTWSMFAVGWMELKD
			AVRARGLLDRSFANMAEPFKVWTENADGSGAVNFLTGMGGFLQA
	`		VVFGCTGFRVTRAGVTFDPVCLSGISRVSVSGIFYQGNKLNFSF
	1		SEDSVTVEVTARAGPWAPHLEAELWPSQSRLSLLPGHKVSFPRS
	1	ļ	AGRIQMSPPKLPGSSSSEFPGRTFSDVRDPLQSPLWVTLGSSSP
	i		TESLTVDPASE*SGTGASETSLGPSLWPRLHPPLLGTLLACHPS
}	ŀ		PAARLSGKVHAAWPEFKAFCL
6846	213	1258	LYFLKTIK*LNRLAEHP*YENEKLTKLRNTIMEQYTRTEESARG
			IIFTKTRQSAYALSQWITENEKFAEVGVKAHHLIGAGHSSEFKP
			MTQNEQKEVISKFRTGKINLLIATTVAEEGLDIKECNIVIRYGL
			VTNEIAMVQARGRARADESTYVLVAHSGSGVIEHETVNDFREKM
1			MYKAIHCVQNMKPEEYAHKILELQMQSIMEKKMKTKRNIAKHYK
			NNPSLITPLCKNCSVLACSGEDIHVIEKMHHVNMTPEFKELYIV
			RENKTLOKKCADYQINGEIICKCGQAWGTMMVHKGLDLPCLKIR
			NFVVVFKNNSTKKQYKKWVELPITFPNLDYSECCLFSDED
6847	1450	348	SMCWNSDRLEMPLIDLALILYPPSYVPYTGHLSDDSLSRKYCLT
0047	1130		WFEDALNGVL*RAEAIQPHCVNAGDRMEKFRQKYWNKLQTLRQQ
	i		PFAYGTLTVRSLLDTREHCLNEFNFPDPYSKVKQRENGVALRCF
			PGVVRSLDALGWEERQLALVKGLLAGNVFDWGAKAVSAVLESDP
	ł		YFGFEEAKRKLOERPWLVDSYSEWLQRLKGPPHKCALIFADNSG
	Ì		IDIILGVFPFVRELLLRGTEVILACNSGPALNDVTHSESLIVAE
1			RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR
1	Į		ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG
1			GRLFSVIFKYEVPAE
6848	19	16	AMWWNSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND
0040			
			LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH
			LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN
			LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK
			LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA
			LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSOAMYDNLALRDGQEGITAFLOKRKPVWSHEPV*VEH
6849	70	821	LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATTAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTFGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLOKRKPVWSHEPV*VEH SLGVDGSCLEOGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC
6849	70	821	LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTEGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLOKRKPVWSHEPV*VEH SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK
6849	70	821	LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTBGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLQKRKPVWSHEPV*VEH SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM
6849	70	821	LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTBGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLQKRKPVWSHEPV*VEH SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM
6849	70	821	LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTEGVALARAVPRKVALEMLFTGEPISAGEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLQKRKPVWSHEPV*VEH SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRILNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ
6849	70	821	LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLQKRKPVWSHEPV*VEH SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRILNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG
			LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVPQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLOKRKPVWSHEPV*VEH SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG
6849	70	821	LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLOKRKPVWSHEPV*VEH SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG ARGLNHEWTFEKLROHISRNAQDKQELHLFMLSGVPDAVFDLTD
			LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATTAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTFGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLOKRKPVWSHEPV*VEH SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL
			LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTEGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLOKRKPVWSHEBV*VEH SLGVDGSCLEGGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG ARGLNHEWTFEKLRQHISRNAQDKGELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI
			LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTEGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLOKRKPVWSHEBPV*VEH SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEILADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG ARGLNHEWTFEKLRQHISRNAQDKGELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAXVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT
			LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTEGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLQKRKPVWSHEPV*VEH SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRILNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG ARGLNHEWFFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KILVINSLKKMMNVAELBLQNCELERIPHAIFSLSNLQELDLKS
			LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVPQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLOKRKPVWSHEPV*VEH SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKLQVTEETAWALQSLGYTCYSRG VKVKGKGGQLCTYFLNTDLTRTGPPSATLG ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKKITCLKLWHNKIVTIPPSITHVKNLESL
			LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLOKRKPVWSHEPV*VEH SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG ARGLNHEWTFEKLRQHTSRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKLVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ
			LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTFGVALLARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLOKRKPVWSHEPV*VEH SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEILADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG ARGLNHEWTFEKLRQHTSRNAQDKGELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVTHNDGT KLLVINSLKKMMNVAELBEQNCELERIPAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKOLFKCIKLRTLNLGQNCITSLPEKVGQLSQ
			LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLOKRKPVWSHEPV*VEH SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLOKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK
6850	2	1235	LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTEGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLOKRKPVWSHEBPV*VEH SLGVDGSCLEGGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVTGAQKPQ YDIWGNTVNVASRMESTOVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG ARGLNHEWTFEKLRQHISRNAQDKGELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI
			LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTEGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLOKRKPVWSHEBPV*VEH SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEILADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG ARGLNHEWTFEKLRQHISRNAQDKGELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAXVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD
6850	2	1235	LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTEGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLOKRKPVWSHEBPV*VEH SLGVDGSCLEGGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVTGAQKPQ YDIWGNTVNVASRMESTOVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG ARGLNHEWTFEKLRQHISRNAQDKGELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI

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			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	I C.
ID	beginning	nucleotide	l clubania hold F=Phenylalanine, Gadijozno,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
)	corresponding	to first	L=Leucine, M=Methionine, N=Methionine
		amino acid	P=Proline, Q=Glutamine, R=Arginine,
	to first	residue of	m.mbroonine V=Valine.
	amino acid		V-Tyrogine, X=Unknown, "-500P
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1			I TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
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1		ļ	TOTAL STATE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
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1			AWASSIHSVSSKSFRDFINBERGHISDLPLLDSPNPWLSSSVTAPSI SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSI
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		1	UNDUTTE STVEETLOOEALIRSREKPLALIQUESITE
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ł	60 1889	1515	mr. OIRRIGETNADDTTV()PMIDQSNRAVSQUEITGT
68			
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68			MGSFVLDGQQHMGTRPAGPMSGMGLTHUDVDGEEOKKOLA
	61 1889	1515	MGSFVLDGQQHMGIRFAGFMSGHGL DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLA DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQ

000	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO;	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	sequence	\=possible nucleotide insertion)
	sequence	<del></del>	MGSFVLDGOOHMGIRPAGPMSGMGMNMGMDGQWHYM
6060	2	471	EEIDREFHNKLKLKEDKLEKQEKPVNGEDKGDSGVDTQNSEGNA
6862		4/1	DEEDPLGPNCYYDKTKSFFDNISCDDNRERRPTWAEERRLNAET
			FGIPLRPNRGRGGYRGRGGLGFRGGRGGGRGGTFTAPRGFRG
	ì		GFRGGRGGREFADFEYRKTTAFGP
		487	POEPALKSEFSQVASNTIPLPLPQPNTCKDNGPCKQVCSTVGGS
6863	2216	467	AICSCFPGYAIMADGVSCEDQDECLMGAHDCSRRQFCVNTLGSF
			YCVNHTVLCADGYILNAHRKCVDINECVTDLHTCSRGEHCVNTL
			GSFHCYKALTCEPGYALKDGECEDVDECAMGTHTCQPGFLCQNT
			KGSFYCQARQRCMDGFLQDPEGNCVDINECTSLSEPCRPGFSCI
			NTVGSYTCQRNPLICARGYHASDDGTKCVDVNECETGVHRCGEG
			QVCHNLPGSYRCDCKAGFQRDAFGRGCIDVNECWASPGRLCQHT
			CENTLGSYRCSCASGFLLAADGKRCEDVNECEAQRCSQECANIY GSYQCYCRQGYQLAEDGHTCTDIDECAQGAGILCTFRCLNVFGS
			GSYQCYCRQGYQLAEDGHTCTDTD&CAQGAGTBCTFRCDNVFGS
			YQCACPEQGYTMTANGRSCKDVDECALGTHNCSEAETCHNIQGS
		}	FRCLRFECPPNYVQVSKTKCERTTCHDFLECQNSPARITHYQLN
			FOTGLLVPAHIFRIGPAPAFTGDTIALNIIKGNEEGYFGTRRLN
			AYTGVVYLQRAVLEPRDFALDVEMKLWRQGSVTTFLAKMHIFFT
			TFAL
6864	2	2933	LADSSPSNLQIIIKELLSMHHQPDPALTKEFDYLPPVDSRSSSG
	1		FVGLRNGGATCYMNAVFQQLYMQPGLPESLLSVDDDTDNPDDSV
	1	<b> </b>	FYQVQSLFGHLMESKLQYYVPENFWKIFKMWNKELYVREQQDAY
		†	EFFTSLIDQMDEYLKKMGRDQIFKNTFQGIYSDQKICKDCPHRY
			EREEAFMALNLGVTSCQSLEISLDQFVRGEVLEGSNAYYCEKCK
			EKRITVKRTCIKSLPSVLVIHLMRFGFDWESGRSIKYDEQIRFE
	1		WMLNMEPYTVSGMARQDSSSEVGENGRSVDQGGGGSPRKKVALT
	1	1	ENYELVGVIVHSGQAHAGHYYSFIKDRRGCGKGKWYKFNDTVIE
			EFDLNDETLEYECFGGEYRPKVYDQTNPYTDVRRRYWNAYMLFY
			QRVSDQNSPVLPKKSRVSVVRQEAEDLSLSAPSSPEISPQSSPF
			PHRPNNDRLSILTKLVKKGEKKGLFVEKMPARIYQMVRDENLKE
			MKNRDVYSSDYFSFVLSLASLNATKLKHPYYPCMAKVSLQLAIC
			FLFQTYLRTKKKLRVDTEEWIATIEALLSKSFDACQWLVEYFIS
	1		SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSI
			HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLI
			LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALI
			VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM
	· I		SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMLH
			FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFBTEN
			GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSH
			WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA
	i	1	YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEI
		1	RSDLDDVDP
6865	1820	1242	DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS
			CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLY
			LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLS
1		1	DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS
		1	PFGQSSVQTIQPKRDS
6866	1571	495	DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIK
	1		IIEGMBEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRK
		Į.	AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLA
]			SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSS
1	(		VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGR
			IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMT
i .	1		GLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKM
			OEIVHKSVVLIPLGAVDDGEHSONEKINRWNYIEGTKLFAAFF)
			QEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFF EMAOLH

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location corresponding	H-Histidine, I=Isoleucine, K=Lysine,
	location	to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	to first	residue of	c_cerine T_Threonine, V=Valine,
	amino acid	amino acid	W-Trophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of		Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence	1704	GTP TMSOPKOKELAGEVROKMLLDYSVYMGRCVPQESRSPQRSP
6867	2833	1704	LOSAESSPTAGKKLPEVPPSEEEEQEAWVNALLGRIFWDFLGEK
			VWSDLVSKKIOMKLSKIKLPYFMNELTLTELDMGVAVPKILQAF
			KPYVDHQGLWIDLEMSYNGSFLMTLETKMNLTKLGKEPLVEALK
	1	l	VGEIGKEGCRPRAFCLADSDEESSSAGSSEEDDAPEPSGGDKQL
			LPGAEGYVGGHRTSKIMRFVDKITKSKYFQKATETEFIKKKIEE
		1	VSNTPLLLTVEVQECRGTLAVNIPPPPTDRVWYGFRKPPHVELK
	ļ		ARPKLGEREVTLVHVTDWIEKKLEQEFQKVFVMPNMDDVYITIM
			HEAMDDRSTSCLLKDPPVEAADOP
		1	RPTRPPTRPEEIKNLILPYISDMNFVQDLCEDFYELFKTDKGFD
6868	1	346	KATFESQMSVMRGQILNLTQALRDGKSPFQLVQIPCVIVERSQG
			GSQGRIVHLSNSFTQTVNCRKPFFSSW
		1610	MYMERMDKRALISFWESVEHLKNANKNEIPQLVGEIYQNFFVES
6869	3	1619	KEISVEKSLYKEIQQCLVGNKGIEVFYKIQEDVYETLKDRYYPS
			FIVSDLYEKLLIKEEEKHASQMISNKDEMGPRDEAGEEAVDDGT
			NQINEQASFAVNKLRELNEKLEYKRQALNSIQNAPKPDKKIVSK
			LKDEIILIEKERTDLQLHMARTDWWCENLGMWKASITSGEVTEE
			NGEQLPCYFVMVSLQEVGGVETKNWTVPKRLSEFHNLHRKLSEC
	}		VPSLKKDQLPSLSKLPFKSIDHTFMEKFENQLNKFLQNLLSDER
			LCQSEALYAPLSPSPDYLKVIDVQGKKNSFSLSSFLERLPRDFF
			SHQEEETEEDSDLSDYGDDVDGRKDALAEPCFMLIGEIFELRGM
	}	ì	FKWVRRTLIALVQVTFGRTINKQIRDTVSWIFSEQMLVYYINIE
	}	1	RDAFWPNGKLAPPTTIRSKEQSQETKQRAQQKLLENIPDMLQSI
			VGQQNARHGIIKIFNALQETRANKHLLYALMELLLIELCPELRV
	}		HLDOLKAGQV
		1566	MAAUVAATRWWOLLLVLSAAGMGASGAPQPPNILLLLMDDMGWC
6870	1	1386	DIGUYGEPSPETPNI,DRMAAEGLLFPNFYSANPLCSPSRAALLI
	i		GDIDIDNGEVTTNAHARNAYTPOEIVGGIPDSEQLLPELLKKAG
			VUSKIVGKWHLGHRPOFHPLKHGFDEWFGSPNCHFGPYDNKARI
			NIDVYRDWEMVGRYYEEFPINLKTGEANLTQIYLQEALDFIKK
			ADHIDEFT, YWAYDATHAPVYASKPFLGTSQRGRYGDAVREIDDS
			TOKILELLODI.HVADNTFVFFTSDNGAALISAPEQGGSNGPFL
			GKOTTFEGGMREPALAWWPGHVTAGQVSHQLGSIMDLFTTSLA
			AGITOPSDRAIDGLNLLPTLLQGRLMDRPIFYYRGDTLMAATL
			OHKAHFWTWTNSWENFROGIDFCPGQNVSGVTTHNLEDHTKLP
			TEHTGROPGERFPLSFASAEYQEALSRITSVVQQHQEALVPAQ
			OLNUCHWAYMNWAPPGCEKLGKCLTPPESIPKKCLWSH
		1126	PMSLNDDIFLKRSEENSSKEVETKOSOTTSIASEDPLQNLCLA
6871	209	1120	OEVLOKAOOSGRSKCLKCGGSRMFYCYTCYVPVENVPIEQIPL
			KI.DI.KIDI IKHPNETDGKSTAIHAKLLAPEFVNIYTYPCIPEY
ı			FKDHEVALIFPGPOSISIKDISFHLQKRIQNNVRGKNDDPDKP
			FKRKRTEEOEFCDLNDSKCKGTTLKKIIFIDSTWNQTNKIFTD
			PLOGLLOVELKTRKTCFWRHQKGKPDTFLSTIEAIYYFLVDYH
ļ			DILKEKYRGOYDNLLFFYSFMYQLIKNAKCSGDKETGKLTH
		459	FGLIMVVLSLIFMKGNCVREDLIFNFLFKLGLDVRETNGLFGN
6872	880	407	KKLITEVFVROKYLEYRRIPYTEPAEYEFLWGPRAFLETSKML
			LRFLAKLHKKDPQSWPFHYLEALAECEWEDTDEDEPDTGDSAH
1		ļ	מעסטססק
		955	DEOAVICSKOKTYDLKIADTSNMLLFIPGCKTPDQLKKEDSHC
6873	1929	755	
			DSNSSKYTTEDLLDQIQASEEEIMTQLQVLNACKIGGYWRILE
	1		DYEMKLLNHVTQLVDSESWSFGKVPLNTCLQELGPLEPEEMIE
1		1	CLKCYGKKYVDBGEVYFELDADKICRAAARMLLQNAVKFNLAE
1	1		QEVWQQSVPEGMVTSLDQLKGLALVDRHSRPEIIFLLKVDDLI
1	1		DNQERFNSLFSLREKWTEEDIAPYIQDLCGEKQTIGALLTKYS
	1	1	I DMODEL DOTE OFFICE TO SEE TO SEE TO SEE
	1	1	SSMONGVKVYNSRRPIS

		······································	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	p=proline, Q=Glutamine, k=Alginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	1 '		\=possible nucleotide insertion)
	sequence	307	DSTADHUNSAAVNVEEGTKNLGKAAKYKLAALPVAGALIGGMVG
6874	1	307	GPIGLLAGFKVAGIAAALGGGVLGFTGGKLIQRKKQKMMEKLTS
		1	SCPDLPSQTDKKCS
			VIGTGERGNSASEKWEIMFNEELGDPFIIIHSISLLNAEEHSIA
6875	1688	349	TLLLRIEKBELDMKGSGFYVSLEWVTISKKNQDNKKYBIIKRDI
		,	TLLLRIEKRELDMKGSGF IVSDEWVII JRKNODNIKTELLIGGE
	1	1	LRGKSVPHYAAIEPDGNGLMIVSYKSLTFVQAGQDLEENMDEDI
			SEKIKEPLYYWQQTEDDLTVTIRLPEDNTKEDIQIQFLPDHINI
	}		VLKDHQFLEGKLYSSIDHESSTWIIKESNSLEISLIKKNEGLTW
		1	PRIVICONOGEI IRDSAOCAAIAERLMHLTSEELNPNPDKEKPP
	1	1	CNAOFI.EECDIFFEESSSLCRFDGNTLKTTHVVNLGSNQYLFSV
		1	IVDPKEMPCFCLRHDVDALLWQPHSSKQDDMWEHIATFNALGYV
		}	QASKRDKKFFACAPNYSYAALCECLRRVFIYRQPAPMSTVLYNR
	1		QASKROKKFFACAPNISIAANCHCHIKKI KEGRQVGQVAKQQVASLETNDPILGFQATNBRLFVLTTKNLFLI
	1	İ	KVNTEN RELIGIOUS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CONCERNOS CO
6876	41	1285	VGEMTLIWRHLLRPLCLVTSAPRILEMHPFLSLGTSRTSVTKLS
0070			LHTKPRMPPCDFMPERYQVIFLVNSGSEANKLAMLMARAHSNNI
		ļ	DIISFRGAYHGCSPYTLGLTNVGIYKMELPGGTGCQPTMCPDVF
			DEDWGGSHCRDSPVOTIRKCSCAPDCCQAKDQYIEQFKDTLSTS
			VAKSIAGPRAEPIOGVNGVVOYPKGFLKEAFELVRARGGVCIAN
	1	1	EVQTGFGRLGSHFWGFQTHDVLPDIVTMAKGIGNGFPMAAVITT
	1	· I	PEIAKSLAKCLQHFNTFGGNPMACAIGSAVLEVIKEENLQENSQ
		1	EVGTYMLLKFAKLRDEFEIVGDVRGKGLMIGIEMVQDKISCRPL
	Ì		PREEVNQIHEDCKHMGLLVGRGSIFSQTFRIAPSMCITKPEVDF
		ì	
}		1	AVEVFRSALTQHMERRAK
6877	1	778	GTSPSPARAYAPPTERKRFYQNVSITQGEGGFEINLDHRKLKTP
60//	1 -		QAKLFTVPSEALAIAVATEWDSQQDTIKYYTMHLTTLCNTSLDN
i			PTOPNKDOLIRAAVKFLDTDTICYRVEEPETLVELQRNEWDP11
			FWAEKPYGVEISSSTSIMGPSIPAKTREVLVSHLASYNTWALQG
			IEFVAAQLKSMVLTLGLIDLRLTVEQAVLLSRLEEEYQIQKWGN
1		1	IEWAHDYELQELRARTAAGTLFIHLCSESTTVKHKLLKE
1			QTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN
6878	931	263	LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAP
		1	LEEDTVTLEVLVAPAVPSCEVPSSALISGIVVEDICOGDICIONILI
ļ		Ĭ	EYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLD
i	1	ì	TGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVIS
l	1		VCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSF
1		İ	TT
L		845	TRYTGESDIMOEFLSESDENYNGVSDVELRVALPDGTTVTVRVK
6879	3	043	KNSTTDOVYOAIAAKVGMDSTTVNYFALFEVISHSFVRKLAPNE
		1	FPHKLYIQNYTSAVPGTCLTIRKWLFTTEEEILLNDNDLAVTYF
			FHQAVDDVKKGYIKAEEKSYQLQKLYEQRKMVMYLNMLRTCEGY
1	1.	1	NEIIFPHCACDSRRKGHVITAISITHFKLHACTEEGQLBNQVIA
		1	NEITFPHCACDSRRKGHVITAISTTHFAIMACTERGERMANHE
i i		1	FEWDEMQRWDTDEEGMAFCFEYARGEKKPRWVKIFTPYFNYMHE
1			CEERVECELKWRKEEY
	2110	1437	RKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISS
6880	2110	1337	MANIVNEKILKEGNOLTESIFIONSKLYFFGILFNGLTLGLQRS
			MDDOIKNCGFFYGHRAFSVALIFVTAFQGLSVAFILKFLDNMFH
			VI MAOVITVI I TTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNAS
1			KPQVPEYAPRQERIRDLSGNLWERSSGDGEELERLTKPKSDESD
1	1		
1			EDTF NDSKWEDIHVITGALKMFFRELPEPLFTFNHFNDFVNAIKQEPR
688	2638	2244	NDSKWEDIHVITGALKMFFKELPEPEFEFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
100.			QRVAAVKDLIRQLPKPNQDTMQILFRHLRRVIENGEKNRMTYQS
			INTURGRELLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR
		850	GIPEAGLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFWLVIN
688	2 1	0.50	OFGNMVTAROEPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT
	1	1	TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSQPYRLVHFEPH
1			
			MRPRRPHQIADLFRPKDQIAYSDTSPFLILSEASLADLNSRLEK

Deginning   coation   coation   coation   coation   corresponding   coation   corresponding   coation   corresponding   corresponding   coation   corresponding   coation   corresponding   coation   corresponding   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No:   location   corresponding   to first   mino acid   residue of   mino acid   residue of   mino acid   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   se				
corresponding to first amino acid amino acid residue of amino acid arion acid sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence	1			
to first amino acid residue of amino acid residue of amino acid sequence    Perfoline, GuGlutamine, Na-Aparagine, amino acid sequence   Sectine, T-Threonine, V-Valine, amino acid sequence   Verifypohan, Y-Yryosine, X-Unknown, *-Stop Codon, /-possible nucleotide deletion, \- possible nucleotide insertion)   Vyossible nucleotide insertion)   Vyossible nucleotide insertion    VYANTNERNIVISGOVYAEDSHOELIGOVELKRYMAGSRCI   LTVVDPTGVWSRREPLETIKLSYRGOPSPEKLIGKSPLIGGYP VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPYTLGO   VENNGTIKVGDPY	NO:			
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amino acid residue of amino acid sequence wityptophan, Y-Yrycosien, X-Wuknown, *-Stop Codon, /-possible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /-yossible nucleotide deletion, /	ł	corresponding	to first	
meino acid sequence  mino acid sequence  mino acid sequence		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
meino acid sequence  mino acid sequence  mino acid sequence		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
amino acid sequence    Codon, /-possible nucleotide deletion,    -possible nucleotide insertion)   EVEATNPERPIVISGODYAEDSWEELIGDVELKRUWAGSEC    LTVOPDTOWNSREPLETIKSYROCPSERKLYGKSPLEGGYP   VLENGTIKVGDPVYLLGG   VLENGTIKVGDPVYLLGG   VLENGTIKVGDPVYLLGG   VLENGTIKVGDPVYLLGG   VLENGTIKVGDPVYLLGG   SIKLKALNGNLKEIFITTYTQVLSLHGMGPGHILGKGGAFPVTONE   ALQLLYDLRYLNIVLTAKODEVESGRSKPDGRIERVTDHLEALI   DPDLDUPTPHANSNLHRLVGRTSVLFGLIVTGHQLAFRSTIF   RNGEPHNIFLLASGIFTGULLEBHTSTKRAASTRNIETKAGTPI   ARC				
Sequence   V=possible nucleotide insertion				
EVAINTEPRIVISCOVYARDSNEDLIJGÖVELKRYMACSRCI   LTYVPDDTOMMSREPLETLIKSYROOPSERKLYKSPIFGÖYY   VLENROTIKYGDPYVILGO    SKIKLNONIKLEFITTYTYGVIJSLIGKGGDTHLOKEGAFPYTONE   ALQLLYDLRYINIVLTAKGDEVKSGRSKPDSRIEKYTDHLEALI   DPPDLDVFTHLISSNIHRIUGRISVLFGLIVTGERGLAFRSSTINS   NSCEPHNIPLLASSINFERLEVITSTRAKSTENIETKAQID   ANC	l		sequence	
LTTVOPDTGMBRREPLETLKSYRQCDPSERKLYGKSPLFGQYF VLENPGTIKKGPPVLLGG   SEROTIKKGPPVLLGG    NSKLKLNQNLKLFTTTYGVJLSLURGRGFHLQKBGAFPVVNG   NSKLKLNQNLKLFTTTYGVJLSLURGRGFHLQKBGAFPVVNG   NSKLKLNQNLKLFTTTYGVJLSLURGRGFHLQKBGAFPVTDHLEALI   DPPDLDVPTHHLSNLHRLVQRTSVLFGLVTGTERQLAPRSSTF   NSGEPHNTLLBHASNLHRLVQRTSVLFGLVTGTERQLAPRSSTF   NSGEPHNTLBHASNLHRLVQRTSVLFGLVTGTERQLAPRSSTF   NSGEPHNTLBHASNLHRLVQRTSVLFGLVTGTERQLAPRSSTF   NSGEPHNTLBLBTYHTTDTTKVCXSKGANASNFGPFGDV   NRC	l	sequence		1 '. *
VLENGTIK/GDPVYLLGQ   SKIKLNONLKIP/TITTYQUS_BIG/KGPGIHLQKEGAFPVYONE   ALQLLYDLRYINTULTAKGDEVKSGRSKPDSTIEKYTDHLEALI   DPPDLDVPTHINSNLHRUGRTSVLFGLIVTGTENQLAFRSTT   NSQEPHNITPLASSQIR FGLIPPISTTSRASSTRAIETKAQTD   NRC				KVKATNFRPNIVISGCDVYAEDSWDELLIGDVELKRVMACSRCI
SERIA   2256   SINGLYDRINGERSPINGERGEPINGERGERINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLYDRINGER   SINGLY	ļ		Į.	LTTVDPDTGVMSRKEPLETLKSYRQCDPSERKLYGKSPLFGQYF
ALQLLYDLRYLANJULTAKODEVESGRSKPDSRIEKTYTHELEALI DPPOLOVPTHILMSNIERLUGHTSVENGLUFTSVENGUTPOLAPSSTF NSQEPHNILPLASSQIRFGLIPLSMTSTRKAKSTRNIETKAQYD ANC  5884 2 99 EFERTTARAVKPRETSEPRAAAQRFCEKFPFL  55085 297 1554 STGQFHHYDLHLDFTYHTTDHTKVCASSKGANASNROPFGDV LCDSPYQLILSAPDFINKSQCBASFMTWTODSPPHYPVPELSTI TVINVITMTTTIQSLFPHLQVFPALONHDYWFQDQLSVYTSKV YNAVANLKEVBLOERATSTLRKGGYTSQKYTHYNRIRIISINTN LYYGPNINTLINKTDRANGFSWLESTLINSCONKEKVYIIAVPV GYLPSSQNITAMBEYYMEKI, DIPFOKYSUVLAGVTHNINGILSINTN LYYGPNINTLINKTDRANGFSWLESTLINSCONKEKVYIIAVPV GYLPSSQNITAMBEYYMEKI, DIPFOKYSUVLAGVTHNINGILSINTN LYYGPNINTLINKTDRANGFSWLESTLINSCONKEKVYIIAVPV GYLDSSQNITAMBEYYMEKI, DIPFOKYSUVLAGVTHNINGILBOYDPB DYKLLDMLGYYIJALTEANLKGSSITMLEKTYNINGILBOYDPB DYKLLDMLGYYIJALTEANLKGSSITMLEKTYNINGILBOYDPB DYKLLDMLGYYIJALTEANLKGSSITMLEKTYNINGILBOYDPB LYGLAKQFTILDSKQFIKYNYFFVSYDSSVTCDRTCKAFQICA IMMLDNISYADCLKQLIYRINY GARYOGSTRELEEGGSSFRELEEGTGSSPACVRGAAPGSEDAFYPTRAK QARVSQELKKAAKRIVSISSGEDTLGDOKREKRETLALLAPPEPB LEKEACERWKRFFRSASATSLTLSSICHOVUKDEKKRGHSIS GGAPEGRYGIIPVCVAARLBYTRAQDVLDAHLSEVNAVRGINSS LLATGGABRILHHANVOKSELEENOTLESGRGSTISSDEDDSGY QVLAATYNQAAQLIKKVGEAQSKETLSGHKOKVTAAKFKLTHRQA VTGSGRFTVEMBLGARVGCSTRINLSYCHOOMITISGHIN DOKIRFWDSKGPHCTOVIPVQGRVTSILSISHDQHBISSGRNT LKVILDLRVSNIRGVPRADGFKCGSDWTKAMFSVLALGSCON LKVILDLRVSNIRGVPRADGFKCGSDWTKAMFSVLALGSCON LKVILDLRVSNIRGVPRADGFKCGSDWTKAMFSVLALGSCON LKVILDL GGQRAAGFTLERGERGGDQSGGGLAAQTPGTSKALAGSCON RVVILMQ  6887 1047 116 WTARFSQRFFREGGRAVPGDPLSTGCSQAQLGGCCPRGFWGPQHG GQCRAAGFTLERGERGGDQSGGGLAAQTPGTSKALAGACH VTSGSPFSTEMBLFYCHTAMFTARATSCALLFRITMENGROQLLTR TYRSGSPFSTEMGPFRGGTGWPEPAVLCLVAVQAMFARLTG TYRSGSPFSTEMGPFRGGTGWPEPAVLCLVAVQAMFARLTG TYRSGSPFSTEMGPFRGTGTGWPEPAVLCLVAVQAMFARLTG TYRSGSPFSTEMGPFRGTGTGWPEPAVLCLVAVQAMFARLTG TYRSGSPFSTEMGPFRGTGTGWPEPAVLCLVAVQAMFARLTG TYRSGSPFSTEMGPFRGTGTGWPEPAVLCLVAVQAPCALLSFBDLT TRANNTUMPEPLDFFTTDTVTHCLANDFRAMINGGGCTLRILL FASNNTUMPEPLDFFTTDTVTHCLANDFRAMTYGGGALHLD LRASSPEDDAFACHTLGFWKAFKFTHILDFTLANDRAGGGTLANDRAGACHLICTSTHAM LDFLENTDTVTHCLANDRAGGGTFRTHATAGRAWTHILDFTTMLH LLSDDIRVALSKLEPEGLITSAVGRNH			1	VLENPGTIKVGDPVYLLGQ
ALQLLYDLRYLANJULTAKODEVESGRSKPDSRIEKTYTHELEALI DPPOLOVPTHILMSNIERLUGHTSVENGLUFTSVENGUTPOLAPSSTF NSQEPHNILPLASSQIRFGLIPLSMTSTRKAKSTRNIETKAQYD ANC  5884 2 99 EFERTTARAVKPRETSEPRAAAQRFCEKFPFL  55085 297 1554 STGQFHHYDLHLDFTYHTTDHTKVCASSKGANASNROPFGDV LCDSPYQLILSAPDFINKSQCBASFMTWTODSPPHYPVPELSTI TVINVITMTTTIQSLFPHLQVFPALONHDYWFQDQLSVYTSKV YNAVANLKEVBLOERATSTLRKGGYTSQKYTHYNRIRIISINTN LYYGPNINTLINKTDRANGFSWLESTLINSCONKEKVYIIAVPV GYLPSSQNITAMBEYYMEKI, DIPFOKYSUVLAGVTHNINGILSINTN LYYGPNINTLINKTDRANGFSWLESTLINSCONKEKVYIIAVPV GYLPSSQNITAMBEYYMEKI, DIPFOKYSUVLAGVTHNINGILSINTN LYYGPNINTLINKTDRANGFSWLESTLINSCONKEKVYIIAVPV GYLDSSQNITAMBEYYMEKI, DIPFOKYSUVLAGVTHNINGILBOYDPB DYKLLDMLGYYIJALTEANLKGSSITMLEKTYNINGILBOYDPB DYKLLDMLGYYIJALTEANLKGSSITMLEKTYNINGILBOYDPB DYKLLDMLGYYIJALTEANLKGSSITMLEKTYNINGILBOYDPB LYGLAKQFTILDSKQFIKYNYFFVSYDSSVTCDRTCKAFQICA IMMLDNISYADCLKQLIYRINY GARYOGSTRELEEGGSSFRELEEGTGSSPACVRGAAPGSEDAFYPTRAK QARVSQELKKAAKRIVSISSGEDTLGDOKREKRETLALLAPPEPB LEKEACERWKRFFRSASATSLTLSSICHOVUKDEKKRGHSIS GGAPEGRYGIIPVCVAARLBYTRAQDVLDAHLSEVNAVRGINSS LLATGGABRILHHANVOKSELEENOTLESGRGSTISSDEDDSGY QVLAATYNQAAQLIKKVGEAQSKETLSGHKOKVTAAKFKLTHRQA VTGSGRFTVEMBLGARVGCSTRINLSYCHOOMITISGHIN DOKIRFWDSKGPHCTOVIPVQGRVTSILSISHDQHBISSGRNT LKVILDLRVSNIRGVPRADGFKCGSDWTKAMFSVLALGSCON LKVILDLRVSNIRGVPRADGFKCGSDWTKAMFSVLALGSCON LKVILDLRVSNIRGVPRADGFKCGSDWTKAMFSVLALGSCON LKVILDL GGQRAAGFTLERGERGGDQSGGGLAAQTPGTSKALAGSCON RVVILMQ  6887 1047 116 WTARFSQRFFREGGRAVPGDPLSTGCSQAQLGGCCPRGFWGPQHG GQCRAAGFTLERGERGGDQSGGGLAAQTPGTSKALAGACH VTSGSPFSTEMBLFYCHTAMFTARATSCALLFRITMENGROQLLTR TYRSGSPFSTEMGPFRGGTGWPEPAVLCLVAVQAMFARLTG TYRSGSPFSTEMGPFRGGTGWPEPAVLCLVAVQAMFARLTG TYRSGSPFSTEMGPFRGTGTGWPEPAVLCLVAVQAMFARLTG TYRSGSPFSTEMGPFRGTGTGWPEPAVLCLVAVQAMFARLTG TYRSGSPFSTEMGPFRGTGTGWPEPAVLCLVAVQAMFARLTG TYRSGSPFSTEMGPFRGTGTGWPEPAVLCLVAVQAPCALLSFBDLT TRANNTUMPEPLDFFTTDTVTHCLANDFRAMINGGGCTLRILL FASNNTUMPEPLDFFTTDTVTHCLANDFRAMTYGGGALHLD LRASSPEDDAFACHTLGFWKAFKFTHILDFTLANDRAGGGTLANDRAGACHLICTSTHAM LDFLENTDTVTHCLANDRAGGGTFRTHATAGRAWTHILDFTTMLH LLSDDIRVALSKLEPEGLITSAVGRNH	6000	2794	2256	NSKLKLNONLKI FITI TVOVI SLHGWGPGIHLOKEGA FPVTONR
DPPDLDVFTPHLMSNLHERLOGTSVLEGUTGTENGLAPRSSTF NSGEPHNILPLASSQIRFGLEPSMTSTRAKSTRIETKAQYD ANC  99 EFERTTARAVKPRETSEPRAAQRFCEKFPFL 6885 297 1554 STGGFRHYTDLHLDFTYHTTDHTTKVCASSKGANASNFGPFGDV LCDSPYGLILSAPDFIKNSGGRASPMINTGDSPHOVVERISTD TVINVITMMTTTGSLFPHIQVPPALGHIDPWPDQDLSVTYSKV YNAVANLKPWLDERAISTLRKGGFYSGKYTTNFNLRIISLNTN LVYGPNINTLIKTTGSLFPHIQVPPALGHIDPWPDQDLSVTYSKV YNAVANLKPWLDERAISTLRKGGFYSGKYTTNFNLRIISLNTN LVYGPNINTLIKTDEANGFEWLESTLINNSGGNKYTNFNLRIISLNTN LVYGPNINTLIKTDEANGFEWLESTLINNSGGNKYTNFNLRIISLNTN LVYGPNINTLIKTDEANGFEWLESTLINNSGGNKYTNFNLRIISLNTN LVYGPNINTLIKTDEANGFEWLESTLINNSGGNKYTNFNLRIISLNTN LVYGPNINTLIKTDEANGFEWLESTLINNSGYFYGDKYTTNFNLRIISLNTN LVYGPNINTLIKTDEANGFEWLESTLINNSGYFYGDKYTTNFNLRIISLNTN LVYGPNINTLIKTDEANGFEWLESTLINLDFYGCHYCHTPTYDIEDLQPBS DYKLLDMIQYYLMLITEANLKGGSIWKLEFILIQTYDIEDLQPBS DYKLLDMIQYYLMLITEANLKGGSIWKLEFYLIQTYDTSDLQPBS DYKLLDMIQYYLMLITEANLKGGSIWKLEFYLIQTYDTSDLQPBS DYKLLDMIQYYLMLITEANLKGGSIWKLEFYLIQTYDTSDLQPBS DYKLLDMIQYYLMLITEANLKGGSIWKLEFYLIQTYDTSDLQPBS DYKLLDMIQYYLMLITEANLKGGSIWKLEFYLIQTYDTSDLQPBS DYKLLDMIQYYLMLITEANLKGGSIWKLEFYLIAGTYDTSDLQPBS DYKLLDMIQYYLMLITEANLKGGSIWKLEFYLIAGTYDTSDLQPBS DYKLLDMIQYYLMLITEANLKGGSIWKLEFYLIAGTYDTSDLQPBS GGRAGGTILFTAGOVLCANLARGHIST LKVIDLRVSNIRGVERAGGSKRELSAMTLEGAGGSITSDVDDBSGY OVLAATYNGAQAUKVGGSAGSKTLSGKKOKYAVARGTSLTSCHANT LKVIDLRVSNIRGVERAGGSKRELSGAMTAVANGTSGSBMT LKVIDLRVSNIRGVERAGGSGRANGTSAVFARFPRSYLLAGSCO GALYI MDVDTGKLESRILQGPHCAAVNAVANCYSGSBMYSVOGGR KVULMG  WTARFSGKFPMEAGAUPDPLSTGCSQAQLGGCCPRGPMGPOHG GQGRAAGFTLERGERGGDQSGPGLAAOTPPTSKQVAMRAFLTG TYRSQSPRSPAGPFRGCTGWWEPAVCLCVAWGPGRILSSBGLYY NASGSHCVDIVELHSCANDFOCOTGPDBARMTOAGTETINLT FARNIVTDMPPDLPFTDELRQRYCLDTWGWPRPDWLLTSFRGG DLARASNITENGNLDBWAGGGITRKDLSASVIATUTTGGAGAHLD LRASHEEDPASVVARKLGATTIGGWYAARRGQPALRGGPRI SL  6888  1 992 FYMYWKRIPHTVVTHCLLNPHALVIKTLPTKLRDALFTVVRVI NFIKGRANNREGGFERGGGDGGFRGFFILLADETHLALDEFKILMS LGASMGRTGMTYSAREKLSAPYRFFPFHQKRIEKNEPHPFI EIILYSDMEGITAABETH LGASMGRTGMTYGASSKKGETHYNILDDIIASKWI LGASHGCDIAHGHT LGASMGRANGAGGSTRAFTYNGAGPSSKGGTHKDDIISL HKABISTUDPRICHTRASKTU LGASMGRANGAGSSK	0003	2754	2230	
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LSASMQRTGMNTVSAREKLSAFVRKFPFWQKRIEKRNFTNFPFL EEIIVSDNEGIFIAAEITLHLQQLSNFFHGYFSIGDLNEASKWI LDPFLFNIDFVDDSYLMKNDLAELRASGQILMEFETMKLEDFWC AQFTAFPNLAKTALEILMPFATTYLCELGFSITFTPQNKVPEAA LILSDDIRVAISKKVPSFLGHH  6889 1 1534 LTLENQIKEEREQDNSESPNGRTSPLVSQNNEQGSTLRDLLTTT AGKLRVGSTDAGIAFAPVYSMGAPSSKSGRTMPNILDDIIASVV ENKIPPSKTSKINVKPELKEEPEESIISAVDENNKLYSDIPHSW ICEKHILWLKDYKNSSNWKLFKECWKQGQPAVVSGVHKKMNISL WKAESISLDFGDHQDLLNCKDSIISNANVKEFWDGFEEVSKRQ KNKSGETVVLKLKDWPSGEDFKTMMPARYBDLLKSLPLPEYCNP EGKFNLASHLPGFFVRPDLGPRLCSAYGVVAAKDHDIGTTNLHI EVSDVVNILVYVGIAKGNGILSKAGILKKFEEEDLDDILRKRLK DSSEIPGALWHIYAGKDVDKIRBFLQKISKBQGLEVLPEHDPIR				IFEMYBEINQFLHHKSSNLVDGFENKEFKIHLAYLADLFKHLNE
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AGKLRVGSTDAGIAFAPVYSMGAPSSKSGRTMPNILDDIIASVV ENKIPPSKTSKINVKPELKEEPEESIISAVDENNKLYSDIPHSW ICEKHILWLKDYKNSSNWKLFKECWKQGQPAVVSGVHKKMNISL WKAESISLDFGDHQADLLNCKDSIISNANVKEFWDGFEEVSKRQ KNKSGETVVLKLKDWPSGEDFKTMMPARYBDLLKSLPLPEYCNP EGKFNLASHLPGFFVRPDLGPRLCSAYGVVAAKDHDIGTTNLHI EVSDVVNILVYVGIAKGNGILSKAGILKKPEEEDLDDILRKRLK DSSEIPGALWHIYAGKDVDKIREFLQKISKBQGLEVLPEHDPIR	1			LILSDDIRVAISKKVPSFLGHH
AGKLRVGSTDAGIAFAPVYSMGAPSSKSGRTMPNILDDIIASVV ENKIPPSKTSKINVKPELKEEPEESIISAVDENNKLYSDIPHSW ICEKHILWLKDYKNSSNWKLFKECWKQGQPAVVSGVHKKMNISL WKAESISLDFGDHQADLLNCKDSIISNANVKEFWDGFEEVSKRQ KNKSGETVVLKLKDWPSGEDFKTMMPARYBDLLKSLPLPEYCNP EGKFNLASHLPGFFVRPDLGPRLCSAYGVVAAKDHDIGTTNLHI EVSDVVNILVYVGIAKGNGILSKAGILKKPEEEDLDDILRKRLK DSSEIPGALWHIYAGKDVDKIREFLQKISKBQGLEVLPEHDPIR	6889	1	1534	LTLENQIKEEREQDNSESPNGRTSPLVSONNEQGSTLRDLLTTT
ENKIPPSKTSKINVKPELKEEPEESIISAVDENNKLYSDIPHSW ICEKHILWLKDYKNSSNWKLFKECWKQGQPAVVSGVHKKMNISL WKAESISLDFGDHQADLLNCKDSIISNANVKEFWDGFEEVSKRQ KNKSGETVVLKLKDWPSGEDFKTMMPARYBDLLKSLPLPEYCNP EGKFNLASHLPGFFVRPDLGPRLCSAYGVVAAKDHDIGTTNLHI EVSDVVNILVYVGIAKGNGILSKAGILKKPEEEDLDDILRKRLK DSSEIPGALWHIYAGKDVDKIRBFLQKISKBQGLEVLPEHDPIR	1	1		
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WKAESISLDFGDHQADLLNCKDSIISNANVKEFWDGFEEVSKRQ KNKSGETVVLKLKDWPSGEDFKTMMPARYBDLLKSLPLPEYCNP EGKFNLASHLPGFFVRPDLGPRLCSAYGVVAAKDHDIGTTNLHI EVSDVVNILVYVGIAKGNGILSKAGILKKPEEEDLDDILRKRLK DSSEIPGALWHIYAGKDVDKIRBFLQKISKBQGLEVLPEHDPIR	1		1	
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EGKFNLASHLPGFFVRPDLGPRLCSAYGVVAAKDHDIGTTNLHI EVSDVVNILVYVGIAKGNGILSKAGILKKPEEEDLDDILRKRLK DSSEIPGALWHIYAGKDVDKIREFLQKISKBQGLEVLPEHDPIR	ì	(		WKAESISLDFGDHQADLLNCKDSIISNANVKEFWDGFEEVSKRQ
EGKFNLASHLPGFFVRPDLGPRLCSAYGVVAAKDHDIGTTNLHI EVSDVVNILVYVGIAKGNGILSKAGILKKPEEEDLDDILRKRLK DSSEIPGALWHIYAGKDVDKIREFLQKISKBQGLEVLPEHDPIR				KNKSGETVVLKLKDWPSGEDFKTMMPARYBDLLKSLPLPEYCNP
EVSDVVNILVYVGIAKGNGILSKAGILKKFEEEDLDDILRKRLK DSSEIPGALWHIYAGKDVDKIREFLQKISKBQGLEVLPEHDPIR				
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PS9#1444KDYZKJUDEF194KT#IDI: POPY14DFAGHUJAA	L	<u> </u>	<u></u>	DOSWYVNKKLRORLLEEYGVRTWTLIQFLGDAIVLPAGALHQVQ

PCT/US00/34263

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
		Bedaciica	\=possible nucleotide insertion)
	sequence		NFHSCIQVTEDFVSPEHLVESFHLTQBLRLLKEEINYDDKLQVK
			NILYHAVKEMVRALKIHEDEVDDMEEN
			THACGMWIPLYLHRALVVHKTAETCNSPPCGAKDSLIFGAITCF
6890	3	667	TGFLGVDTGAGATRWCRLKTQRADPLVCAVGMLGSAIFICLIFV
	l _i		AAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAV
		(	
			ALQSFTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYA
			LMLCPFVVVLGGMFFLATALFFVSDRARAEQQVNQLAMPPASVK
			V
6891	1980	1262	LRIHQELLSKELKLLRGITIESIIHIGLAAGKEQFMQDASNVMQ
<del>-</del>		1	LLLKTQSHLYNMEDNNPEVRQAAAYGLGVMAQFGGDDYRSLCSE
			AVPLLVKVIKRAHSKTKKNVIATENCISAIGKILKFKPNCVNVD
	1	1	EVLPHWLSWLPLHEDKEEAIQTLSFLCDLIESNHPVVIGPNNSN
	1		LPKIISIIAEGKINETINYEDPCAKRLANVVRQVQTSEDLWLEC
			VSQLDDEQQEALQELLNFA
2000	<del> </del>	876	RSVAAASGPGAWGTDHYCLELLRKRDYEGYLCSLLLPAESRSSV
6892	3	0,0	FALRAFNVBLAQVKDSVSEKTIGLMRMQFWKKTVEDIYCDNPPH
		1	OPVAIELWKAVKRHNLTKRWLMKIVDEREKNLDDKAYRNIKELE
			NYAENTOSSLLYLTLEILGIKDLHADHAASHIGKAQGIVTCLRA
			NYAENTQSSEETETETETETATAAAAAAAAAAAAAAAAAAAAAAA
	•		TPYHGSRRKVFLPMDICMLHGVSQEDFLRRNQDKNVRDVIYDIA
			SQAHLHLKHARSFHKTVPVKAFPAFLQTVSLEDFLKKIQRVDFD
		<u> </u>	IFHPSLQQKNTLLPLYLYIQSWRKTY
6893	1	842	DGERKSMSVERTFSEINKAEEQYSLCQELCSELAQDLQKERLKG
	}	i	RTVTIKLKNVNFEVKTRASTVSSVVSTAEEIFAIAKELLKTEID
		1	ADFPHPLRLRLMGVRISSFPNEEDRKHQQRSIIGFLQAGNQALS
			ATECTLEKTDKDKFVKPLEMSHKKSFFDKKRSERKWSHQDTFKC
	1		EAVNKQSFQTSQPFQVLKKKMNENLEISENSDDCQILTCPVCFR
	1		AQGCISLEALNKHVDECLDGPSISENFKMFSCSHVSATKVNKKE
	1		NVPASSLCEKQDYEAH
6894	1742	1463	TTLCKPLVPREHQFYETLPAEMRKFTPQYKGKSQLLEGLPHWRG
0034	1,42		DVRDRGHGRPWQPSLEPSLPPTLCFPSLSSFSSSWPSAQHLTPS
			VENPW
	- 0270	478	VTYVELCDLASPTALLIMRTVLDLIVEDLQSTSEDKEQQYTSQT
6895	2379	* 10	TRLLALLYALASHKACKLAILHLINGTIKGDERYAEIFQDLLAL
(			VRSPGDSVIRQQCVEYVTSILQSLCDQDIALILPSSSEGSISEL
	1		EQLSNSLPNKELMTSICDCLLATLANSESSYNCLLTCVRTMMFL
1		Ì	AEHDYGLFHLKSSLRKNSSALHSLLKRVVSTFSKDTGELASSFL
1		1	EFMRQILNSDTIGCCGDDNGLMEVEGAHTSRTMSINAAELKQLL
1		1	QSKEESPENLFLELEKLVLEHSKDDDNLDSLLDSVVGLKQMLES
1		1	SGDPLPLSDQDVEPVLSAPESLQNLFNNRTAYVLADVMDDQLKS
1			MWFTPFQAEEIDTDLDLVKVDLIELSBKCCSDFDLHSELERSFL
			SEPSSPGRTKTTKGFKLGKHKHETFITSSGKSEYIEPAKRAHVV
ł			PPPRGRGGGGGGGIRPHDIFRQRKQNTSRPPSMHVDDFVAAES
1			KEVVPQDGIPPPKRPLKVSQKISSRGGFSGNRGGRGAFHSQNRF
1			FTPPASKGNYSRREGTRGSSWSAQNTPRGNYNESRGGQSNFNRG
<b>!</b>			PLPPLRPLSSTGYRPSPRDRASRGRGGLGPSWASANSGSGGSRG
1	1		KFVSGGSGRGRHVRSFTR
	<del></del>		GNIVIOKKKYNKOHIIPLENVTIDSIKDEGDLRNGWLIKTPTKS
6896	ı	. 555	FAVYAATATEKSEWMNHINKCVTDLLSKSGKTPSNEHAAVWVPD
			SEATVCMRCQKAKFTPVNRRHHCRKCGFVVCGPCSEKRFLLPSQ
		Ì	
			SSKPVRICDFCYDLLSAGDMATCQPARSDSYSQSLKSPLNDMSD
ł		1	DDDDDDSSD
		1	
6897	3	920	GDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHY
6897	3	920	AGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVL
6897	3	920	AGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVL SLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRTYRGRLA
6897	3	920	AGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVL

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ID Degiming	=Cvsteine, D=Aspartic Acid, E=
location   Glutamic Acid	, F=Phenylalanine, G=Glycine,
Additional Hamistidine.	I=Isoleucine, K=Lysine,
Instruction to first Instruction, Ma	Methionine, N=Asparagine,
be first   mino acid   P=Proline, O=	Glutamine, R=Arginine,
S-Serine T=T	hreonine, V=Valine,
amino acid W=Trvptophan.	Y=Tyrosine, X=Unknown, *=Stop
codon /=poss	ible nucleotide deletion,
\=nossible nu	cleotide insertion)
I.RI.FI.AMEKGRHN	MEYECPYLVYVPVVAFRLEPKDGKGVFAVDGE
TMVSEAVOGOVHE	NYFWMVSGCVEPPPSWKPQQMPPPEEPL
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6898 919 346 QKTVTAVASLIKU	LEMOTDINGGSLKPVRTAAKTTWFIMGILNPA
CGFLISLARYGWI	GCSLGFQSPRKEIQWESLTTSAAEGAHPSPL
MDUFNDASCKVSC	OVGGOTSDEALSMLSEGSDASTIEIHTASESC
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6899 120 827 MKVRKNNDAYLLI	CAYARSILTVPWVELGGKVSVNCAKTGYSASI
LENGELITSDRO	HRVTAEVKHNITNTVVCRVQGEWNSVLEFTYS
THITKPIIGKL	AVTKKRVRPLBKQDPFESRRLWKNVTDSLRES
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HKPLWKIIPTTQ	RSSTSALHHALEESASLLTMFWRAALPSTHIP
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	HDVLKKARTNLEVRKLLHQSEAPSLSPTHHHP
LADLVGDSWPAL	RFUEK
6901 1 201 DDNMVQRLETDF	KMTLQQQSTLEQWAAWLDNVMMQALKPYEGRP
SFPKAARQFLLK	WSFYRYHLGFS
6902 2 267 GAPPPPPSQPPR	QPPQAAPSSHPHSDLTFNPSSALEGQAGAQGA
SDMPEPSLDLLP	ELTNPDELLSYLDPPDLPSNSNDDLLSLFENN
1 0 3 0 3 1	IHILVIDQMVQNFQDESCFLFSTVKAESSDGI
l l l l l HTTLK	TOWARD I LO
6904 464 2092 MEASLPVSLSCV	LACGDVEGKFDILFNRVQAIQKKSGNFDLLLC
VCNFFGSTODAE	WEEYKTGIKKAPIQTYVLGANNQETVKYFQDA
DGCELAENITYL	GRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF
SPKDVSSLRMML	CTTSQFKGVDILLTSPWPKCVGNFGNSSGEVD
TKKCGSALVSSL	ATGLKPRYHFAALEKTYYERLPYRNHIILQEN
AQHATRFIALAN	VGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD
VTENPYRKSGQE	ASIGKQILAPVEESACQFFFDLNEKQGRKRSS
TGRDSKSSPHPK	QPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH
CYLALAKGGLSD	DHVLILPIGHYQSVVELSAEVVEEVEKYKATL
RRFFKSRGKWCV	VFERNYKSHHLQLQVIPVPISCSTTDDIKDAF
ITQAQEQQIELL	EIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR
IKKNFPLQFGRE	VLASEAILNVPDKSDWRQCQISKEDEETLARR
FRKDFEPYDFTI	DD DO
6905 1 226 VSKTGEAETITS	HYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI
VAGLVOTVLYCE	)FFYLYITKVLKGKKLSLPA
6906 3 611 SYDDHNGHIDFI	TAASNLRAKMYSIEPADRFKTKRIAGKIIPAI
ATTTATVSGLVA	LEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET
TEVRKTKIRNGI	[SFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE
PTMVVQGVKMLY	YVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV
SFAPDIDGDEDI	LPGPPVRYYFSHDTD
2228 LPGVPVWAAGAI	FRESSGEESTSHLIMSRRSQRLTRYSQGDDDGS
SSSGGSSVAGSO	OSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS
DAHTSYYSESLY	VHESWFPPRSSLEELHGDANWGEDLRVRRRRGT
GGSESSRASGL ¹	VGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS
SSRIRSAVSRAC	GSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA
SULDVEVLTRRI	FSSLKTFLWFLLPLLLTCLTYGAWYFYPYGLQ
TPUDAT.VQUWA:	AKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL
בססו באו אשני ביי ביי ביי ביי ביי ביי ביי ביי ביי ב	SSNWQKEAMRLERLELRQGAPGQGGGGGLSHED
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i i mistrociuoni	CELEBOTE VIOLET CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRA
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SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	/A-Alanine, C=Cvsteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	LaLeucine, MaMethionine, NaAsparagine,
	to first	amino acid	P=Proline, O=Glutamine, R=Arginine,
	amino acid	residue of	Sacerine TaThreonine, Valline,
	residue of	amino acid	W-Truntonhan, Y-Tyrosine, X-Unknown, *=Stop
	amino acid	sequence	Codon. /=possible nucleotide deletion,
	1	sequence	\=possible nucleotide insertion)
	sequence		APEAAASLSLTLOKEGVIGVTEEOVHHIVKQALQRYSEDRIGLA
			DYALESGGASVISTRCSETYETKTALLSLFGIPLWYHSQSPRVI
			LQPDVHPGNCWAFQGPQGFAVVRLSARIRPTAVTLEHVPKALSP
	1		NSTISSAPKDFAIFGFDEDLQQEGTLLGKFTYDQDGEPIQTFHF
			QAPTMATYQVVELRILTNWGHPEYTCIYRFRVHGEPAH
			QVPSAAWLMAVCGLGSRLGLGSRLGLQGCFGAARLLYPRFQSRG
6908	3	780	POGVEDGDRPQPSSKTPRIPKIYTKTGDKGFSSTFTGERRPKDD
			QVFEAVGTTDELSSAIGFALELVTEKGHTFAEELQKIQCTLQDV
			QVFEAVGTTDELSSAIGFALEDVIEWSHIFAEEDQRIQCIEQUI
			GSALATPCSSAREAHLKYTTFKAGPILELBQWIDKYTSQLPPLT
			AFILPSGGKISSALHFCRAVCRRAERRVVPLVQMGETDANVAKF
		1	LNRLSDYLFTLARYAAMKEGNQEKIYKKNDPSAESEGL
6909	3	409	GRLLAVGTDLYGQRSSAPEQELLVQDATPVSNSLLPEKAFSDIP
0,00			SPYLRGTIKMMQAVRQAFQDQDDRRTWDGRPLTMAATFDDCLYA
	1		LCVVDTIKRSSQTGEWQNIAIMTEEPELSPAYLISEAMRRSRMS
			LYC
6910	1	1068	LVPVVVIDSYYYGKLVIAPLNIVLYNIFTPHGPDLYGTEPWYFY
9310	•		LINGFLNFNVAFALALLVLPLTSLMEYLLQRFHVQNLGHPYWLT
			LAPMYIWEIIFFIOPHKEERFLFPVYPLICLCGAVALSALQHSF
		į	LYPOKCYHFYFORYRLEHYTYTSNWLALGTYFLFGLLSFSRSVA
			LPRGYHGPLDLYPEFYRIATDPTIHTVPEGRPVNVCVGKEWYRF
			PSSFLLPDNWQLQFIPSEFRGQLPKPFAEGPLATRIVPTDMNDQ
			NLEEPSRYIDISKCHYLVDLDTMRETPREPKYSSNKEEWISLAY
	ì		RPFLDASRSSKLLRAFYVPFLSDQYTVYVNYTILKPRKAKQIR
			KSGG GEDAEEMETGNVANLISIFGSSFSGLLRKSPGGGREEEEGEESG
6911	1184	966	PEAAEPGQICCDKPVLRDMNPWSTAIVAF
			AMKPVETHSFOMLFTILSTGSALKAQSYEDAYRCIKSSILLGS
6912	1	844	SGGTDIISCFMGHNFSLPVYKGEIQARNLGMAVEAWNEEGKAV
	•	į	GESGELVCTKPIPCQPTHFWNDENGNKYRKAYFSKFPGIWAHGI
			YCRINPKTGGIVMLGRSDGTLNPNGVRFGSSEIYNIVESFEEV
	ì		YCRINPKIGGIVMLGRSDGTLNPNGVRFGSSEITHIVESTEEV
			DSLCVPQYNKYREERVILFLKMASGHAFQPDLVKRIRDAIRMGI
			SARHVPSLILETKGIPYTLNGKKVEVAVKQIIAGKAVEQGGAF
	İ		NPBTLDLYRDIPELQGF
6913	1643	. 1558	KKSHEESHKEELSYGAQASLPLPCSDFR
6914	1251	615	ELAAECKSAGYPGTLIPYRCDLSNEEDILSMFSAIRSQHSGVD
6314	1231	1	CINNAGIARPDTILSGSTSGWKDMFNVNVLALSICTREAYQSM
	Ì	<b>\</b>	ERNVDDGHIININSMSGHRVLPLSVTHFYSATKYAVTALTEGL
			QELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQM
		{	CLEDEDUAEAVIYVISTPAHIOIGDIOMRPTEQVT
			CRELERYTHI, TWVI, TSTYOGGILMYGALVLFESEFVHVVAISF
6915	254	652	ALILTELLMVALTVRTWHWLMVVABFLSLGCYVSSLAFLNEYF
		ì	VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLA
			GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISF
6916	254	652	GRSLSFKTFLIWVLISITUGGIEMIGALVDFESEFVRVVAISF
			ALILTELLMVALTVRTWHWLMVVABFLSLGCYVSSLAFLNEYF
1			VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLA
6917	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISF
1 372.	1		ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYF
1			VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLA
	30	921	PEAGTRSWREPDPEDLRRFLLSAACRSFPQWLPGGGGGQVSSC
6918	28	321	DTDVPYLLLAVKSEPGRFAERQAVRETWGSPAPGIRLLFLLGS
			VGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLA
1		1	LGRHCPTVSFVLRAQDDAFVHTPALLAHLRALPPASARSLYLG
1			VFTQAMPLRKPGGPFYVPESFFEGGYPAYASGGGYVIAGRLAF
1	1		LLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPADF
		1	PPKWWWKAWLLLEDAIIGECTKWTQTALAWTTOT DIVERTIN
		l l	ADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC

WO 01/53312	Amino acid segment containing signal peptide  Amino acid segment containing signal peptide  D=Aspartic Acid, E=  Amino acid segment containing signal peptide  Amino acid segment containing signal peptide  Amino acid segment containing signal peptide  Amino acid segment containing signal peptide  Amino acid segment containing signal peptide  Amino acid segment containing signal peptide  Amino acid segment containing signal peptide
	Amino acid segment containing signal peptitos  Amino acid segment containing signal peptitos  (A=Alanine, C=Cysteine, D=Aspartic Acid, E=  (A=Alanine, C=Cysteine, D=Aspartic Acid, F=Phenylalanine, G=Glycine,  Amanic Acid, F=Phenylalanine, K=Lysine,  Amanic Acid, F=Phenylalanine, K=Lysine,  Amanic Acid, F=Phenylalanine, K=Lysine,
7.77	Amino acid segment containing Variatic Acid, Landon Amino acid segment containing Variatic Acid, Landon Amino Acid, Fephenylalanine, GeGlycine, Glutamic Acid, Fephenylalanine, Kelysine, Glutamic Acid, Fephenylalanine, Ne
Dredicted	Aria acide
nucleot nucleotis	H=Histidine, M=Methionine, N=Arginine,
ID   correspond	
NO: location to first	Perion, Tethies magine, Assetion,
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acia   amino	Code ible nuclear processing the same was a same with the same of the same was a same with the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of
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ACFSASE*  ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* ACFSASE* AC
QRWYSTI ACRMITAFTPFLINGROUND DIEDTLYQMEKLADLEELED ACRMITAFTPFLINGROUND DIEDTLYQMEKLADLEELED ACRMITAFTPFLINGROUND DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES DE PROPERTIES D
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SUNLHCTLPFFFT.  SUNLHCTLPFFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SUNLHCTLPFTT.  SU
SDDDCFS.MVEGPNFLKKLEQSFMCVCC
DCLDRSTON SKGR SKGR SKGR DRDHSQCGGIRRVALARVSSVKLISKAKIRTVKMTFIIVLMIIV DRDHSQCGGIRRVALARVSSVKLISKAKIRTVKMTFIIVLMIIV DRDHSQCGGIRRVALARVSSVKLISKAKIRTVKMTFIIVLMIIV DRDHSQCGGIRRVALARVSSVKLISKAKIRTVKMTFIIVLMIIV CWTPFFFVQMMSVWDANAPKRASAFIIVMLIASLNSCCNPWLIS CWTPFFFVQMMSVWDANAPKRASAFIIVMLIASLNSCSVFVLS LFTGLIFFELVQRFLCCSASYLKGRRLGETSASKKSNSSSFVLS LFTGLIFFELVQRFLCCSASYLKGRRLGETSASKKSNSSSFVLS LFTGLIFFELVQRFLCCSASYLKGRRLGETSASKKSNSSSFVLS
CWTPFFT CUTTIVORPLCCSASYBROAD
6934 3030 LFTGHLFHELVORFILECON- HRSSSQRSCSQPSTA
HRSSSUR
-70
572

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	S=Serine, T=Threonine, v=vailne,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
6935	886	543	NSALYVAGGNDGTSCLNSVERYSPKAGAWESVAPMNIRRSTHDL
6935	000		VAMDGWLYAVGGNDGSSSLNSIEKYNPRTNKWVAASCMFTRRSS
			VCVAVLELINEPPPSSPTLSVSSTSL
		567	RSHRRQFLSRALLEFFGKSHPPPHRLFRKSLNVGLHYSHIPFLT
6936	1347	367	TCLHFLRKRLQKGEVGLSVETSKPQVPVGGLSRKKVPQEPWATV
			MEKRLQEAQLYKEEGNQRYREGKYRDAVSRYHRALLQLRGLDPS
	1		MEKKLQEAQLYKEEGNQKIKEGKIKDAVSKIIIG MEQHACOS
	1		LPSPLPNLGPQGPALTPEQENILHTTQTDCYNNLAACLLQMEPV
		1	NYERVREYSQKVLERQPDNAKALYRAGVAFFHLQDYDQARHYLL
			AAVNRQPKDANVRRYLQLTQSELSSYHRKEKQLYLGMFG
6027	+	727	AVEFRCCPGRDPACFARGWRLDRVYGTCFCDQACRFTGDCCFDY
6937	1	1 '-'	DRACPARPCEVGEWSPWSGCADQCKPTTRVRRRSVQQEPQNGGA
			DCDDLEERAGCLEYSTPOGODCGHTYVPAFITTSAFNKERTRQA
			TSPHWSTHTEDAGYCMEFKTESLTPHCALENRPLTRWMQYLREG
	1	1	YTVCVDCQPPAMNSVSLRCSGDGLDSDGNQTLHWQAIGNPRCQG
			TWKKVRRVDQCSCPAVHSFIFI
		J	TWKKVRKVDQCSCPAVASFIFI  NSRKLELAERVDTDFMQLKKRRQSSEKENDSGTLDTVGAVVVDH
6938	3	719	NSRKLELAERVDTDFMQLKARRQSSERENDSGT LIDT VOAV VER
			EGNVAAAVSSGGLALKHPGRVGQAALYGCGCWAENTGAHNPYST
			AVSTSGCGEHLVRTILARECSHALQAEDAHQALLETMQNKFISS
			PFLASEDGVLGGVIVLRSCRCSAEPDSSQNKQTLLVEFLWSHTT
		ţ	ESMCVGYMSAQDGKAKTHISRLPPGAVAGQSVAIEGGVCRLGEP
			SELTLQAECEASQRHFRT
	J	810	KVTAPRRPORYSSGHGSDNSSVLSGELPPAMGRTALFHHSGGSS
6939	3	1 010	CVESTERDSEATGSASSAPDSMSESGAASPGARTRSLKSPKKRA
	ļ		TGLQRRRLI PAPLPDTTALGRKPSLPGQWVDLPPPLAGSLKEPF
		l l	EIKVYEIDDVERLQRPRPTPREAPTQGLACVSTRLRLAERRQQR
	l	l l	LREVQAKHKHLCEELAETQGRLMLEPGRWLEQFEVDPELEPESA
		1	EYLAALERATAALEQCVNLCKAHVMMVTCFDISVAASAAIPGPQ
	Ì		
	<b>\</b>	1	BVDV
6940	1188	496	GKMAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQ
0,710			VVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAV
		i	LADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFLVGIEGSLKGS
	Ì	}	TYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLI
		ì	KTKAIVNASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILS
	Į.		RVTPDOSKPEN
		200	SLSRADSDPHGPHTCGHVLNVIIGSNVLALAEAQRQAEALGYQA
6941	1	713	VVLSAAMQGDVKSMAQFYGLLAHVARTRLTPSMAGASVEEDAQI
		]	VVLSAAMQGDVKSMAQFIGHLARVAKIKUIFSVAAASVAAASVAASVAASVAASVAASVAASVAASVAAS
			RGGRNQELALRVGAELRRWPLGPIDVLFLSGGTDGQDGPTEAAC
		Ì	RGGRNQELALRYGAELKKWYLGYIDVDFLSGGIDGQUGYIEAFA
	1	1	AWYTPELASQAAAEGLDIATFLAHNDSHTFFCCLQGGAHLLHT
	[		MTGTNVMDTHLLFLRPR
6942	1	246	GDYVERYDPKTDTWTMGAPLSMPTNAVGGCLLGDRLYADGGYD
0942	·   •	1	OTVINTMESYDPOTNEWTOMASLNIGRAGACVVVIKQP
		739	DMATGDGAKTLAIHVKALTADSIRITWKATLPASSFRLSWLRLG
6943	. 1	137	HSPAGGSITETLVQGDKTEYLLTALEPKPTYIICMVTMETTNA
			VADETPVCAKAETADSYGPTTTLNQEQNAGPMASLPLAGIIGG.
			VALVFLFLVLGAICWYVHQAGELLTRERAYNRGSRKKDDYMES
			TKKDNSILBIRGPGLQMLPINPYRAKEEYVVHTIFPSNGSSLC
			TKKDNSILKIKGPGLQMLPINPIKAKEEIVVATIFFBAGSSIC
			ATHTIGYGTTRGYRDGGIPDIDYSYT
6944	960	156	VANILLNGVKYESELTGSSERAEQPLSVGRLCSTICNMPKALR
0 244		1	LCVNHFLGWLSFEGMLLFYTDFMGEVVFQGDPKAPHTSEAYQK
1		1	NSGYTMGCWGMCIYAFSAAFYSAILEKLEEFLSVRTLYFIAYL
		1	FCLCTGLATLSRNLYVVLSLCITYGILFSTLCTLPYSLLCDYY
		1	SKKFAGSSADGTRRGMGVDISLLSCQYFLAQILVSLVLGPLTS
	1		VGSANGVMYFSSLVSFLGCLYSSLFVIYEIPPSDAADEEHRPL
			INV

WO 01/53312

				Amino acid segment containing signal peptide
SEO	Pred	icted	Predicted end	Amino acid segment containing signific Acid, E= (A=Alanine, C=Cysteine, D=Aspartic Acid, E= (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	begi	nning	nucleotide	
NO:	nucl	eotide	location	
NO:	1000	tion	corresponding	M=Methionine, N=Asparage
1	corr	esponding	to first	I n need the Original net residing to
1	1 2011	irst	amino acid	
	1 60 1	no acid	residue of	I V-Throathe XSULKhowit
	amı	idue of	amino acid	Codon, /=possible nucleotide deletion,
	res	ique or	sequence	\=possible nucleotide insertion)
	amı	no acid	201	
	seq	uence	179	EGEDRGLPRTMGAALGIGIALAWPERGARTLEERLOLGIHGL HSKPGPARPVPLKKRGYDVTRPNDLNKKGMAFTLEERLOLGIHGL
6945	7	2067		HSKPGPARPVPLKKRGTDVTRAPHLAKONAT IPPCFLSQDVQLLRIMRYYERQOSDLDKYIILMTLQDRNEKLFY IPPCFLSQDVQLLRIMRYYERQOSDLDKYIILFRRPRGLFITIHDKG
	1		\	IPPCFLSQDVQLLRIMRITERQQSDLDAR TERRPRGLFITIHDKG
	1			RVLTSDVEKFMPIV YTYTVGDACUITGDD GCYGMGIPVGKLA
	1			HLATMLNSWPEDNIKAVVVTDGERINGBODDI.YIGLKHORVHGK
	1			HLATMLNSWPEDNIKAVVVTDERTIGEBELLRDPLYIGLKHQRVHGK LYTACGGVNPQQCLPVLLDVGTNNEELLRDPLYIGLKHQRVHGK
	1		- {	AYDDLLDEFMQAVTDKFGINCUIQFEDITION CATHVFGFOGAGEAAM
	- }		1	AYDDLLDEFMQAVTDKFGINCHTGFEGKLSNHVFGFQGAGEAAM CMFNDDIQGTASVAVAGILAALRITKNKLSNHVFGFQGAGEAAM G\IAHLLVMALE\KEGVPKA\EATRKIW\MVDF\KGLIVQGRDH G\IAHLLVMALE\KEGVPKA\EATRKIW\MVDF\KGLIVQGRDH
	l l			G IAHLLVMALE KEGVPKA EATRK IN WORLD THEAL FTE
	1			G\IAHLLVMALE\KEGYPKA\EEVIRLVKPTAIIGVAAIAEA\FTE LNHEKEMFAQD\HPEVNSLEEVIRLVKPTAIIGVAAIAEA\FTE
	1			LNHEKEMFAQD\HPEVNSLEEVVRLVAECTA\EKCYRVTEGPRGF QILRDMASFHERP\IIFALSNPTSKAECTA\EKCYRVTEGPRGF QILRDMASFHERP\IIFALSNPTSKGEGNNA*RVPRGWQLGVHSPG
	1		1	QILRDMASFHERP\TIFALSNPTSKA_BUAA\TVPRGWQLGVHSPG FAS\GSPF*GVLIWEMGKTFIPGGRGNNA*RVPRGWQLGVHSPG FAS\GSPF*GVLIWEMGKTFIPGGRGNLYP\PLST\IR
	1			FAS\GSPF+GVLIWEMGKTFIPGGRSANH XV GDPGHIP\DEIFLPDSRAKLPQEVSEQHLSQGRLYP\PLST\IR GDPGHIP\DEIFLPDSRAKLPQEVSEQHLYQGRLYP\PLST\IR
	-		1	ATTER DIATKUFD*GIRANDV \SIIPB"
	- 1			YDSFYT/VDSYIWAQGKAMNVQTV
	ı			YDSFYT/VDSYIWAXGRAMNVQIV SCEYSGITVAPGDPCPGVAHLAPSMASDTPESLMALCTDFCLR SCEYSGITVAPGDPCPGVAHLAPSMASDTPESLMALCTDFCLR
6946		133	2551	SCEYSGITVAPGDPCPGVAHLAPSMASDIT  SCEYSGITVAPGDPCPGVAHLAPSMASDIT  CDRLVNEYVELVNAAC  NLDGTLGYLLDKETLRLHPDIFLPSBITU.RED\LVQD\QD\LE
6946	<b>'</b>			NLDGTLGYLLDKETLRLHPDIFERSBI (CDM) LVQD\QD\LE NF\EPHE\SFFNPLFRDPKQPASRRIHL\RED\LVQD\QD\LE NF\EPHE\SFFNPLFRDPKQPASRRIHL\RED\LVQD*AFFG
l	- 1			NF\EPHE\SFFNPLFRDPRKQPASKITH\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
1	- 1		1	AIRKQDL\VEL\VLTN\CEKESARSDTIQVLVKDFTFEGFSRLR C\TNILLLRKENPGGL\CEBEYLFNFTCQVLVKDFTFEGFSRLR
1	1		1	C\TNILLLRKENPGGL/CEDEYLFRY LCVB F\LKLGRMIDWVPVES\LLRPLNSLAALDLSGIQTSDAA\FLTQ F\LKLGRMIDWVPVES\LLRPLNSLAALDLSGIQTSDAA\FLTQ
1	- 1			F\LKLGRMIDWVPVES\LLKPLNSIARIDLESCHELSS WKDSL\VSLVL\YNMDLSDDHIR\VIVQLHKLRHLDISRDRLSS WKDSL\VSLVL\YNMDLSDDHIR\VIVQLHKLRHLDISRDRLSS
1	- 1		<b>!</b>	WKDSL\VSLVL\YMMDLSDBHIK\VI\VQLIMBLENCSISKIGKR YYKFKLTREVLSLFVQKLGNLMSLDISG\HMILENCSISKIGKR
1	1			YYKFKLTREVLSLFVQKIGNLMSLDISG(NMLDS) EAGQTSI\EPSK\SSIIPFRGFEGGPLQF\LGVF*GIFCGRLTH
1	1			EAGQTSI\EPSK\SSIIPFRGFEGGPDUT\LSTRIP. IPAYKVSGDKNEEQVLNAIEAYTEHRPEITSRAINLLIFDIARIE IPAYKVSGDKNEEQVLNAIEAYTEHRPEITSRAINLLIFDIARIE
1			(	IPAYKVSGDKNEEQVLNALEAYIBARTTSAALFYLTNSEYRSE RCNQLLRALKLVITALKCHXYDRNIQVTGSAALFYLTNSEYRSE RCNQLLRALKLVITALKCHXYDRNIQVTLORNCCLTLCNFSIPEELEF
1	- 1			RCNQLLRALKLVITALKCHKYDRNIQVIOSITECHTSIPEELEF QSVKLRRQVIQVVLNGMESYQEVTVQRNCCLTLCNFSIPEELEF QSVKLRRQVIQVVLNGMESYQEVTLCNALVCQVDNDHKEA
1	- 1			QSVKLRRQVIQVVLNGMESQESIQRIAVHLCNALVCQVDNDHKEA QYRRVNELLLSILNPTRQDESIQRIAVHLCNALVCQVDNDHKEA
1	1			QYRRVNELLLSILNPTRQDESIQXIAVNECHESW\SALWNITDETPD VGKMGFVVTMLKLTQKKLDKTCDQVMEFSW\SALWNITDETPD VGKMGFVVTMLKLTQKKLDKTCDQVMEFSW\SALWNITDETPD
1	- 1		)	VGKMGFVVTMLKLTQKKLLDKTLTQVHIFTOK NCEMFLNFNGMKLFLDCLNEFPEKQELHRNMLGLLGNVAEVKEL NCEMFLNFNGMKLFLDCLNEFPEKQELHRNMLGLLGNVAEVKEL
1	- 1		ł	NCEMFLNFNGMKLFLDCLNEFFERQUEVSYNACGVLSHIMFDGFEA RPQLMTSQFISVFSNLLESKADGIEVSYNACGVLSHIMFDGFEA
1	- 1			RPQLMTSQFISVFSNLLES KADGINSRNINYRSFEPILRLLPQ WGVCEPQREBYEERMWAAIQSWDINSRNINYRSFEPILRLLPQ
1	- 1			WGVCEPQREKVEERMWAAIQSWDINSKRATHING GISPVSQHWATWALYNLVSVYPDKYCPLLIKEGGMPLLRDIIKM
1	1			GISPVSQHWATWALINDVSVII
- 1	- 1		}	GISPVSQHMATMALITIEHCSNFKEENMDTSR ATARQETKEMARKVIEHCSNFKEENMDTSR TSVSTIPRGLASARPQSRSWRCCPVWRRSPGRARGRGLKMLNVP TSVSTIPRGLASARPQSRSWRCCPVWRRSPGRARGRGLKMLNVP
1	- 1		1682	TSVSTIPRGLASARPOSKSWKCEPVAKARPO SQSFPAPRSQQRVASGGRSKVPLKQGRSLMDWIRLTKSGKDLTG SQSFPAPRSQQRVASGGRSKVPLKZIEGFVYNVSPYMEYHPGGE
69	147	2	100-	SQSFPAPRSQQRVASGGRSKVFIRGSRVANVSPYMEYHPGGE
1				LKGRLIEVTEEELKKHNKRDDCHTCIMLKEGLVGRMAIKPAVLK
				DELMRAAGSDGTELFDQVARWVNIESHDESYDWFOTDSLVTI
}				DYREEEKKVLNGMLPKSQVTDTLAKEGFSTTSTLLSYTYW/R*A
- 1				DYREEEKKVINGMLPKSQVTDILAKGSTOTHY*GLLISYTYW/R*A /EHIY*TEGYQFRLNNS*SSE*FLYSRNY*GLLISYTYW/R*A /EHIY*TEGYQFRLNNS*SSE*FLYSRNY*GLLISYTYW/R*A
Ì			<b> </b>	/EHIY*TEGYQFRLNNS*SSE*FIJSKNIV MRFRKIFLCGL/CESVGKIEIVLQKKENTSWDPLGHPLKNHNSL
1		1	1	MRFRKIFLCGL/CESVGKIEIVTHDTRLFCLMLPPSTHLQVPIGQ IPRKDTGLYYRKCQLISKEDVTHDTRLFCLMLPPSTHLQVPIGQ IPRKDTGLYYRKCQLISKEDVTHDTRLFCLMLPPSTHLQVPIGQ
\				IPRKDTGLYYRKCQLISKEDVTHUIKELDHILL HVYLKLPITGTEIVKPYTPVSGSLLSEFKEPVLPNNKYIYFLIK
- {		}	\	HVYLKLPITGTEIVKPYTPVSGSLLSEFACE IYPTGLFTPELDRLQIGDFVSVSSPEGNFKISKFQELEDLFLLA
- 1				IYPTGLFTPELDRLQIGDFVSVSSFAGR TVETEDIIWRSQLE AGTGFTPMVKILNYALTDIPSLRKVKLMFFNKTEDDIIWRSQLE AGTGFTPMVKILNYALTDIFFNGKYGHISPALLSEFLKRNLDK
Į		1		
}				KLAPKDKRLDVEFVLSAFIDENFSKNEIHSFTA SKVLVCICGPVPFTEQGVRLHDLNFSKNEIHSFTA
1				SKVLVCICGPVPFTEDGVRULHDINGSKYSMYHGKEGVPHEAKSF PDGAHSFFPDEYFTCSSLCLSCGVGCKKSMYHGKEGVPHEAKSF
L		104	58	PDGAHSFFPDEYFTCSSLCLSCGVG KASHMAN CRYSHQYDNRVYTCKACYBRGEEVSVVPKTSASTDSPWMGLAKY
	6948	1 104		CRYSHQYDNRVYTCKACYBRGBEVSVVVKTEIVHVWPG AWSGYVIECPNCGVYYRSRQYWFGNQDPVDTVVRTEIVHVWPG AWSGYVIECPNCGVYYRSRQYWFGNQDPVDTVVRTEIVHVWPG
1		1	1	AWSGYVIECPNCGVVYRSQIWFGNOF: DGFLKDNNNAAQRLLDGMNFMAQSVSBLSLGPTKAVTSWLTDQ: DGFLKDNNNAAQRLLDGMNFMAQSVSBLSLGPTKAVTSWLTDQ:
]		1	1	DGFLKDNNNAAQRLLDGMNFNAQSVBBBBBB APAYWRPNSQILSCNKCATSFKDNDTKHHCRACGBGFCDSCSSI APAYWRPNSQILSCNKCATSFKDNDTKHHCRACGBGFCDSCSSI
1		1		APAYWRPNSQILSCNKCATS FALMDIAMECT TRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGTSGR*RRETTRPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYRGT*RTPVSCYR
1		1	}	TRPVPERGWGPAPVRVCDMCIEARC
		1		QETVB CONCOURSE TRANSPORTER CONCOURSE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE P
1		_	465	QETVE  6 GLRLCLSRPLTRPGDDSVGGSAMASGAGGVGGGGGGKIRTRRCI QGPIKPYQQGRQQHQGILSRVTESVKNIVPGWLQRYFNKNEDV
1				
-	6949	152	403	OGPIKPYQQGRQQHQGTLSKVILGVI

		Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	H=H1stidine, I=1soleucine, k=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		- "	Codon, /=possible nucleotide deletion,
	amino acid	sedneuce	\=possible nucleotide insertion)
	sequence	l	/=possible nucleotide insertion/
		T	SCSTDTSEVPRWPENKEDHLVYADEESSNITDGRITPEPAVSNT
	ł	ĺ	EEPSTTSTAST\YPDVLTRVSLYRSHLNFSMLESPALHCQPSTS
	ł		SAFPIGSSGFSLVKBIKDSTSQHDDDNISTTSGFSSRASDKDIT
	<b>\</b>	1	VSKNTSLPPLWSPEAERSHSLSQHTATSSKKPAFNLSAFGTLSP
	Į.	1	SLGNSSILKTSQLGDSPFYPGKTTYGGAAAAVRQSKLRNTPYQA
	1	1	PVRRQMKAKQLSAQSYGVTSSTARRILQSLEKMSSPLADAKRIP
	1	1	PVRKQMKAKQLSAQS1GV1351AKK111QS1BKM3511AAMK11
		1	SIVSSPLNSPLDRSGIDITDFQAKREKVDSQYPPVQRLMTPKPV
	1	1	SIATNRSVYFKPSLTPSGEFRKTNQRIDKKCSTGYEKNMTPGQN
	1	ì	REQRESGFSYPNFSLPAANGLSSGVGGGGGKMRRERHAFVASKP
			LEEEEMEGPVLPKISLPITSSSLPTFNFSSPEITTSSPSPINSS
			QALTNKVQMTSPSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTF
			SVPVAKTAELSGSSSTLEPIISSSAHHVTTVNSTNCKKTPPEDC
			PARAWLARDOGGGTTDERITGGGGGTTDGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
			EGPFRPAEILKEGSVLDILKSPGFASPKIDSVAAQPTATSPVVY
			TRPAISSFSSSGIGFGESLKAGSSWQCDTCLLQNKVTDNKCIAC
		}	QAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVIGT
	1	Į	WDCDTCLVQNKPEAIKCVACETPKPGTCVKRALTLTVVSESAET
	}		MTASSSSCTVTTGTLGFGDKFKRPIGSWECSVCCVSNNAEDNKC
	1		VSCMSEKPGSSVPTSSSSTVPVSLPSGGSLGLEKFKKPEGIWDC
	ì	i	ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASS
	i	1	ELCLYUNADSTREMEESARPSTRESPRENT TOUGED COUNTY
		1	SFKFGVSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGYINP
			MSEGF*FSKHIVGFKFGVSSESKPEEVKKDSKNDNFKFGLSFGL
			SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR
	1	ł	VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA
		1	TKGGFSFGNVEPASLPSASVFVLGRTEEKQQEPVTSTSLVFGEG
		1	KLTMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE
		l l	SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS
		Į.	SECPARATEARGAQINI IADQGAAREDDSTIMASSOOSSIII
	}	1	AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST
		ļ	SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG
	<b>\</b>	į	ATTTSSSAGSSFVFGTGPSAPSASPAFGANQTPTFGQSQGASQP
	Į.		NPPGFGSISSSTALFPTGSQPAPPTFGTVSSSSQPPVFGQQPSQ
	1	<b>\</b>	SAFGSGTTPNSSSAFQFGSSTTNFNFTNNSPSGVFTFGANSSTP
	1	1	AASAQPSGSGGFPFNQSPAAFTVGSNGKNVFSSSGTSFSGRKIK
ĺ		1	
1		_	TAVRRK
6950	2585	411	PRPGSRSGLCRRAGERGAVRAGGLSRRTRAE * IMDELHYQDTDS
1			DVPEQRDSKCKVKWTHEEDEQLRALVRQFGQQDWKFLASHFPNR
1			TDOOCOYRWLRVLNPDLVKGPWTKEEDQKVIELVKKYGTKQWTL
1	İ		IAKHLKGRIGKQCRERWHNHLNPEVKKSCWTEEEDRIICEAHKV
1	ì		LGNRWAEIAKMLPGRTDNAVKNHWNSTIKRKVDTGGFLSESKDC
1	ì	l	KPPVYLLLELEDKDGLQSAQPTEGQGSLLTNWPSVPPTIKEEEN
i	1	i	KPPVILLEDEDEDADGEDGSAQFIEGGGSBETHILDVILLETTE
1	1 .	1	SEEELAAATTSKEQEPIGTDLDAVRTPBPLEEFPKREDQEGSPP
1	1	1	ETSLPYKWVVEAANLLIPAVGSSLSEALDLIESDPDAWCDLSKF
1		I	DLPEEPSAEDSINNSLVQLQASHQQQVLPPRQPSA\LVPSVTEY
1	}		RLDGHTISDLSRSSRGELIPISPSTEVGGSGIGTPPSVLKRQRK
1	1		RRVALSPYTENSTSLSFLDSCNSLTPKSTPVKTLPFSPSQFLNF
1	1		WNKQDTLELESPSLTSTPVCSQKVVVTTPLHRDKTPLHQKHAAF
			MNYOTTPETED SOTIOTAL AND ALTERNATION AND DOLDHA BEDT AB
1	i	1	VTPDQKYSMDNTPHTPTPFKNALEKYGPLKPLPQTPHLEEDLKE
1		l	VLRSEAGIELIIEDDIRPEKOKRKPGLRRSPIKKVRKSLALDIV
1		1	DEDMKLMMSTLPKSLSLPTTAPSNSSSLTLSGIKEDNSLLNQGF
1	]		LQAKPEKAAVAQKPRSHFTTPAPMSSAWKTVACGGTRDQLFMQE
1	1		KARQLLGRLKPSHTSRTLILS
			AGPDDTMKRSLQALYCQLLSFLLILALTEALAFAIQEPSPRESL
	1940	239	QVLPSGTPPGTMVTAPHSSTRHTSVVMLTPNPDGPPSQAAAPMA
6951			OVI.PSGTPPGTMVTAPHSSTRHTSVVMLTPNPDGPPSQAAAPMA
6951		l l	9,2,0
6951			TPTPRAEGHPPT\TPSPPSLRQ*PPPILKAP/SSTGPAPAAMAT
6951			TPTPRAEGHPPT\TPSPPSLRQ*PPPILKAP/SSTGPAPAAMAT TSSKPEGRPRGOAAPTILLTKPPGATSRPTTAPPRTTTRRPPRP
6951			TPTPRAEGHPPT\TPSPPSLRQ*PPPILKAP/SSTGPAPAAMAT TSSKPEGRPRGQAAPTILLTKPPGATSRPTTAPPRTTTRRPPRP PGSSRKGAGNSSRPVPPAPGGHSRSKEGQRGRNPSSTPLGQKRP
6951			TPTPRAEGHPPT\TPSPPSLRQ*PPPILKAP/SSTGPAPAAMAT

Deginning nucleotide location corresponding to first amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid acid acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid acid acid acid acid acid acid acid	ID beginuclioca corrector faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for the faminin sequence for	nning ectide ation responding first no acid adue of no acid nence	eginning nucleotide location corresponding to first amino acid residue of amino acid equence nucleotide location corresponding to first amino acid residue of amino acid sequence	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)  TVPSNTSWAPTTTSLGPAKDKPGLRRAAQGGGSTFTSQGGTPDA TAASGAPVSP/PSCPSAFSAPPPR*PTGPQP**LLAYCYP\CT SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTTPQAP THPSRVSESTISGAKEETVA\PSP*PTGCPVLSPQWYPQPQAIS STAWSPPGPGSLGQQGTSPMWPRGTNRSTEPPSA*ARWISPG*S WPSACPSPP\LCPADGVLHEBEEEDRQPGEQPEAYGNNTHHPGT TFQQAC\RGAAPGEIPVPLKPLRTQLSEPRSPANGDYRDTGMVP C  PESEGESGEMTDRYTIHSQLEHLQSKYIGT\ATPTPPSGSG\CE PTPRLVILLHGPLRPSQLLRHCGE*EQSASPLQLDGKDASALWT ASRQARGELRLCLTTAVRGTSPSVSPVCQSS NWGKTRALASGKHVPFGKQTNPNKS/VHCDS*G**RRETTQDES FSPHFRGKMGGVV\KLEKELENTEQPVGGNEG*EHEVTGNLNSD
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SRPLETSSGYFTAATGFTPAAPDTSVSAPSGGIPGGASTTPQAI THESKVSESTISCAKETVALPSP + PROFULSGWYPGPQAIL STAWSPOPGSLCQGGTSPWBRGTNSTEPPSA*ARWISGO*S WPSACPSPP\LCPADGVLHEBEEDGRGPGGDEPSA*ARWISGO*S WPSACPSPP\LCPADGVLHEBEEDGRGPGGDEPSA*ARWISGO*S WPSACPSPP\LCPADGVLHEBEEDGRGPGGDEPSA*ARWISGO*S WPSACPSPP\LCPADGVLHEBEEDGRGPGGDEPSA*ARWISGO*S PTERLVILLINGPLRPSGLLEHGGS*SGAGIPGDTATAVGNTHHEGG PTERLVILLINGPLRPSGLLEHGGS*SGASTLQLDGKDASALW ASKQARGELSLCLTTAVAGTSPSVSPVCGG ASKQARGELSLCLTTAVAGTSPSVSPVCGG ASKQARGELSLCLTTAVAGTSPSVSPVCGG  6953 1512 349 NGKTFALASGKRVPFGKGTNDNKS_VHCDS*G**RETTORE FSPHPRGKMGGVV\KLEKELENTGPVGKGG**SHEVTTOKASI PSPHPRGKMGGVV\KLEKELENTGPVGKGG**SHEVTGNLASI PSPHPRGKMGGVV\KLEKELENTGPVGKGG**SHEVTGNLASI PSPHPRGKMGGVV\KLEKELENTGPVGKGG**RETSHATFNSKLL BVLNMESLFYTNNEGPSSAGKOLTGSFPVYPAGILLVCNNCA YRLLEAGTFSVKKWALRRONFDLEVVLGRERERTAKSRCDI BTFSEKQARALTREREKKRLKRRLEKMDWMLRAGFGQDPSAM ALAAENNFPGLPVGSVGLBGCMGFTDGRARGLGDREMARIKA AIETPEKQARALTREREKKRLKRRLEKMDWMLRAGFGQDPSAM ALAAENNFPGLPVGSVGLBGLGMGMFTEGRAGDBABRCTY PSRAPPATYKPULAGPRASAQTGARSPAPRCTYP PSRRRRRL PGRAPPAG**AAPAPTKYMLAGPASAQTGARSPAPRCTYP PSRRRRRL PGRAPPAG**AAPAPTKYMLAGPASAQTGARSPAPRCTYP PSRRRRRL PGRAPPAG**AAPAPTKYMLAGPASAQTGARSPAPRCTYP PSRRRRRL PGRAPPAG**AGGRQPSTGT**PFVGVGGARSPRREETTFGNPIPI AS*RAGWG**PGF/FEWGL**PGCGGREBREREGTTFGNPIPI AS*RAGWG**PGF/FEWGL**PGCGGREBREREGTTFGNPIPI AS*RAGWG**PGF/FEWGL**PGCGGREBREREGTTFGNPIPI AS*RAGWG**PGF/FEWGL**PGCGGREBREREGTTFGNPIPI AS*RAGWG**PGF/FEWGL**PGCGGREBREREGTTFGNPIPI AS*RAGWG**PGF/FEWGL**PGCGGREBREREGTTFGNPIPI AS*RAGWG**PGF/FEWGL**PGCGGREBREREGTTFGNPIPI AS*RAGWG**PGF/FEWGL**PGCGGREBREREGTTFGNPIPI AS*RAGWG**PGF/FEWGL**PGCGGREBREREGTTFGNPIPI AS*RAGWG**PGF/FEWGL**PGCGGREBREREGTTFGNPIPI AS*RAGWG**PGF/FEWGL**PGCGGREBREREGTTFGNPIPI AS*RAGWG**PGGPFFFTAADFDSTARTATGSSDD**AS*NU UNGAMSTGI UNGAMSTGI UNGATTGT  TSSECUTION**GARGATTTATGSSDD**AS*NU**AS*RAGWG**GGGGGGPTGGAPPNCVAS*TUYPHATGGGARAFTATATGSSDD**AS*NU**AS*RAGWG**GGGGGGGAPTGGGGGGAPTGGGGGGGAPTGGGGGGGGGG	6953			SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTTPQAP THPSRVSESTISGAKEETVA\PSP*PTGCPVLSPQWYPQPQAIS STAWSPPGPGSLGQQGTSPMWPRGTNRSTEPPSA*ARWISPG*S WPSACPSPP\LCPADGVLHEBEEEDRQPGEQPEAYGNNTHHPGT TPQQAC\RGAAPGEIPVPLKPLRTQLSEPRSPANGDYRDTGMVP C PESEGESGEMTDRYTIHSQLEHLQSKYIGT\ATPTPPSGSG\CE PTPRLVLLLHGPLRPSQLLRHCGE*EQSASPLQLDGKDASALWT ASRQARGELRLCLTTAVRGTSPSVSPVCQSS NWGKTRALASGKHVPFGKQTNPNKS/VHCDS*G**RRETTQDES FSPHFRGKWGGVV\KLEKELENTEQPVGGNEG*EHEVTGNLNSD
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### ### ##############################	6953			WPSACPSPP\LCPADGVLHEBEEEDRQPGEQPEAYGNNTHHPGT TFQQAC\RGAAPGEIPVPLKPLRTQLSEPRSPANGDYRDTGMVP C PESEGESGEMTDRYTIHSQLEHLQSKYIGT\ATPTPPSGSG\CE PTPRLVLLLHGPLRPSQLLRHCGE*EQSASPLQLDGKDASALWT ASRQARGELRLCLTTAVRGTSPSVSPVCQSS NWGKTRALASGKHVPFGKQTNPNKS/VHCDS*G**RRETTQDES FSPHFRGKMGGVV\KLEKELENTEQPVGGNEG*EHEVTGNLNSD
TPQQAC\RGAAPGEIPVPLKPLRTQLSEPRSPANGDYRDTGMVI C C C PSS2 658 304 PESEGESGEMTDRYTIHSQLEHLQSKYIGT\ATPTPPSGSG\Ci PTTRLVLLLHGPLRRSQLLRHCCG* ** \$Q\$ASPLQLGKASASLAV. ASRQARGELRICLTTAVKTSTPSVSPVCQSS ASRQARGELRICLTTAVKTSTPSVSPVCQSS FSPHFRGKMGOVV\LUKEKLENTGPPGVGNGG* ** SHEVTGNENS FSPHFRGKMGOVV\LUKEKLENTGPPGVGNGG* ** SHEVTGNLNSI PLLELCQCPLCQLDCGSREQLIAHVYQHTAAVVSAKSIM\CDW GRALSSPGSLGGRHLLHSEDQRSRCAVCGARFTSHATFNSEKLI, EVLNMESLPTHNEGESSAGEKAI AFPDVYPAGILLVCNNCA YRKLLEAGTPSVKRWALRRQNEPLEVRLQRUERERTAKKSRRD\ ETPEEREVERRDRERKRLQPMOETDGERRETQRDERMRIKK AIETPEKRQARLIREREAKRLKRRLDEKMDMALRAQFGQDPSAM ALAAEMNFFQLPVSGVELDSQLLGKMAFEEQNSSSLH PPPFTITISHPREAGT* ** AG* KRSGDSECSPVEG* A** TRAAAQ PFQR* ** PWTEGNS* PQASAVATFCGGASPAAPRCTP* ** PSRKHRRL PFQR* ** PAFA* ANPARTKWALGAPSA* PQCAAPLS* PPAPPLI** T* CAGAAARGR* PRRRS* PPR* TPGGCSWSEPT* PPAVSASAQTV DAG* ** AGG** GQRQRPSTGR** ** PPGVGGAGSHREEGT* PCONPIPE AS* ** RAGWGR** ** PGF* /* REWGL** EPCGEEMSGPGGAPPNCVGS VMQAMSTGI  FFGRGYORAQVAGAPVGHWGTRARQVKTGGRRARRTMFFLGQ WRSSGSWSTKTEDGWKCESCSOKLERENNHCHISHSILINGS GEIFNNEEHEYAS KKRKKOHFFROLTMOSFYREKWIVVIKESE GEIFNNEEHEYAS KKRKKOHFFROLTMOSFYREKWIVVIKESE GEIFNNEEHEYAS KKRKKOHFFROLTMOSFYREKWIVVIKEDGLOSTLCI  N** PSREVCISGKWQYLDPJ FIRNYSKLATTATGSSDD** ASE \N LTLSDLPJLIMLNNTLVR* PSDGWDITT.GQVTPTIJMLSBCDQL KKLCOYHPAEKQCFGHLIJBEKGHIEWAYALQKULPASESCOKLERENTGON GDTLHFCRHCS* LIFWKDSGHPCTAADPDSCTPTVS PQHFIDLF F GTSTS IFAS PTS PVLGESVLQDNSFDLNNGSDAEQEEMETQS GDTLHFCRHCS* LIFWKDSGHPCTAADPDSCTPTVS PQHFIDLF F SPKAS PVTSPAAAFPTASPANKDVSS FLETTADVE EI TGEGI ASGGOVMRRR TAT PEEVELPLQHGWRREVYLAVENSUVPPTAS PEISERVCPAASTVVSSPAVFSVSSPAVLPAVSLEVPLTAS TSPKAS PVTSPAAAFPTASPANKDVSS FLETTADVE EI TGEGI ASGGOVMRRR TAT PEEVELPLQHGWRREVYLAKSKSHRQGET FXVKRGRGRPPKVIT ITLLISKRGHIEWKKLEAQFELMEEDKAR AKSKKMRQKVQRGECOTTIQQAANKRKGETKSLKQELKKK KAEKKKKRGKVQRGECOTTIQQAANKRKGETKSLKQELKK KAEKKGKTKQEKLKEXVKREKKEVTKMEKEETYKAAPACK KAEKKGKTKQEKLKEXVKREKKEKVTKMEKEETYTKAAPACK CLTUPPGSATSCULTUPPGTSTCOLLINGENGERPSVCOSLKLILGEKVSE GLTLPGGARSDCLLTIVEFIHSTGKVLGFPDAKUVPSLGVLGE LCCOBSLGGROPQLLTIVEFIHSTGKVLGFPDAK	6953			TFQQAC\RGAAPGEIPVPLKPLRTQLSEPRSPANGDYRDTGMVP C PESEGESGEMTDRYTIHSQLEHLQSKYIGT\ATPTPPSGSG\CE PTPRLVLLHGPLRPSQLLRHCGE*EQSASPLQLDGKDASALWT ASRQARGELRLCLTTAVRGTSPSVSPVCQSS NWGKTRALASGKHVPFGKQTNPNKS/VHCDS*G**RRETTQDES FSPHFRGKMGGVV\KLEKELENTEQPVGGNEG*EHEVTGNLNSD
C C PESSEGSEMITORYTIHSQLEHLQSKYIGT\APPTPPSGSG\CI PESSEGSEMITORYTIHSQLEHLQSKYIGT\APPTPPSGSG\CI PTRIVILLHOPIRPSGLIRHGGB*EQSASPLQLDGKDASALW: ASRQARGELRICLITAVRGTSPSVSPVCQSS  6953 1512 349 NWKTRALASGKHYPFKGKINPINKS\VICES*G**RRETTQDE: FSPHPFGKMGGWV\KLEKELENTEQPVGGNEG*EREVITANVSASYM\CDW\GRALSSPGSLGRHLLIHSEQPVGGNEG*EREVITANVSASYM\CDW\GRALSSPGSLGRHLLIHSEQRSNCAVGGRFTSHATFNSEKL: EVLIMESLETTSVRINDEGPSSAEGKOIAFSPFYYPAGILLVCINICAS YRLLEACTPSVRIKAMLRRQNDELEVRIQRIEBERTAKKSRRD\EVTYNINEGPSSAEGKOIAFSPFYYPAGILLVCINICAS YRLLEACTPSVRIKAMLRRQNDELEVRIQRIEBERTAKKSRRD\ETTPEREVRIRHDREARRILGROREMMILKA AIETPEKRQARLIREREAKRIKRRLEKMDMALRAQFGQDPSAM. ALABENTFQLPVSGVELDSGLIGBMAFEERNASPGGDPSAM. ALABENTFQLPVSGVELDSGLIGBMAFEERNASSSHA PPOFFITFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	6953			C PESEGESGEMTDRYTIHSQLEHLQSKYIGT\ATPTPPSGSG\CE PTPRLV1LLHGPLRPSQLLRHCGE*EQSASPLQLDGKDASALWT ASRQARGELRLCLTTAVRGTSPSVSPVCQSS NWGKTRALASGKHVPFGKQTNPNKS/VHCDS*G**RRETTQDES FSPHFRGKMGGVV\KLEKELENTEQPVGGNEG*EHEVTGNLNSD
6952 658 304 PESEGSGEMTDRYTHISQLERLOSKYIGT\APPTPPSGSG\C\C PTPRIVILLIHGPIRPSQLIRHCGE*QQSASPLQLDGKDASALW: ASRQARGELRICLITAVRGTSPSVSPVCQSS  1512 349 NWGKTRALASGKHVPFCKGTNPNKS/VICDS*G*RETTODGE FSPHPFGKWGGVV\LEKELENTEQPVGKWGG*eHEVTGNINSI FSPHPFGKWGGVV\LEKELENTEQPVGKWGG*HEVTGNINSI FSPHPFGKWGGVV\LEKELENTEQPVGKWGG*HEVTGNINSI BEVLMWSSLFTVHNEGPSSAGKGNIAFSPFVYPAGILLVCNNCA- YRKILEAGTPSVRKWALRRONDFLEVRIQRIEBERTAKKSRRDI ETYBERGVRRMGTDGRARRICLORREMANIKA AIETYBEKQARLIREREAKRLORRICEKMDWHLRAQFGQDPSAM- ALAABMNFFQLPVSGVELDSQLIGMMAFEQNORSSIH PPPFITIFFHFREGAT*AG*KRSGBGCSPFVEQ**A*TRAAAO *PQR*RWTEGNSPQASAVATPGQGASPAAPRCTP*PSRRHRRL- PGARPPAG**APAPTKWMLAGPASAPQPGAAPLSPPAGPASAAQTP DAG**AGGR*GGRQRPSTGR*PPGVGSWSEPRTPPAVSASAQTP DAG**AGGR*GGRQRSTGR*PPGVGSWSEPRTPPAVSASAQTP DAG**AGGR*GFQRGRSTGR*PPGVGGAGRSERREGTIPGNPHP AS**RAGWGR*PGP/REWGL*EPQGEWSGGGGFGGAPPNOVGS VMQAMSTGI  6955 1968 782 PPGGRQVRAGAPVGHWGTGRRARRTRMFFLGQ WRSFGWSHIKTEDGWKRCESCSKLERENNICHISHSIILNSE GEIFNNEHEYASKKRKKDHFRNDTNTOSFYRERWIYVHKEST ERHGYCTLGEAFNRLDFSSAIQDIRFRTVVVKLQLILAKSQLT LSGVAQKNYFNILDKIVQKVLDDHNYPRLIKDLLQLIAKSQLT LSGVAQKNYFNILDKIVQKVLDDHNYPRLIKDLLQLIAKSQLT AN**RSFVCIISGKHGYLDLPIRNYSRLATTAGSDD*ASE\N LLILSDLPIHMINNILYRPSDONDITILGGVYPTIYMISBDRQL KKLCQYHFAEKQFCRHLILSEKGHIEWKLMYFALQKHYPAEXG GDTHFCRICSILFFKNOSGHPCTAADPDSCTTPUSPQHFIDLF F  6956 8605 3839 OTSTSIFASFTSPPVLGESVLÖNDSFDLNNGSDAEQEEMETG STPRASFVTSPAAPFTASPANDVSSFLETTAVEEITGGGL AGSGDWMRRIATEREWRLPCHGWRREVIKKGSRRGGET YYGPCGRMKQFPEVIKLISENGHRREVRIKKGSRRGGET YYGPCGRMKQFPEVIKLISENGHRREVRIKKGSRRGGET YYGPCGRMKQFPEVIKLISENGHRRERRATKE PKYKRGGRPPKVKTELLNRTDNRFLKKLRAPCKX ARSKKMRGKYVGRGECOTTIOGQARNKKRGETKSLKQKEAKKK KAEKEKKTYGEKLKEKVMKKEKEVYKKKEKEKTKSKLKAPACKX KAEKEKKTYGEKLKEKVMKKEKEVYKKKEKKEKEVKKKKAPACKX KAEKEKKTYGEKLKEKVKMKEKEVYKKKEKEKEVKKKARCKCACK KALACKTYGEKLKEKVKMKEKEVYKKKEKEKEVKKKARCKECOTKSLCQCEAKK CALKKGRGPPKYKLTELLHRTDNRFLKKLEAQETINEEDKAR ARSKKKWRGKVOGGECOTTIOGQARNKRGGETKSLKQKEAKYK KAEKEKKTYGEKLUKLKALALIPDFFSYCOSLKILIGEKVSE GLTLPSGAFSDCLITVELHSFGKVLGFDPAKGVGFGLOTKSLCQCEAK	6953			PESEGESGEMTDRYTIHSQLEHLQSKYIGT\ATPTPPSGSG\CE PTPRLVLLLHGPLRPSQLLRHCGE*EQSASPLQLDGKDASALWT ASRQARGELRLCLTTAVRGTSPSVSPVCQSS NWGKTRALASGKHVPFGKQTNPNKS/VHCDS*G**RRETTQDES FSPHFRGKMGGVV\KLEKELENTEQPVGGNEG*EHEVTGNLNSD
PTPRLVLILHOPLRPSCLERHGE* EQSASPLQLOKDASALM* ASRQARGERICLITAVRGTSBSVPQGSS  NWKKTRALASGKHVPFGKQTNPNKS/VHCDS*G**RRETTODE* FSPHFRGKMGGVV\KLEKELENTEQPVGGMEG**ERETTODE* FSPHFRGKMGGVV\KLEKELENTEQPVGGMEG**ERETTODE* FSPHFRGKMGGVV\KLEKELENTEQPVGGMEG**ERETTODE* FSPHFRGKMGGVV\KLEKELENTEQPVGGMEG**ERETTODE* FSPHFRGKMGGVV\KLEKELENTEQPVGGMEG**ERETTAKTSTRTD* PLELECQPLCQLLOCGSREQLIAHVTAVAVSAXYM\CDW. GRALSSPGSLGRHLLIHISEDGKSNCAVCGARFTSHATTPNSKYM\CDW. ARLALEAGTPSVRKMALRRQNEPLEVRLQRLERETAKKSRDI ETTEEREVURRMDREAGRIQAMGETDEGRARRLQRDREAMRLKA ARTEPEKRGARLIREREAKRLKRRLEKMDMMLRAQFGOPSAM. ALAAEMNFPOLEVGVVELDSOLLGKMAFEEONSSILH PPPFTITSHPREAGT**AG**KRSGDSECSFPVEQ*A*TRAAAO! **POR**RHTGMSPOASAVATPGGGASPAPRCTP**PSRRHRRL PGARPPAG**AAPAPTKWLLAGPASAPQGGAPAPRCTP**PSRRHRRL PGARPPAG**AAPAPTKWLLAGPASAPQGGAPAPRCTP**PSRRHRRL PGARPPAG**AAPAPTKWLLAGPASAPQGGAPAPRCTP**PSRRHRRL PGARPPAG**AAPAPTKWLLAGPASAPQGGAPAPRCTP**PSRRHRRL PGARPAGA**GGRQRQRPSTGR**PGVGGGASERRRGGTIPONPIP AAS**RAGWGR**PGP/REMCL**EPQGEMMSGRGGAPPROVGS *WOQMSTGI **ORG**GGRQRQRPSTGR**PGVGGAGGASHRRRGTIPONPIP AS**RAGWGR**PGP/REMCL**EPQGEMMSGRGGAPPROVGS *WOQMSTGI **ORG**GGRQRQRYSTGR**PGVVGGGAGRSHRRRGTIPONPIP AS**RAGWGR**PGP/REMCL**EPQGEMMSGRGGAPPROVGS **WOQMSTGI **ORG**GGRQRQRYSTGR**PARRRTMFFLGQ **WRSPGWKRYTCHOPKTRAGVVTGGRRRARRTMFFLGQ **WRSPGWKRYTCHOPKTRAGVVTGGRRRARRTMFFLGG **GETINNESHEYASKKRKXDHFRNDTNTQSFYREKWIYVHKEST* ERHGYCTLGEARNRLDFSSALQINRFRLYNCLLQLIAKSQLT /**N*SRSVCISGKHQYLDLPIRNYSRLATTATGSDD**ASE*\M* LITLSDLPLHMLNNILYRPSDMDIITLGQVTPTLYMLSBDRQL KKLCQYHFAEKQFCCHLILSEKGHLEWKLMYFALQKHYPAKEQ GDTLHFCRIGSILFFKWDGGHPCTAADPDSCTTPVSPQHFIDLF* F **GSSSVTTSPAAPPTASPANKDVSSFLETTAAVEEITGBGL AAGSGDWMRRIATEEREKTLOHGMRREVXIKKGSRRNGGET TYGGCGKRMKQFFPVKKGRPPFWKIKGSHRNGGT TYGGCGKRMKQFFPVKKGRRPPKTKLKGLAGETLINEEDKAR AASKKMRGXVORGECOTTIOGQARNKRRGETVKSLKGKRAKK KAEKEKKTKQEKLKEKVMRKKEKEVTKAKKKARPACKA KAEKEKKTKQEKLKEKVARKKKEKEVTKAKKKARPACKA KAEKEKKTKQEKLEKVARKKKEKEVTKAKKARPACKA KAEKEKGKTKQELGELLHELINGENVLIGEVOSE** GLTLPSGAFFSDCLTTVELLISFGKULGEVOSE** GLTLPSGAFFSDCLTTVELLISFGKULGEVOSE** GLTLPSGAFFSDCLTTVELLISFGKULGEVOS	6953			PTPRLVLLLHGPLRPSQLLRHCGE*EQSASPLQLDGKDASALWT ASRQARGELRLCLTTAVRGTSPSVSPVCQSS  NWGKTRALASGKHVPFGKQTNPNKS/VHCDS*G**RRETTQDES FSPHFRGKMGGVV\KLEKELENTEQPVGGNEG*EHEVTGNLNSD
ASRQARGELRICLTTAVRGTSPSVSPVCQSS  1512  349  NWGKTRALASGKHVPFGKOTNPKK5/VHCDS -0** RRETTODE: FSPHFRGKWGGVV\ KLEKELENTEQVGGNEG* EHEVTGNLNSI PLLELQCPLCQLDGGSREQLIAHVYQHTHAVVSAKSYM\CPW GRALSSPGSLGRILLIHSEDGRSNCAVCGRAFTSHATTNSKL\ EVLNMESLPTVHNEGPSSAEGKDI AFSPFVYPAGILLVCUNCA\ YRKLLEAQTPSVRKWALRRQNEPLEVRLQRLERERTAKKSRDI ETPEREQRARLIGRERAKRIKKRIERUMDHIRAOFGGOPSAM. ALAAEMNFFQLPVSGVELDSQLLGKMAFEEONSSGLH PPPFFITSHPREAGT* AG* KRSGDSECSFFVEQ* A*TRAAAQ\ **ALAEMNFFQLPVSGVELDSQLLGKMAFEEONSSGLH PPPFFITSHPREAGT* AG* KRSGDSECSFFVEQ* A*TRAAAQ\ **PQR*RRTEGNSPQASAVATEGGASPAAPRCTP* PSRRHRRL PGARPPG**APPAPTYPMLAGPBASAPQPGAPLISPAPPLIKT\ **CAGAARGR*PRCDR*SPRFTFGGCSWSEDRTPPAVSASAQTP DAG**AGGR*GQRQRSTGR**PFTPGGCSWSEDRTPPAVSASAQTP DAG**AGGR*GQRQRSTGR**PFTPGGCSWSEDRTPPAVSASAQTP DAG**AGGR*GQRQRSTGR**PFTPGGCSWSEDRTPPAVSASAQTP DAG**AGGR*GQRQRSTGR**PFTPGGCSWSEDRTPPAVSASAQTP DAG**AGGR*GQRQRSTGR**PFTPGGCSWSEDRTPPAVSASAQTP DAG**AGGR*GQRQRSTGR**PFTPGGCSWSEDRTPPAVSASAQTP DAG**AGGR*GQRQRSTGR**PFTPGGCSWSEDRTPPAVSASAQTP DAG**AGGR*GQRQRSTGC**PFTPGGCSWSEDRTPPAVSASAQTP DAG**AGGR*GQRQRSTGC**PFTPGGCSWSEDRTPPAVSASAQTP DAG**AGGR*GQRQRSTGC**PFTPGGCSWSEDRTPPAVSASAQTP DAG**AGGR*GQRQRSTGC**PPTPGGCSWSEDRTPPAVSASAQTP DAG**AGGR*GQRQRSTGC**PFTPGGCSWSEDRTPPAVSASAQTP DAG**AGGR*GQRQRASTGC**PFTPAVSACAQTP DAG**AGGR*GQRQRSTGC**PFTPATAVVSKLLQLLSSTLCI /N*SSRSVCISGRHQ**LDDP**IRNSRLATATGGSDD**ASE\N LTLSDDP**LINLILYRPBGMDITLGQVTPTLYMLSEDRGL KKLCQYHFASKQFCRILLISEKGHLEWKLMYFALQKHYPAKSQ GDTLHFCRCSILFWKDSGHPCTAADPDSCTFTPVSPGHFIDF F  6956  3605  3639  OTSTSIFASPTSPPVLGESVLQDNSPDLNRGSDAEQEEMETGS DFPPSLTQAPADGSSTICLHPATSPAVSPTTSAVSLVVSPAX TSPKASPVTSPAAAFTTASPANKDVSSFLTTADVSEITGGLI AGSGDVMRRITATPEEVKLPQHGWRREVXIKKGSHRQGET YGPGGKRMKQFPBVIKXLSRNVVHSVRREHFSSFRPMYGDF EERDTPEGCLQWVQLSAEETSRIQATIGKRGRPRNTEKARTKE PKVKRGRGRPPKVKITELLINKTDNRPIKKLEAQETINEEDKAR AKSKKWRQKVGRGECCTTIQQQANKKKQETKSLQKEAKKK KAEKKKKKNGKVGKKKEKVEKKKKKEKEETKALKKCHKEKETKALKKUKKKEKETKALKKCHKEKETKALKKKKKKEKTKALKEKTKALKTHKALPPGFINADPSKCHALKGCHAKKKALKECTKALKTKALKTHKALPDGFISNGCALLIGEKKKETTALAUCHALAGATALAGGLILGEGGALLAGGGGGGGGGGGG	6954	1512	1512 349	ASRQARGELRLCLTTAVRGTSPSVSPVCQSS  NWGKTRALASGKHVPFGKQTNPNKS/VHCDS*G**RRETTQDES FSPHFRGKMGGVV\KLEKELENTEQPVGGNEG*EHEVTGNLNSD
1512   349   NWGKTRALASGKHVPFGKOTNPNKS/VHCDS-GS-RRETTODE   FSPHFRGKMGGVV, KLEKELENTEQPVGGNEG-EHEVTGDLNS-    FSPHFRGKMGGVV, KLEKELENTEQPVGGNEG-EHEVTGDLNS-    GRALSSPGSLGRHLLIHSEDGRSNCAVCGRFTSHATENSEKL-   BVLNMESLPTVINEGPSSAEGKIL AFSPPVYPAGILLVCNNCA-   YRKLLEAGTFSVRKWALRRQNEPLEVRLQRLERERTAKKSRDI-   BTEBEREVRMRDRBAKRLQRMGETDEGRARRLQRDRBAMRLK-   AIETPERGARLIREREAKRIKRELEMMDMLRAGPGGVPSM-   ALAAEMNFFQLPVSGVELDSQLLGKMAFEEQNSSSLH-   ALAAEMNFFQLPVSGVELDSQLLGKMAFEEQNSSSLH-   PPPFFITFSHPREAGT-8G-KRSGDSECSPFVEG-R-TRAAAQ-   PPQR-RRTEGNSPQASAVATEGGASPAAPRCTP+PSRRHRRL-   PGR-PAG-AAPAPTKPMLAGPASAAPQCGASPASASATP-PSRRHRRL-   PGR-PAG-AAPAPTKPMLAGPASAAPQCGASPLSPAPBLIRT-   *CAGAAARGPRRDRSPRTPGGCSWEPRTPPAVSASAQTP-   DAG-AAGGR-GQRGRSTGR-PPGVGGAGRSHRREGTIPGNPHP-   AS-*RAGWQR-PGG-RESTGR-PPGVGGAGRSHRREGTIPGNPHP-   AS-*RAGWQR-PGG-RESTGR-PPGVGGAGRSHRREGTIPGNPHP-   AS-*RAGWQR-PGG-RESTGR-PPGVGGAGRSHRREGTIPGNPHP-   AS-*RAGWQR-PGG-RESTGR-PPGVGGAGRSHRREGTIPGNPHP-   AS-*RAGWQR-PGG-RESTGR-PPGVGGAGRSHRREGTIPGNPHP-   AS-*RAGWQR-PGG-RESTGR-PGGGAGRSHRREGTIPGNPHP-   AS-*RAGWQR-PGG-RESTGR-PPGVGGAGRSHRREGTIPGN-PG-WGS-PGG-RESTGR-PGG-PGGAPPNQVGS-   WQAMSTGI-PGG-RESTGR-PFG-PGG-RESTGR-PGG-PGGAPPNQVGS-PGG-PGG-PNQVGS-PGG-PGG-PNQVGS-PGG-PGG-PNQVGS-PGG-PGG-PNQVGS-PGG-PGG-PGG-PNQVGS-PGG-PGG-PGG-PNQVGS-PGG-PGG-PGG-PNQVGS-PGG-PGG-PGG-PNQVGS-PGG-PGG-PGG-PGG-PGG-PGG-PGG-PGG-PGG-P	6954	1512	1512 349	NWGKTRALASGKHVPFGKQTNPNKS/VHCDS*G**RRETTQDES FSPHFRGKMGGVV\KLEKELENTEQPVGGNEG*EHEVTGNLNSD
FSPHFRGKMGGVV_KLEKLENTTOPUGGRG* ENEVTGNINSI  PLLELCQCPLCQLCGSREQLIAHVYQHTAAVVSAKSYM_CPW  GRALSSPGSLGRHLLIHSEDGRSNCAVCGARTSHATFNSEKLI  BVINMSSLFTVINGGPSSAEGKDIAFSPYPYAGGILLVCNNCA  YRKLLEAQTPSVKRWALERQNEDLEVELQRIEGERTAKKSREDL  ETPEEREVRRMRDREAKRLKRRLEKMUMULRAGFGGDPSAM  ALAAEMNFFQLEVSGVELDSQLLGKMAFEEQNSSSLH  ALAAEMNFFQLEVSGVELDSQLLGKMAFEEQNSSSLH  ALAAEMNFFQLEVSGVELDSQLLGKMAFEEQNSSSLH  PPPPFIIFSHPREAGT*AG*KRSGDSEGSPVEQ*A*TRAAAO  *PQR*RNTEGNSPQASAVATPGGGASPAPRCTP*PSRHRRL PGARPPAG*APAPPKKPLLAGPASAPQPGAPLISPPAPPLIKT  *CAGAAARGPRRDRSPPRTTGGCSNSEGFTYPAVSASAQTP DAG*AGGR*GQRQRPSTGR*PPGGGSNSEGFTYPAVSASAQTP DAG*AGGR*GQRQRPSTGR*PPGGGSNSEGFTYPAVSASAQTP AS*LAGWQR*PGP/REWGL*EPQGEBMSGPGGPGAPPNQVGS VMQAMSTGI  ### PPP PP PP PP PP PP PP PP PP PP PP PP	6954	1512	1512 349	FSPHFRGKMGGVV\KLEKELENTEQPVGGNEG*EHEVTGNLNSD
FSHFRGMGGVV_KLERLENTEQPUSGCS*ELENTGNINSS PLLELCQCELCQLDGSREQLIANYQHTAAVVSAKSYM_CPW GRALSSPGSLGRHLLIHSEDQRSNCAVCGARFTSHATFNSEKL BVLNMGSLFTVINNEGPSSAEGKDIAFSPBYPAGILLVCHNCA YRKLLEAOTPSVKWALERQNEDFLEVELQRLERERTAKKSRROL ETPEEREVRRMRDREARRLQRMGETDEQRARRLGRDERAMRIK AIETPEKRQARIIREREAKRLKRRLEKHDWHLRAQFGQDPSAM ALAAENNFFQLEVSCVELDSQLLGKMAFEEQNISSIH  6954 819 1 PPPFFIIFSHPREAGT*AG*KRSGDSSCSPVEO*A*TRAAAO *PPR*RWTEGNSPQASAVATPGQGSASAPAPCTP*PSRHRRL PGARPPAG*AAPAPTKFWLLAGPASAPQFBAAPLS*PAPPLIFT *CAGAAARGPRRDRSPPRTPGGCSNSEBTTPPAVSASAQTP DAG*AGGR*GQRQRPSTGR*PPGGGSRSEBTTPPAVSASAQTP DAG*AGGR*GQRQRPSTGR*PPGGGSRSEBTTPPAVSASAQTP DAG*AGGR*GQRQRPSTGR*PPGGGSRSEBTTPPAVSASAQTP DAG*AGGR*GQRQRPSTGR*PPGGGSRSEBTTPPAVSASAQTP DAG*AGGR*GQRQRPSTGR*PPGGGSRSEBTTPAVSASAQTP DAG*AGGR*GGRQRPSTGR*PPGGGSRSEBTTPAVSASAQTP DAG*AGGR*GGRQRPSTGR*PPGGGSRSEBTTPAVSASAQTP DAG*AGGR*GGRQRPSTGR*PPGGGSRSEBTTPAVSASAQTP DAG*AGGR*GGRQRPSTGR*PPGGGSRSERTPAVSASAQTP DAG*ARGR*GGRQRPSTGR*PPGGGSRSERTPAVSASAQTP DAG*ARGR*GGRQPSTGR*PPGGGSRSERTPAVSASAQTP DAG*ARGR*GGRQPSTGR*PRGGTSGGRGRARARTMFFLGQ WRSPGWSWIKTEDGWKCTSCSQKLEENHHCHISHSIIINSE GEINNEEHEYASKKRKKDHFRNITTGSFYREKWIYVHKEST ERHGYCTLGEAFNRLDFSSAIQDTRRNYVVKLLQLIAKSQLT LSGVAQKNYFNILDKIVQRVLDDHHNYEIKKDLQDLSSTLCI /N*RSRVCISGKRYLDLPINTYSRLATTATGSSDD*ASE_W LTLEDDLPLHHLNNILVRFDGWDIITIGQVTPTLYMLSEDRQL KKLCQYHFASKQYCDRITTIGQVTPTLYMLSEDRQL KKLCQYHFASKQPCRHLILISEKGHLEWKLMYFALQKHYPAKEQ GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPGHFIDLF PC TSTSIFASPTSPFVLGESVLQDNSFDLINMGSDAEQEEMETQS DFPPSLTQPAPDQSSTIQLHPATSPAVSPTSAVSLVVSPAA PEISPEVCPAASTYVSPAVFSVSSPLSAVLPAVSLEVPLITAS TSPRASVTSPAAAFTTSAPANKDVSSPLETTADVEEITGGGI ASGSGDWMRRIATPEEVKLPLQHGWRREVIKKGSHRWQGFT YGPGGKRMKQFPSVKXLSRNVVHSVREEHFSFSPRMVGDF EERDTPEGLQNVQLSABEIPSRIQAITGKGGRPNTYTEKARTKE PKVKRGKGRPPKVKITELLNKTDNRPLKKLEAQETINEDKAK AKSKKNRNGRVQGGECQTTIQQQANKRKGSTKSLKQKEAKKK KAKKKNRGKVQRGECQTTIQQQANKRKGSTKSLKQKEAKKK KAKKKKRKGKTKGSKLKEKVKRKEKEVTKKAKEEVTKARPACYK KTLATQRLEERQRQQMILEEMKKPTEDMCLTDHQPLPPSRY GLTLPSGAFSDCLTIVEFLHSTGWLLGFPDAKOYPSLGVLQGE KTLATQRLEERQRQMILLEEMKKPTEDMCLTDHQPLPPSRY GLTLPSGAFSDCLTIVE	6954			FSPHFRGKMGGVV\KLEKELENTEQPVGGNEG*EHEVTGNLNSD
GRALSSPGLIGRILLIHSEDCRSNCAVCGARFTSHATNSEKL EVINMESLPTVHNEGPSSAEKGI JAFSPPVYPAGILLUCNNCA. YRKILEAQTPSVKKWALRRQNSPLEVRLQRIEBERTAKKSRRDI ETPEEREVRRMRDREAKRLQRMGETDEGRARRLQRDREAMRI.KA AIETPEKRQARLIREREAKRLKQRMMLRAQFGQDPSAM. ALAAEMIFFQLPVSGVELDSQLIGKMAFTEGNSSSLH  6954 819 1 PPPPFIIPSHPREAGT*AG*KRSGDSECSPFVG***A*TRAAO. **PQR*RHTEGNSPQASAVATPGGGASPAAPRCTP*PSRHRRL FGARPPAG**AAPAPTKPWLAGPASAPQGAAPLS*PAPPLIRT **CAGAAARGRPRDRS\$PRPTPGGCSWSEPRTPPAVSASAQTP* DAG**AGGR**GQRQRPSTGR**PPGVGGASPAAPRCTP*PSRHRRL **PPAG**AAPAPTKPWLAGPASAPQGGAPLS*PAPPLIRT **CAGAAARGRPRDRS\$PRPTPGGCSWSEPRTPPAVSASAQTP* DAG**AGGR**GQRQRPSTGR**PPGVGGAGSPAPPROPYGS VMQAM*GII **PPGRQVRAQVAGAPVGHWGTRARQVKTGGRRRARRTMFFLGQ** WRSPGWSWINTEDGWKRCESCSKLERENNICNISHSIILMSE GEIFNNEHEYSASKKRKÜHFRNDTNTOSFYREKWIYVHKEST ERHGYCTLGBAFNRLDFSSAIQDIRRFNYVVKLLQLIAKSQLT LIGGVAQKNYFNILDKIVQRVLDDHHNPRLIKDLLQDLSSTLCI /N*RSREWCISGKHQYLDLPIRNSKLATTATGSSDD**ASE_VN KKLCQYHFAEKQFCRHLIJSEKGHIEWKLMYFALQKHYRAKQ GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLF F  6956 8605 3839 OTSTSIFASPTSPPVLGESVLQDNSFDLNNGSDAEQEEMETQS DFPPSLTQPADQSSTIQLHPATSPAVSPTSPAVSLVVSPAA PEISBEVCPAASTTVVSPAVFSVVSPASSAVLPAVSLEVPLTAX TSPKASPVTSPAAAFPTASPANKDVSSFLETTADVEEITGGGL ASGSGDWARRIATPEEVRLPLGHGMRREVRIKKSHRWGGTT YYGPCGKKMKQFPEVIKYLSRNVVSREHFSFSPRMPVGDF EERDTPEGLQWVQLSAEEIPSRIQATIGKGRPRNTEKARTKE PKVKRGRGRPPKVXITELLHKTDNRPLKKLEAQETLNEEDKAK AKSKKMRQKVQRGECQTTIQGARNKKRGETKSLKQKEAKKK KAEKKKKRIKQVQRGECQTTIQGARNKKRGETKSLKQKEAKKK KAEKKKRIKQKVQRGECQTTIQGARNKKRGETKSLKQKEAKKK KAEKKKKRIKQKVQRGECQTTIQGARNKKRGETKSLKQKEAKK KAEKKKKRIKQKVQRGECQTTIQGARNKKRGETKSLKQKEAKK KAEKKKGKTRGEKGKLKEVKNEKKEKEVMMKSKEEVTKAKAPACKA KTLATQRRLEERQRQMILEEMKKPTEDMCLTDHQPLPDFSRV GLTLPSGGAFSDCLTIVEFLISFGKVLGFDPAKDVPSLGVLQLLQCGSLGEVQDLLVRLLIKAAAHDPGFPSYCOSLKILGEKVES  CLTLPSGGAFSDCLTIVEFLISFGKVLGFDPAKDVPSLGVLQLCGGSLGEVQDLLVRLLIKAAAHDPGFPSYCOSLKILGEKVES  CLTLPSGGAFSDCLTIVEFLISFGKVLGFDPAKDVPSLGVLQLCCGGSLGEVQDLLVRLLIKAAAHDPGFPSYCOSLKILGEKVES	6955			
GRALSSPGLIGRILLIHSEDCRSNCAVCGARFTSHATNSEKL EVINMESLPTVHNEGPSSAEKGI JAFSPPVYPAGILLUCNNCA. YRKILEAQTPSVKKWALRRQNSPLEVRLQRIEBERTAKKSRRDI ETPEEREVRRMRDREAKRLQRMGETDEGRARRLQRDREAMRI.KA AIETPEKRQARLIREREAKRLKQRMMLRAQFGQDPSAM. ALAAEMIFFQLPVSGVELDSQLIGKMAFTEGNSSSLH  6954 819 1 PPPPFIIPSHPREAGT*AG*KRSGDSECSPFVG***A*TRAAO. **PQR*RHTEGNSPQASAVATPGGGASPAAPRCTP*PSRHRRL FGARPPAG**AAPAPTKPWLAGPASAPQGAAPLS*PAPPLIRT **CAGAAARGRPRDRS\$PRPTPGGCSWSEPRTPPAVSASAQTP* DAG**AGGR**GQRQRPSTGR**PPGVGGASPAAPRCTP*PSRHRRL **PPAG**AAPAPTKPWLAGPASAPQGGAPLS*PAPPLIRT **CAGAAARGRPRDRS\$PRPTPGGCSWSEPRTPPAVSASAQTP* DAG**AGGR**GQRQRPSTGR**PPGVGGAGSPAPPROPYGS VMQAM*GII **PPGRQVRAQVAGAPVGHWGTRARQVKTGGRRRARRTMFFLGQ** WRSPGWSWINTEDGWKRCESCSKLERENNICNISHSIILMSE GEIFNNEHEYSASKKRKÜHFRNDTNTOSFYREKWIYVHKEST ERHGYCTLGBAFNRLDFSSAIQDIRRFNYVVKLLQLIAKSQLT LIGGVAQKNYFNILDKIVQRVLDDHHNPRLIKDLLQDLSSTLCI /N*RSREWCISGKHQYLDLPIRNSKLATTATGSSDD**ASE_VN KKLCQYHFAEKQFCRHLIJSEKGHIEWKLMYFALQKHYRAKQ GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLF F  6956 8605 3839 OTSTSIFASPTSPPVLGESVLQDNSFDLNNGSDAEQEEMETQS DFPPSLTQPADQSSTIQLHPATSPAVSPTSPAVSLVVSPAA PEISBEVCPAASTTVVSPAVFSVVSPASSAVLPAVSLEVPLTAX TSPKASPVTSPAAAFPTASPANKDVSSFLETTADVEEITGGGL ASGSGDWARRIATPEEVRLPLGHGMRREVRIKKSHRWGGTT YYGPCGKKMKQFPEVIKYLSRNVVSREHFSFSPRMPVGDF EERDTPEGLQWVQLSAEEIPSRIQATIGKGRPRNTEKARTKE PKVKRGRGRPPKVXITELLHKTDNRPLKKLEAQETLNEEDKAK AKSKKMRQKVQRGECQTTIQGARNKKRGETKSLKQKEAKKK KAEKKKKRIKQVQRGECQTTIQGARNKKRGETKSLKQKEAKKK KAEKKKRIKQKVQRGECQTTIQGARNKKRGETKSLKQKEAKKK KAEKKKKRIKQKVQRGECQTTIQGARNKKRGETKSLKQKEAKK KAEKKKKRIKQKVQRGECQTTIQGARNKKRGETKSLKQKEAKK KAEKKKGKTRGEKGKLKEVKNEKKEKEVMMKSKEEVTKAKAPACKA KTLATQRRLEERQRQMILEEMKKPTEDMCLTDHQPLPDFSRV GLTLPSGGAFSDCLTIVEFLISFGKVLGFDPAKDVPSLGVLQLLQCGSLGEVQDLLVRLLIKAAAHDPGFPSYCOSLKILGEKVES  CLTLPSGGAFSDCLTIVEFLISFGKVLGFDPAKDVPSLGVLQLCGGSLGEVQDLLVRLLIKAAAHDPGFPSYCOSLKILGEKVES  CLTLPSGGAFSDCLTIVEFLISFGKVLGFDPAKDVPSLGVLQLCCGGSLGEVQDLLVRLLIKAAAHDPGFPSYCOSLKILGEKVES	6955			PLLELCQCPLCQLDCGSREQLIAHVYQHTAAVVSAKSIM\CPVC
EVLNMESLPTVNNEGPSSAEGKDIAFSPPVYPAGILLVCNNCA YRKLLEAGTPSVRKWALRRQNE PLEVRLQRLERERTAKKSRRDI ETPEEREVRMRDREAKRLQRMGETDEGRARRLGRDREBMALK AIETPEKRQARLIREREAKRLKKRLEKHDMMLRAGFGOP SAM. ALAAEMNFPCLPVSGVELDSQLLIGMAFEEQNSSLH  1 PPPFIIPSIPREAGT*AG*KRSGDSECSPVEO*A*TRAAAO *PQR*RWTEGNSPQASAVATPGQGASPAAPRCTP*PSRRHRRL PGARPPAG*AAPAPTKYWLAGPASAPQCGASPAPAPCTP*PSRRHRRL *CAGAARGRERRERDSSPPTRGGCSWSEPRTPPAVSASAQTP DAG*AGGR*GQRQRPSTGR*PGVGGGWSEPRTPPAVSASAQTP DAG*AGGR*GQRQRPSTGR*PGVGGGWSEPRTPPAVSASAQTP DAG*AGGR*GQRQRPSTGR*PGVGGGWSEPRTPPAVSASAQTP VMQAMSTGI  6955  1968  782  PPGRRQVRAQVAGAPVGHWGTRARQVKTGGRRRARRIMFFLGQ WRSPGWSHIKTEDGWKRCESCSCKLERENNHCNISHSILLNSE GEIFNNEEHEYASKKKKDHFROIDTTOGSFYREKMIYVHLSE ERHGYCTLGEAFNRLDFSSAIQDIRRFNYVVKLLQLIAKSQLT LSGWAQKNYFNILDKLVQKVLDDHHNPRLIKDLLQDLSSTLCI /N*RSREVCISGKHQYLDLPIRNYSRLATTATGSSDD*ASE\N LITLSDLPILHMLNNILVRFSDGNDIITLGQVTFTLYMLSEDRGL KKLCQYHFAEKQFCRHLILSEKGHIEWKLMYFALQKHYPAKBQ GDTLHFCRHGSILFWKDSGBPCTAADPDSCFTPVSPQHFIDLF F  6956  8605  3839  QTSTSIFASPTSPPVLGESVLQDNSFDLNNGSDAEQEEMETQS DFPPSLTQPADDQSSTIQLHPATSPAVSPTTSFBAVLVVSPRA PEISPEVCPAASTVVSPAVSPVSTPASAVLPAVSLEVPLTAS TSPRASPVTSPAAAFTASPANKDVSSFLETTADVEEITGGI ASGSGDWRRRIATPESVRLPLQHGWREVTIKKGSHRWQGST YYGPCGKRMKQFPEVIKXLSRNVVHSVREHFSFSPRMPVGDF EERDTPBELQWOLSABEIPSRIQAITGKRGRPRNTEKARTKE PKVKRGGGRPPKVKITELLNKTNNEPLKKLEAQEFILNEDDKAR AKSKKKMRQKVQRGECQTTIQGQARNKRKGETWSLKQKEAKK KAEKGKGTKQEKLKEXVKRRKKKKVMMKSKEVTKAKRACKK KTLATQRLEERQRQQMILEEMKKPTEDHCLTTHQFLPFSRC CLTLDESGAFSDCLTIVEFLLSFGKVLGFDPAKDVPSLGVLQEC CLCOGSLGEVQDLLVTLLKKAALHDPGFPSYCOSLKILGEKVSE	6955		i	GRALSSPGSLGRHLLIHSEDORSNCAVCGARFTSHATFNSEKLP
### ETPEREVREMPREAKRLORMOETDECRARRLORDERAMELK AIETTPEKQARLIREREAKRLKRIEKMDMMLRAQFGODPSAM ALAAEMMFFQLPVSGVELDSQLLGKMAFEECNSSSLH  #### 1	6955		I	EVLNMESLPTVHNEGPSSAEGKDIAFSPPVYPAGILLVCNNCAA
### ETPEREVRIMERBEAKRLORMOETDECRARRLOGDERAMELK AIETPEKQARLIREREAKRLKRIEKMDMMLRAQFGODPSAM ALAAEMMEPGUPVSGVELDSQLLOKMAFEECNSSSLH  6954 819 1 PPPPFIIPSHPREAGT*AG*KRSGDSECSPPVEQ*A*TRAAQI *POR*RMTECNSPQASAVATEGGASAPARRCTEP*SERRHRIL PGARPPAG*AAPAPTKWHAGPASAPQPGAAPLSPPAPPLIRT *CAGAAARGRPRRDSPRPRTPGGCSWSEPRTPPAVSASAQTP DAG*AGGR*GGRQRSTGR*PPGGGSGSSHRRREGTIPGNPHP AS*RAGWGR*PGP/REWGL*EPQGBEMSGPGGAPPNQVGS VMQAMSTGI  6955 1968 782 PPGRRQVRAQVAGABVGHWGTRARQVKTGGRRRARRIMPFLGQ WRSPGWSWIKTEDGWKRCESCSQKLERENNHCNISHSIILNSE GEIFNNEEHEVASKKRKDHFRNDTNTGSFTREKWIYHKEST ERHGYCTLGEAFNRLDFSSAIQDIRFFNYVVKLLQLIAKSQUT LSGVAQKNYFNILDKIVQRVLDDHHNPRLIKDLLQLLSTLCI /N*RSREVCISGSKHQYLDFIRNYSRLATTATGSSDD*ASE\N LTLSDLPLHMLNNILYRPSDGWDITLGQVTPTLYMLSEDRQL KKLCQYHPAEKQFCCHLLILSEKGHLEWKLMYFALQKHYPAKEQ GDTLHFCRHCSILFWKDSGHPCTAADPSCFTPVSPQHFIDLF F  6956 8605 3839 QTSTSIFASPTSPPVLGESVLQDNSFDLNNGSDAEQEEMETQS DFPPSLTQPAPDQSSTIQLHPATSPAVSPTTSPAVSLVVSPAA PEISFEVCPAASTVVSPAVFSVVSPASSAVLPAVSLEVPLTAS TSPKASPVTSPAAFPTASPANKDVSSFLETTADVEEITGEGL ASGSGDVWRRIATETEEVRLELQHWRREVXIKKSSHRWGGET YGGGGKRWKQPFEVIKYLSRNVYHSVRREHFSFSPRMPVGDF EERDTPEGLQWVQLSAEEIPSRIQAITGKRGRRRNTEKARTKE PKVKRGRGRPPKVKITELLNKTDNRPLKKLEAQETLNEEDKAK AKSKKMRQKVQRGECQTTIQGARNKRKGETKSLKQKEAKKK KAEKKKRTKQEKVQRGECQTTIQGQARNKRGETKSLKQKEAKKK KAEKKKTKCREKKEKVKMKEKEEVTKAKPACKA KTLATQRRLEERQRQMILEENKKPTEDMCLTDHGPLPDFSRY GLTLPBGAFSDCLTIVEFLHSPGKVLGFDPAKDVPSLGVLQEC LCQGDSLGEVQDLLVELLKAALHDPGFFSYCQSLKLIGEKVSE	6955	\ \		YRKLLEAGTPSVRKWALRRQNEPLEVRLQRLERERTAKKSRRDN
Aletpekroarlirerearrikerekmdmilraofgoddsam. Alaaemsffolpvsgveldsoliskmafeeonssslh  PPPFFIIFSHPREAGT-%a*KRSGDSECSFVEO-%a*Traaao  *PQR*RWTEGNSPQASAVATPGQGASPAPRCTP*PSRRHRRL PGARPPAG-*AAPAPIKPWLAGPASAPORPAPPLIRT *CAGAAARGPRERDRSPRTPTOGGCSWSEPRTPPAVSASAOTP DAG*AGGR*GQRQRPSTGR*PPGVGGAGRAPHNOVGS VMOAMSTGI  PPGRRQVRAQVAGAPVGHWGTRARQVKTGGRRARRTMFFIGQ WRSPGWSHIKTEDGWRRCESCSKLERENHHCNISHSILINSE GEIPNNEEHEYASKKRKOHFRNDTNOSFYREWIYVHKEST ERHGYCTLGEAFNRLDFSSAIQDIRFNYVVKLLQLIAKSQLT LSGVAQKWYFNILDKTVQKVLDDHHNPRLIKDLLQDLSSTLGI /N*RSREVCISGKHQYLDDJPIRNYSRLATTATGSDD*ASE\N LTLSDLPLHMLNNILYRPSDGWDIITLGQVTPTLYMLSEDRQL KKLCQYHFAEKQFCRHLILSEKGHIEWKLMYFALOKHYPAREQ GDTLHFCRHCSILFWKDSGHPCTAADPDSCTTPVSPQHFIDLF F  6956  8605  3839  QTSTSIFASPTSPPVLGESVLQDNSPDLNNGSDAEQEEMETQS DFPPSLTQPADPOSSTIQLHPARTSPAVSPTTSPAVSLVVSPA PEISPEVCPAASTVVSPAVSTVSPASSAVLPAVSLEVPLTAS TSPKASPVTSPAAAFPTASPANKDVSSFLETTADVEEITGEGL ASGSGDVMRRRIATPEEVRIPLOHGWRREVXIKGSHRWQET YYGPCGKRMKQFPEVIKYLERNVHSVRREHFSFSPRMPVGGF YYGPCGKRMKQFPEVIKYLERNVHSVRREHFSFSPRMPVGGF YYGPCGKRMKQFPEVIKYLERNVHSVRREHFSFSPRMPVGGF PKYKRGRGRPPKVKITELLMKTDNRPLKKLEAQETINEEDKAR AKSKKMRQRVQRGECQTTIQGQARNKRKDETKSLKQKEAKKK KAEKERGKTKQEVLKEKVKRRKKEKEVTKAKREETVKAKPACKA KAEKERGKTKQEVLKEKVVKRRKKETEDMCLTDHOPLPDFSRV GLTLPEGAFSDCCTTIVEFLHSFGKVLGFDPAKDVPSLGVLGEC KTLATQRRLEERGRQQMILEEMKKPTEDMCLTDHOPLPDFSRV GLTLPEGAFSDCCTTIVEFLHSFGKVLGFDPAKDVPSLGVLGEC	6955			ETPEEREVRRMRDREAKRLORMQETDEQRARRLQRDREAMRLKR
ALAZEMSFFQLPVSGVELDSQLLGWAFEEQNSSSLH  1 PPPFFITSHPREAGT*AG*KRSGDSECSPPVEQ*A*TRAAAQ)  *PPQR*RWTEGMSPQASAVATPGGGASPAAPRCTP*PSRRHRRL PGARPPAG*AAPAPTKPWLAGPASAPQPGAAPLSPPAPPLIRT. *CAGAAARGRPRRDRSPRTTRTGGGWSEPFTPPAVSASAQTP DAG*AGGR*GQRQRPSTGR*PPGGGWSEPFTPPAVSASAQTP DAG*AGGR*GQRQRPSTGR*PPGGGWSEPFTPAVSASAQTP AS*RAGWQR*PGP/REWGL*EPQGBEMSGPGGAPPNQVGS VMQAMSTGI  PFGRRQVRAQVAGAPVGHWGTRARQVKTGGRRARRTMFFLGQ WRSPGWSWIKTEDGWKRCESCSCKLERENNHCNISHSILINSE GEIPNNEEHEYASKKRKKDHFRNDTNTQSFYREKWIYVHKEST ERHGYCTLGEAFNRLDFSSAIQDIRFNYVVKLLQLIAKSQLT LSGVAQKNYFNILDKLYQXVLDDHHNPRIKDLLQDLSSTLGI /N*RSREVCISCKHQYLDLPIRNYSRLATTATGSSDD*ASE\N LTLSDLPLHMLNNILVRFSDGNDITTLGQVTPTLYMLSEDRQL KKLCQYHFAEKQFCRHLILSEKGHIEWKLMYFALQKHYPAKEQ GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLF F  6956  8605  3839  OTSTSIFASPTSPPVLGESVLQDNSFDLNNGSDAEQEEMETQS DFPPSLTQPAPDQSSTIQLHPATSPAVSPTTSPAVSLVVSPAA PEISPEVCPAASTVVSPAVFSVVSPASSAVLPAVSLEVPLTAS TSPKASPVTSPAAAFPTASPANDVSSFLETTADVEITTGGLI ASGSGDVMRRRIATPEEVLPLQHGWRREVRIKKGSHRWQGET YGGPCGKRMKQFPEVIKYLSRNVVHSVRREHFSFSPRMPVGDF EERDTPEGLQWVQLSAEEIPSRIQAITGKRGRPRNTEKARTKE PKVKRGRGRPPKVKITELLMKTDNRPLKKLEAQETLNEEDKAK AKSKKMRQKVQRGECTTIQGQARRKKQFTESLKQKEAKKK KAEKEKGKTKQERLKEKVKREKKEKVKMKKEKEEVTKAKPACKA KTLATQRRLEERQRQOMILEEMKKPTEDMCLTDHQPLPDFSRV GLTLPBGAFSDCLTIVEFLHSFGKVLGFDPAKDVPSLGVLQEC	6955	1		AIETPEKROARLIREREAKRLKRRLEKMDMMLRAQFGQDPSAMA
1 PPPPFIIPSHPREAGT*AG*KRSGDSECSPPVEQ*A*TRAAAO  *PQR*RWTEGNSPQASAVATPGQGASPAAPRCTP*PSRRHRRL PGARPPAG*AAPAPTKWLAGPASAAPPGGASPAAPRCTP*PSRRHRRL *CAGAAAGRPRAGRSPRPRTPGGCSWSEPRTPPAVSASAQTP DAG*AGGR*GQRQRPSTGR*PPGVGAGGRSHRREGTIPGNPHP AS*RAGWQR*PGP/REWGL*EPQGEEMSGPGGPGAPPNQVGS VMQAMSTGI  *PPPREQVRAQVAGAPVGHWGTRARQVKTGGRRARRIMFFLGQ WRSPGWSWIKTEDGWKRCESCSQKLERENHCNISHSIILNSE GEIFNNEEHYASKKKKKDHFRNDTNTQSFYREKWIYVHKEST ERHGYCTLGEAFRRLDFSSATQDIRRFNYVWKLLQLTAKSQLT LSGVAQKNYFNILDKIVQKVLDDHNPRLIKDLLQDLSSTLCI /N*RSREVCISGRHQYLDLPIRNYSRLATTATGSSDD*ASE\N LTLSDLPLHMLNNILYRPSDGWDIITLGQVTPTJYMLSEDRQL KKLCQYHFAEKQPCRHLILSEKGHTEWKLMYFALQKHYPAREQ GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLF F  6956  8605  3839  QTSTSIFASPTSPPVLGESVLQDNSFDLNNGSDAEQEEMETQS DFPPSLTQPAPDQSSTIQLHPATSPAVSPTTSPAVSLVVSPAA PEISPEVCPAASTVVSPAVFSVSPASSAVLPAVSLEVPLTAS TSPKASPVTSPAAAFPTASPANKDVSSFLETTADVEEITGEGL AGSGDVMRRIATPEEVRLPLQHGWRREVRIKKGSIRWQGET YYGPCGKRMKQFPEVIKYLSRNVVHSVRREHFSFSPRMPVGDF EERDTPEGLQWVQLSAEEIPSRIQAITGRGRPRNTEKARTKE PKVKRGRGRPPKVKITELLNKTDNRPLKKLEAQETLNEEDKAK AKSKKMRQKVQRGEQTTIQQQARNKRKQETKSLKQKEAKKK KAEKEKGKTKQEKLKEVKREKEKVKMKEKEEVTKAKPACKA KTLATQRRLEERQRQQMILEEMKKPTEDMGLTDHQPLPDFSRV GLTLPBGAFSDCLTIVEFLHSFGKVLGFDPAKDVPSLGVLQEG	6955			ALAAEMNFFOLPVSGVELDSQLLGKMAFEEQNSSSLH
*PQR*RWTEGNSPQASAVATEGGASPAAPRCTP*PSRRHRRL PGARPPAG*AAPAPTKPWLAGPASAPQPGAAPLSPAPPLIRTL *CAGAAARGPRRADRSPRPRTPGGCSWSEPRTPAVSASAQTP DAG*AGGR*GQRQRPSTGR*PPGVGGAGRSHRREGTIPGNPHP AS*RAGWQR*PGP/REWGL*EPQGEEMSGPGGPGAPPNQVGS VMQAMSTGI  PPGRRQVRAQVAGAPVGHWGTRARQVKTGGRRARRIMPFLGQ WRSPGWSWIKTEDGWKRCESCSQKLERENNHCNISHSIILNSE GEIFMNEEHEYASKKRKKDHFRNDTNTQSFYREKWIYVHKEST LSGVAQKNYFNILDKIVQKVLDDHHNPRLIKDLLQDLSSTLCI /N*RSREVCISGKHQYLDLPIRNYSRLATTATGSSDD*ASE\N LTLSDLPLHMLNNILYRPSDGWDIITLGQVTPTLYMLSEDRQL KKLCQYHFAEKQFCRHLILSEKGHTEWKLMYFALQKHYPAREQ GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLF F  6956 8605 3839 QTSTSIFASPTSPPVLGESVLQDNSFDLNNGSDAEQEEMETQS DFPPSLTQPAPDQSSTIQLHPATSPAVSPTTSPAVSLVVSPAA PEISPEVCPAASTVVSPAVFSVVSPASSAVLPAVSLEVPLTAS TSPKASPVTSPAAAFPTASPANKDVSSFIETTADVEEITGEGL AGSGGDVMRRRIATPEEVRLPLQHGWRREVRIKKGSKRWQGET YYGPCGKRMKQFPEVIKYLSRNVVHSVRREHFSFSPRMPVGDF EERDTPEGLQWVQLSAEEIPSRIQATTGRRGRPRNTEKARTKE PKVKRGGRRPPKVRITELLINKTDNRPLKKLEAQETILNEEDKAK KAEKEKGKTKQEKLKEVKREKEKVKMKEKEEVTKAKPACKA KTLATQRRLEERQRQQMILEEMKKPTEDMGLTDHQPLPDFSRV GLTLPBGAFSDCLTIVEFLHSFGKVLGFDPAKDVPSLGVLQEG LCGGDSLGEVQDLLVRLKAALHDPGFPSYCQSLKILGEKVSE	6955		010	PPPPFIIPSHPREAGT*AG*KRSGDSECSPPVEQ*A*TRAAAQN
PGARPPAG*AAPAPTKPMLAGPASAPQGAAPLSPPAPPLIRT  *CAGAAARGRRRDRSPRPTPGGCSWSEPRTPPAVSASAQTP DAG*AGGR*GQRQPSTGR*PPGVGGAGRSHRREGTIPGNPHP AS*RAGWQR*PGP/REWGL*EPQGBEMSGPGGPAPPNQVGS VMQAMSTGI  PPGRRQVRAQVAGAPVGHWGTRARQVKTGGRRARRIMPFLGQ WRSPGWSWIKTEDGWKRCESCSQKLERENNHCNISHSIILNSE GEIFNNEEHEYASKKRKDHFRNDTNTQSFYREKWIYVHKEST ERHGYCTLGEAFNRLDFSSAIQDIRRFNYVVKLLQLIAKSQLT LSGVAQKNYFNILDKIVQRVLDDHHNPRLIKDLLQDLSSTLGL /N*RSREVCISGKHQYLDLPIRNYSRLATTATGSSDD*ASE\N LTLSDLPLHMLNNILYRFSDGWDIITLGQVTPTLYMLSEDRQL KKLCQYHFAEKQFCRHLILSEKGHIEWKLMYFALQKHYPAREQ GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLF F  6956  3839  OTSTSIFASPTSPPVLGESVLQDNSFDLNNGSDAEQEEMETQS DFPPSLTQPAPDQSSTIQLHPATSPAVSPTTSPAVSLVVSPAA PEISPEVCPAASTVVSPAVSVVSPASSAVLPAVSLEVPLTAS TSPKASPVTSPAAAFPTASPANKDVSSFLETTADVEEITGBGL ASGSGDVMRRIATTEEVKLPLQHGWRREVRIKKGSHRWQGET YYGPCGKRMKQFPEVIKYLSRNVVHSVRREHFSFSPRMPVGDF EERDTTEGLQWVQLSAEEITSRIQAITGKRGRPRNTEKARTKA PKVKRGRGPPPVVKITELLNKTDNRPLKKLEAQETLMEEDKAK ARSKKKMRQKVQRGECQTTIQGQARNKRKQETKSLKQKEAKKK KAEKEKGKTKQEKLKEKVKREKKEKVKMKEKEEVTKAKPACKA KTLATQRRLEERQRQMILLEMKKPTEDMCLTDHQPLPDFSRV KAEKEKGKTKQEKLKEKVKREKKEKVKMKEKEEVTKAKPACKA KTLATQRRLEERQRQMILLEMKKPTEDMCLTDHQPLPDFSRV GLTLPSGAFSDCLTIVVFFLHSFGKVLGFDPAKDVPSLGVLQEG GLTLPSGAFSDCLTIVVFFLHSFGKVLGFDPAKDVPSLGVLQEG GLTLPSGAFSDCLTIVVFFLHSFGKVLGFDPAKDVPSLGVLQEG LCOGDSLGEVQDLLVVLLKAALHDPGFFSYCOSLKILGEKVGE		619	819	*POR*RWTEGNSPOASAVATPGQGASPAAPRCTP*PSRRHRRLP
*CAGAARGRPRRDRSPRPTFGGCSWSEPRTPPAVSASAQTP DAG*AGGR*GQRQRPSTGR*PPGVGGAGRSHRREGTIPGNPHP AS*RAGWQR*PGP/REWGL*EPQGBEMSGPGGPGAPPNQVGS VMQAMSTGI  6955 1968 782 PPGRRQVRAQVAGAPVGHWGTRARQVKTGGRRARRTMPFLGQ WRSPGWSWIKTEDGWKRCESCSOKLERENNHCNISHSIILNSE GEIFNNEEHEYASKKKKDHFRNDTNTQSFYREKWIYVHKEST ERHGYCTLGEAFNRLDFSSALQDIRRFNYVVKLLQLIAKSQLT LSGVAQKNYFNILDKIVQKVLDDHHNPRLIKDLLQDLSSTLCI /N*RSREVCISGKHQYLDLPIRNYSRLATTATGSSDD*ASE\N LTLSDLPHHMLNNILYRFSDGMDIITLGQVTPTLYMLSEDRQL KKLCQYHFAEKQFCRHLILSEKGHIEWKLMYFALQKHYPAKEQ GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLF F  6956 8605 3839 QTSTSIFASPTSPPVLGESVLQDNSFDLNNGSDAEQEEMETQS DFPPSLTQAPDQSSTIQHPATSPAVSPTTSPAVSLVVSPAA PEISPEVCPAASTVVSPAVFSVVSPASSAVLPAVSLEVPLTAS TSPKASSVTSPAAAFPTASPANKDVSSFLETTADVEEITGEGL ASGSGDVMRRIATPEEVRLPLQHGWRREVRIKKGSHRWQGET YYGPCGKRMKQFPEVIKYLSRNVVHSVRREHFSFSSRMPVGDF EERDTPPEGLQWVQLSAEEIPSRIQAITGKRGRPRNTEKARTKE PKVKRGGGRPPKVKITELLNKTDNRPLKKLEAQETLNEEDKAK AKSKKKNRQKVQRGECQTTIQGQARNKRKQETKSLKQKEAKKK KAEKEKGKTKQEKLKEKVKREKKEVVKMKEKEEVTKAKPACKA KTLATQRRLEERQRQQMILEENKKPEDMCLTDHQPLPDFSRV GLTLPSGAFSDCLTIVEFLHSFGKVLGFDPAKDVPSLGVLGEG LCGGDSLGEVQDLLVRLLKAALHDPGFPSYCQSLKILGEKVSE GLTLPSGAFSDCLTIVEFLHSFGKVLGFDPAKDVPSLGVLGEG			ļ	PGARPPAG*AAPAPTKPWLAGPASAPQPGAAPLSPPAPPLIRTR
DAG*AGGR*GQRQRPSTGR*PPGVGGAGRSHRREGTIPGMPHP AS*RAGWQR*PGP/REWGL*EPQGEEMSGPGGPGAPPNQVGS VMQAMSTGI  PPGRRQVRAQVAGAPVGHWGTRARQVKTGGRRARRIMPFLGQ WRSPGWSWIKTEDGWKRCESCSQKLERENNHCNISHSIILNSE GEIFNNEEHEVASKKRKKDHFRNDTNTQSFYREKWIYVHKEST ERHGYCTLGBAFNRLDFSSAIQDIRRFNYVVKLLQLIAKSQLT LSGVAQKNYFNILDKTVQKVLDDHNMPRLIKDLLQDLSSTLGI /N*RSREVCISGKHQYLDLPIRNYSRLATTATGSSDD*ASE\N LTLSDLPLHMLNNILYRPSDGMDIITLGQVTPTLYMLSEDRQL KKLCQYHFAEKQFCRHLILBEKGHIEWKLWFALQKHYPAKEQ GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLF F  6956  8605  3839  QTSTSIFASPTSPPVLGESVLQDNSFDLNNGSDAEQEEMETQS DFPPSLTQPAPDQSSTIQLHPATSPAVSPTTSPAVSLVVSPAA PEISPEVCPAASTVVSPAVFSVVSPASAVLPAVSLEVPLTAS TSPKASPVTSPAAFPTASPANKDVSSFLETTADVEEITGBGL ASGSGDVMRRRIATPEEVRLPLQHGWRREVRIKKGSHRWQGET YYGPCGRMKQFPEVIKYLSRNVVHSVRREHFSFSPRMPVGDF EERDTPEGLQWVQLSAEEIPSRIQAITGKRGRPRNTEKARTKE PKVKRGRGRPPKVKITELLNKTDNRPLKKLEAQETLNEEDKAR AKSKKKNRQKVQRGECCTTIQGQARNKRKQETKSLKQKEAKKK KAEKEKGKTKQEKLKEXVKREKKEVVKMKEKEEVTKAKPACKA KTLATQRRLEERQRQQMILEEMKKPTEDMCLTDHQPLPDFSRV GLTLPSGAFSDCLTIVEFLHSFGKVLGFDPAKDVPSLGVLGEG LCQGDSLGEVQDLLVRLLKAALHDPGFPSYCQSLKILGEKVSE				*CAGAAARGRPRRDRSPRPRTPGGCSWSEPRTPPAVSASAQTPS
AS*RAGWQR*PGP/REWGL*EPQGBEMSGPGGPGAPPNQVGS VMQAMSTGI  PFGRRQVRAQVAGAPVGHWGTRARQVKTGGRRARRIMFFLGQ WRSPGWSWIKTEDGWKRCESCSCKLERENNHCNISHSIILNSE GEIFNNEEHEYASKKRKKDHFRNDTNTQSFYREKWIYVHKEST ERHGYCTLGEAFNRLDFSSAIQDIRRFNYVVKLLQLIAKSQLT LSGVAQKNYFNILDKIVQRVLDDHHNPRLIKDLLQDLSSTLGI /N*RSREVCISKHQYLDLPIRNYSRLATTATGSSDD*ASE\N LTLSDLPHHMLNNILYRPSDGWDIITLGGVTPTLYMLSEDRQL KKLCQYHFAEKQFCRHLILSEKGHIEWKLMYFALQKHYPAKEQ GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLF F  G956 8605 3839 QTSTSIFASPTSPPVLGESVLQDNSFDLNNGSDAEQEEMETQS DFPPSLTQPAPDQSSTIQLHPATSPAVSPTTSPAVSLVVSPAA PEISPEVCPAASTVVSPAVFSVVSPASSAVLPAVSLEVPLTAS TSPKASPVTSPAAAFPTASPANKDVSSFLETTADVEEITGGL ASGSGDVMRRRIATPEEVKLPLQHGWRREVRIKKGSHRWQGET YYGPCGKRMKQFPEVIKYLSRNVVHSVRREHFSFSPRMVGDF EERDTPEGLQWVQLSAEEIPSRIQAITGKRGRPRNTEKARTKE PKVKRGRGRPPKVKITELLNKTDNRPLKKLEAQETLNEEDKAK AKSKKKMRQKVQRGECQTTIQGQARNKRKQETKSLKQKEAKKK KAEKEKGTTKQEKLKEKVKREKKEKVKMKEKEVTKAKPACKA KTLATQRRLEERQRQMILEEMKKPTEDMCLTDHQPLDFSRV GLTLPSGAFSDCLTIVEFLHSFGKVLGFDPAKDVPSLGVLOGG GLTLPSGAFSDCLTIVEFLHSFGKVLGFDPAKDVPSLGVLOGG LCGGDSLGEVQDLLVRLLKAALHDPGFPSYCQSLKILGEKVSE		ļ		DAG*AGGR*GORORPSTGR*PPGVGGAGRSHRREGTIPGNPHPR
VMQAMSTGI  PPGRRQVRAQVAGAPVGHWGTRARQVKTGGRRRARRIMFFLGQ WRSPGWSWIKTEDGWKRCESCSQKLERENNHCNISHSIILNSE GEIFNNEEHEYASKKRKKDHFRNDTNTQSFYREKWIYVHKEST ERHGYCTLGEAFNRLDFSSAIQDIRRRNYVVKLLQLIAKSQLT LSGVAQKNYFNILDKIVQKVLDDHHNPRLIKDLLQDLSSTLCI /N*RSREVCISGKHQYLDLPIRNYSRLATTATGSSDD*ASE\N LTLSDLPLHMINNILYRFSDGWDIITLGQVTPTLYMLSEDRQL KKLCQYHFAEKQFCRHLILBEKGHIEWKLMYFALQKHYPAKEQ GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLF F  6956  8605  3839  OTSTSIFASPTSPPVLGESVLQDNSFDLNNGSDAEQEEMETQS DFPPSLTQPAPDQSSTIQLHPATSPAVSPTTSPAVSLVVSPAA PEISPEVCPAASTVVSPAVFSVSPASSAVLPAVSLEVPLTAS AGSGDVMRRRIATPEEVRLPLQHGWRREVRIKKGSHRWQGET YYGPCGKRMKQFPEVIKYLSRNVVHSVRREHFSFSPRMPVGDF EERDTPEGGLQWVQLSAEEIPSRIQAITGKRGRPRNTEKARTKE PKVKRGRGRPPKVKITELLNKTDNRPLKKLEAQETLNEEDKAK AKSKKKMRQKVQRGECQTTIQGQARNKRKQETKSLKQKEAKKK KABKEKGKTKQEKLKEKVKREKKEKVKMEKEETKALPQLEDGAK KTLATQRRLEERQRQMILEEMKKPTEDMCLTDHQPLPDFSRV GLTLPSGAFSDCLTIVEFLHSFGKVLGFPPAKDVPSLGVLOEG LCOGDSLGEVQDLLVELLKAAHHDPGFPSYCQSLKILGEKVSE			i	AS*RAGWOR*PGP/REWGL*EPOGEEMSGPGGPGGAPPNQVGSS
6955  1968  782  PFGRRQVRAQVAGAPVGHWGTRARQVKTGGRRRARTMFFLGQ WRSPGWSWIKTEDGWKRCESCSQKLERENHCHISHSIILNSE GEIFNNEEHEYASKKRKKDHFRNDTNTQSFYREKWIYVHKEST ERHGYCTLGEAFNRLDFSSAIQDIRRFNYVVKLLQLIAKSQLT LSGVAQKNYFNILDKIVQKVLDDHHNPRLIKDLLQDLSSTLCI /N*RSREVCISGKHQYLDLPIRNYSRLATTATGSSDD*ASE\N LTLSDLPLHMLNNILYRFSDGWDIITLGQVTPTLYMLSEDRQL KKLCQYHFAEKQFCRHLILSEKGHIEWKLMYFALQKHYPAKEQ GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLF F  6956  8605  3839  QTSTSIFASPTSPPVLGESVLQDNSFDLNNGSDAEQEEMETQS DFFPSLTQPAPDQSSTIQLHPATSPAVSPTTSPAVSLVVSPAA PEISPEVCPAASTVVSPAVFSVVSPASSAVLPAVSLEVPLTAS TSPKASPVTSPAAAFPTASPANKDVSSFLETTADVEEITGEGL ASGSGDVMRRRIATPEEVRLPLQHGWRREVRIKKGSHRVGGET YYGPCGKRMKQFPEVIKYLSRNVVHSVRREHFSFSPRMPVGDF EERDTPEGLQWVQLSAEEIPSRIQAITGKRGRPRNTEKARTKE PKVKRGRGRPPKVKITELLNKTDNRPLKKLEAQETLNEEDKAK AKSKKMRQXVQRGECQTTIQGQARNKRKQETKSLKQKEAKKK KABKEKGKTKQEKLKEKVKREKKEKVKMEKEEVTKAXPACKA KALKEKGKTKQEKLKEKVKREKKEKVKMEKEEVTKAXPACKA KALKEKGKTKQEKLKEKVKREKKEKVKMEKEEVTKAXPACKA GLTLPSGAFSDCLTIVEFLHSFGKVLGFPPAKDVPSLGVLOEG GLTLPSGAFSDCLTIVEFLHSFGKVLGFPPAKDVPSLGVLOEG LCOGDSLGEVQDLLVELLKAALHDPGFPSYCQSLKILGEKVSE			i	
WRSPGWSWIKTEDGWKRCESCSQKLERENNHCNISHSIILNSE GEIFNNEEHEYASKKRKKDHFRNDTNTQSFYREKWIYVHKEST ERHGYCTLGEAFNRLDFSSAIQDIRRFNYVVKLLQLIAKSQLT LSGVAQKNYFNILDKIVQKVLDDHHNPRLIKDLLQDLSSTLCI /N*RSREVCISGKHQYLDLPIRNYSRLATTATGSSDD*ASE\N LTLSDLPLHMLNNILYRPSDGWDIITLGQVTPTLYMLSEDRQL KKLCQYHFAEKQFCRHLILSEKGHIEWKLMYFALQKHYPAKEQ GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLF F  6956 8605 3839 QTSTSIFASPTSPPVLGESVLQDNSFDLNNGSDAEQEEMETQS DFFPSLTQPAPDQSSTIQLHPATSPAVSPTTSPAVSLVVSPAA TSPKASPVTSPAASFTASPANKDVSFLETTADVEEITGGL ASGSGDVMRRRIATPEEVRLPLQHGWRREVRIKKGSHRWQGET YYGPCGKRMKQFPEVIKYLSRNVVHSVRREHFSFSPRMPVGDF EERDTPEGLQWVQLSAEEIPSRIQAITGKRGRPRNTEKARTKE PKVKRGRGRPPKVKITELLIKTDNRPLKKLEAQETLNEEDKAK AKSKKMRQXVQRGECQTTIQGQARNKRKQETKSLKQKEAKKK KAEKKGKTKQSKLKEKKVKKEKKEEVVTKAKPACKA KTLATQRRLEERQRQQMILEEMKKPTEDMCLTDHQPLPDFSRV GLTLPSGAFSCDLTIVEFLHSFGKVLGFDPAKDVPSLGVLQEG LCQGDSLGEVQDLLVRLLKAALHDPGFPSYCQSLKILGEKVSE		1000	792	PPGRROVRAOVAGAPVGHWGTRAROVKTGGRRRARRTMPFLGQD
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ERHGYCTLGEAFNRLDFSSAIQDIRRFNYVVKLLQLIAKSQLT LSGVAQKNYFNILDKIVQKVLDDHHNPRLIKDLLQDLSSTLCI /N*RSREVCISGKHQYLDLPIRNYSRLATTATGSSDD*ASE\N LTLSDLPLHMLNNILYRFSDGWDIITLGQVTPTLYMLSEDRQL KKLCQYHFAEKQFCRHLILSEKGHIEWKLMYFALQKHYPAKEQ GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLF F  6956 8605 3839 QTSTSIFASPTSPPVLGESVLQDNSFDLNNGSDAEQEEMETQS DFPPSLTQPAPDQSSTIQLHPATSPAVSPTTSPAVSLVVSPAA PEISPEVCPAASTVVSPAVFSVVSPASAVLPAVSLEVYLTAS TSPKASPVTSPAAFPTASPANKDVSSFLETTADVEEITGEGL ASGSGDVMRRRIATPEEVRLPLQHGWRREVRIKKGSHRWQGEI YYGPCGKRMKQFPEVIKXLSRNVVHSVRREHFSFSPRMPVGDF EERDTPEGLQWVQLSAEEIPSRIQAITGKRGRPRNTEKARTKE PKVKRGRGRPPKVKITELLNKTDNRPLKKLEAQETLNEEDKAK AKSKKMRQXVQRGECQTTIQGQARNKRKQETKSLKQKEAKKK KAEKEKGKTKQEKLKEXVKMKEKEEVTKAKPACKA KTLATQRRLEERQRQQMILEEMKKPTEDMCLTDHQPLPDFSRV GLTLPSGAFSCDLTIVEFLHSFGKVLGFDPAKDVPSLGVLQEG LCQGDSLGEVQDLLVRLLKAALHDPGFPSYCQSLKILGEKVSE	6956		<b>\</b>	GETFNNEEHEYASKKRKKDHFRNDTNTQSFYREKWIYVHKESTK
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LCOGDSLGEVQDLLVRLLKAALHDPGFPSYCQSLKILGEKVSE				KITATOKKUBEKOKOONI DEGAMAKE EDINGI IDIQEBER SKAF
LCQGDSLGEVQDLLVRLLKAALHDPGFPSYCQSLKILGEKVSB			I	GLTDPSGAKSDCDTIVELTMSIGKVDGFDVAKDVKSDGVDGGD
THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O				LCQGDSLGEVQDLLVKLLKAALHDPGFPSICQSLKILGEKVSKI
PLTRDNVSEILRCFLMAYGVEPALCDRLRTOPFOAGPPOQUAG				PLTRDNVSEILRCFLMAYGVEPALCDRLRTQPFQAQPPQQKAAV
LAFLVHELNGSTLIINEIDKTLESMSSYRKNKWIVEGRLERLE				LAFLVHELNGSTLIINEIDKTLESMSSYRKNKWIVEGRLRRLKT
VLAKRTGRSEVEMEGPEECLGRRRSSRIMEVTSGMEBEEEEES				VLAKRTGRSEVEMEGPEECLGRRRSSRIMEVTSGMEBEEEEESI
AAVPGRRGRRDGEVDATASSIPELERQIEKLSKRQLFFRKKLI				
SSQMLRAVSLGQDRYRRRYWVLPYLAGIFVEGTEGNLVPEEVI	]			AAVPGRRGRRDGEVDATASSIPELERQIEKLSKRQLFFRKKLLH
				AAVPGRRGRRDGEVDATASSIPELERQIEKLSKRQLFFRKKLLH SSQMLRAVSLGQDRYRRRYWVLPYLAGIFVEGTEGNLVPEEVIK KETDSLKVAAHASLNPALFSMKMELAGSNTTASSPARARGRPRK

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	Codon, /=possible nucleotide deletion,
	amino acid	sequence	Codon, /=possible nucleocide defection,
	sequence		\=possible nucleotide insertion)
			TKPGSMQPRHLKSPVRGQDSEQPQAQLQPEAQLHAPAQPQPQLQ
			LQLQSHKGFLEQEGSPLSLGQSQHDLSQSAFLSWLSQTQSHSSL
		į	LSSSVLTPDSSPGKLDPAPSQPPEEPEPDEAESSPDPQALWFNI
		1	SAQMPCNAAPTPPPAVSEDQPTPSPQQLASSKPMNRPSAANPCS
	<b>\</b>		PVQFSSTPLAGLAPKRRAGDPGEMPQSPTGLGQPKRRGRPPSKF
	1	1	FKQMEQRYLTQLTAQPVPPEMCSGWWWIRDPEMLDAMLKALHPR
			GIREKALHKHLNKHRDFLQEVCLRPSADPIFEPRQLPAFQEGIM
			SWSPKEKTYETDLAVLQWVEELEQRVIMSDLQIRGWTCPSPDST
	1		REDLAYCEHLSDSQEDITWRGRGREGLAPQRKTTNPLDLAVMRL
			AALEONVERRYLREPLWPTHEVVLEKALLSTPNGAPEGTTTEIS
			YEITPRIRVWRQTLERCRSAAQVCLCLGQLERSIAWEKSVNKVT
			CLVCRKGDNDEFLLLCDGCDRGCHIYCHRPKMEAVPEGDWFCTV
			CLAQQVEGEFTQKPGFPKRGQKRKSGYSLNFSEGDGRRRRVLLR
			GRESPAAGPRYSEEGLSPSKRRRLSMRNHHSDLTFCEIILMEME
			SHDAAWPFLEPVNPRLVSGYRRIIKNPMDFSTMRERLLRGGYTS
	Į.	Ì	SEEFAADALLVFDNCQTFNEDDSEVGKAGHIMRRFFE\SRWEEF
			YQGKQGQSVRQGRWGVTLWHLPPTFQTKTCHFHLLMLPWVQTQV
}			RYNPDF
6957	82	3514	HLIVAMPEPTKKEENBVPAPAPPPEEPSKEKEAGTTPAKDWTLV
6957	02	-	ETPPGEEQAKQNANSQLSILFIEKPQGGTVKVGEDITFIAKVKA
	1		EDLSEKPTINGSRKWMDLASKAGKHLQLKBTFERHSRVYTFEMQ
l	1		IIKAKDNFAGNYRCEVTYKDKFDSCSFDLEVHESTGTTPNIDIR
			SAFKRSGEGQEDAGELDFSGLLKRREVKQQEEEPQVDVWELLKN
}	}		TKPSEYEKIAFQYESPTCSGMLKRLKRSIREEKKSAAFAKILDP
1		ļ	VYQVDKGGRVRFVVELADPKLEVKWNKNGQELRPSTKYIFEDTR
1			COSILNIDNCOMTDDSEYYVTAGDEKCSTELLVREPPIMVTKQL
ł			EDTTDYCGERVELECEVSEDDAQVKWFKNGBEIILVQTRYRIRV
			EGKKHILIIEGATKADAADYSVMTTGGQSSAKLSVDLKPLKILT
1			PLTDQTVNLGKEICLKCEISENIPGKWTKNGLPVQESDRLKVVH
1			KGRIHKLVIDHALTEDEGDYVFAPDAYNVTLPAKVHVIDPPKII
Ì			LDGLDADNTVTVIAGNKLRLEIPISGEPPPKAMWSRGDKAIMEG
			SGRIRTESYPDSSTLVIDIAERDDSGVYHINLKNEAGEAHASIK
	1	1	VKVVDFPDPPVAPTVTEVGDDWCIMNWEPPAYDGGSPILGYFIE
	1	1	RKKKQSSRWMRLNFDLCKETTFEPKKMIEGVAYEVRIFAVNA\1
	1		GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI
	}	-{	GAAGLDGYVLEYCFEGSTSAKQSDENGEAAYDLPAEDWIVANKD
			LIDKTKFTITGLPTDAKIFVRVKAVNAAGASEPKYYSQPILVKE
		1	IIEPPKIHSPKHLKQTYIRRVGDRVILVIPFQGKPRPELTWKKD
}		}	GAELDKNQINIRNSETDTIIFIRKAERSHSGKYDLQVKVDKFVE
			TASIDIRIIDRPGPPQIVKIEDVWGRNVALTWTPPKDDGNAAIT
			GYTIQKADKKSMEWLRVIEHIIEPVPHTELVIGNEYYFRVFSEN
}		1.	MCGLSEDATMTKESAVIARDGKIYKNPVYEDFDFSEAPMFTQPL
1			VNRLCHSGYMATLNCSVRGNPKPKITWMKNKVAIVDDPRYRMFS
1	İ		NQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKVIAQ
			PRISRVKTEGSQGSSAMDFSVKVDIEKEVTCPICLELLTEPLSL
6958	274	1663	DCGHSFCQACITAKIKESVIISRGESSCPVCQTRFQPGNLRPNR
1			HLANIVERVKEVKMSPQEGQKRDVCEHHGKKLQIFCKEDGKVIC
			WVCELSQEHQGHQTFRINEVVKECQEKLQVALQRLIKENQEAEK
		Í	LEDDIRQERTAWKNYIQIBRQKILKGFNEMRVILDNEEQRELQK
		}	PEDDIKÉRKIHMENTIÁTPEÁVITOGODS GALTEDI UDDI DUGGARM
	1		LEEGEVIVLDNLAAATDQLVQQRQDASTLISDLQRRLRGSSVEM
	Į.	1	LQDVIDVMKRSESWTLKKPKSVSKKLKSVFRVPDLSGMLQVLKE
		<b>}</b>	LTDVQYYWVDVMINPGSATSNVAISVDQRQVKTVRTCTFKNSNP
		)	CDFSAFGVFGCQYFSSGKYYWEVDVSGKIAWILGVHSKISSLNK
1		1	RKSSGFAFDPSVNYSKVYSRYRPQYGYWVIGLQNTCEYNAFEDS
			SSSDPKVLTLFMAV\LPVVLGFS
6959	i	1469	SLVHVVEFGRGIBDFPYLFFQLTHCQQRICSVTQAGVQWCDHSS
ردر د			

Predicted   Predicted end   Deginning   Deginning   Deginning   Deginning   Decation   Decation   Corresponding   Decation   Corresponding   Decation   Corresponding   Decation   Corresponding   Decation   Corresponding   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decatio	, E= ne,  Stop  SPPNVT GLPLS AQCGL VGGLSV ILLELG KEQVIH MVNYMQ NKGPFF DIRSDV
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence nce Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence	DEPONT  GLPLS  AQCGL  VGGLSV  VLLELG  KEQVIH  MVNYMQ  NRGPFF  DIRSDV
location corresponding to first amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence s	Stop  DPPNVT  GLPLS  AQCGL  GGLSV  KLLELG  KEQVIH  MVNYMQ  MKGPFF  DIRSDV
to first amino acid residue of amino acid sequence  L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *= Codon, /=possible nucleotide deletion, \	LPPNVT EGLPLS LAQCGL VGGLSV VLLELG KEQVIH MVNYMQ NRGPFF DIRSDV
to first amino acid residue of amino acid sequence  P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *= Codon, /=possible nucleotide deletion, _possible nucleotide insertion)  LQPQTPGLNQSSHLSLLSSRDYRMLSSFNEWFWQDRFWL WTSLEDRDGRVYPHPQDLLAALPLALVLLAMRLAFERFI RWLGVRDQTRRQVKPNATLEKHFLTEGHRPKEPQLSLLF TLQQTQRWFRRRRNQDRPQLTKKFCEASWRFLFYLSSF\ LYHESWLWAPVMCWBRYPNQLTLSCPAADSEA\SLYWWY FYLSLLIRLPFDVKRKGGGPSSIKPRPHYDPPSTA\DFF HFVAVILMTFSYSANLLRIGSLVLLLHDSSDYLLEACKO YQQVCDALFLIFSFVFFTTRLVLFPTQILYTTYYESIST GYYFFNGLLMLLQLLHVFWSCLILRMLYSFMKKGQMEKI EESDSSEEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVI RHTTAT  AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLL PCSDPERKRFRRNSESESGSEASSPDYFGPPAKNGVASI KEENPRRA\SKAVEESSDEERQRDLPAQRGEESSEBEE TRKKPVVKKQAPGKASVSRKQAREESEERSEAEPVQRTA KGTKSLKESEQESEEEILAQKKEQREEEVEEEERBDE PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEEQK DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDGS KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKN	LPPNVT EGLPLS LAQCGL VGGLSV VLLELG KEQVIH MVNYMQ NRGPFF DIRSDV
amino acid residue of amino acid sequence  S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Codon, /=possible nucleotide deletion, \ -possible nucleotide insertion)  LQPQTPGLNQSSHLSLLSSRDYRMLSSFNEWFWQDRFWL WTSLEDRDGRVYPHPQDLLAALPLALVLLAMRLAFERFI RWLGVRDQTRRQVKPNATLEKHFLTEGHRPKEPQLSLLFTLQTQRWFRRRRNQDRPQLTKKFCEASWRFLFYLSSFVLYHESWLWAPVMCWDRYPNQLTLSCPAADSEA\SLYWWY FYLSLIRLPFDVKRKGGGPSSIKPRPHYDPPSTA\DFF HFVAVILMTFSYSANLLRIGSLVLLLHDSSDYLLEACK YQQVCDALFLIFSFVFFTTRLVLFPTQILYTTYYESIST GYYFFNGLLMLLQLLHVFWSCLILRMLYSFMKKGQMEKI EESDSSEEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVWRHTTAT  AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYL HLEPEKQALKRLVEEEPLKMQVDEAASREDKLDLTKKK PCSDPERKRFRRNSESESGSEASSPDYFGPPAKNGVASI KEENPRRA\SKAVEESSDEERQRDLPAQRGEESSEBEE TRKKPVVKKQAPGKASVSRKQAREESEESEAEPVQRTA KGTKSLKESEQESEEILAQKKEQREEEVEEEEKEBDE PRTRSNGRRKSAREERSCKQKSQAKRLLGGSDSEEEQK DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDGS KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKN	LPPNVT EGLPLS LAQCGL VGGLSV VLLELG KEQVIH MVNYMQ NRGPFF DIRSDV
residue of amino acid sequence    W=Tryptophan, Y=Tyrosine, X=Unknown, *=Codon, /=possible nucleotide deletion,    -possible nucleotide insertion    LQPQTFGLNQSSHLSLLSSRDYRMLSSFNEWFWQDRFWL    WTELEDRDGRVYPHPQDLLAALPLALVLLAMRLAFERFI     RWLGVRDQTRRQVXPNATLEKHFLTEGHRPKEPQLSLLF     TLQQTQRWFRRRRNQDRPQLTKKFCEASWRFLFYLSSFI     LYHESWLWAPVMCWDRYPNQLTLSCPAADSEA\SLYWW]     FYLSLLIRLFPDVKRKGGGPSSIKPRPHYDPPSTA\DFF     HFVAVILMTFSYSANLLRIGSLVLLLHDSSDYLLEACK     YQQVCDALFLIFSFVFTTRLVLFFTQILYTTTYESISI     GYYFFNGLLMLQLLHVFWSCLILRMLYSFMKKGQMEKI     EESDSSEEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRV     RHTTAT	LPPNVT EGLPLS LAQCGL VGGLSV VLLELG KEQVIH MVNYMQ NRGPFF DIRSDV
codon, /=possible nucleotide deletion, /=possible nucleotide insertion)  LOPOTPGLNQSSHLSLLSSRDYRMLSSFNEWFWQDRFWL WTELEDRDGRVYPHPQDLLAALPLALVLLAMRLAFERFI RWLGVRDQTRRQVKPNATLEKHFLTEGHRPKEPQLSLLY TLQQTQRWFRRRRNQDRPQLTKKFCEASWRFLFYLSSF\ LYHESWLWAPVMCWDRYPNQLTLSCPAADSEA\SLYWWY FYLSLLIRLPFDVKRKGGGPSSIKRRPHYDPPSTA\DFF HFVAVILMTFSYSANLLRIGSLVLLLHDSSDYLLEACM YQQVCDALFLIFSFVFTTRLVLFPTQILYTTYYESIS GYYFFNGLMLLQLLHVFWSCLILRMLYSFMKKGQMEKI EESDSSEEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVI RHTTAT  AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRYLL PCSDPERKRFRPNSESESGEASSPDYFGPPARNGVASI KEENPRRA\SKAVEESDEERQRDLPAQRGEESSEEEE TRKKPVVKKQAPGKASVSRKQAREESEESEAEPVQRTA KGTKSLKESEQESEEILAQKKEQREEEVEEEEKEEDE PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDEEEGK DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDGS KGSRWMARLGSTSGEESDLEREVSDSEAGGPQGERKN	LPPNVT EGLPLS LAQCGL VGGLSV VLLELG KEQVIH MVNYMQ NRGPFF DIRSDV
possible nucleotide insertion   -possible nucleotide insertion   -poptpglnqsshlsslssrdyrmlssfnewfwqdrfwl    -poptpglnqsshlsslssrdyrmlssfnewfwqdrfwl    -poptpglnqsshlsslssrdyrmlssfnewfwqdrfwl    -poptpglnqsyphpqdllaalplalvllamrlaferfi    -poptpglnqsyphpqdllaalplalvllamrlaferfi    -poptpglngrqrrqnqdrpqltkkfccaswrflfylssfv	AQCGL VGGLSV VLLELG KEQVIH MVNYMQ NRGPFF DIRSDV
LQPQTFGLNQSSHLSLLSSRDYRMLSSFNEWFWQDRFML WTELEDRDGRVYPHPQDLLAALVLLAMRLAFERFI RWLGVRDQTRRQVKPNATLEKHFLTEGHRPKEPQLSLLF TLQQTQRWFRRRRNQDRPQLTKKFCEASWRFLFYLSSFV LYHESWLWAPVMCWDRYPNQLTLSCPAADSEA\SLYWWY FYLSLLIRLSPDVKRKGGGPSSIKPRPHYDPPSTA\DFF HFVAVILMTFSYSANLLRIGSLVLLLHDSSDYLLEACK YQQVCDALFLIFSFVFFYTRLVLFPTQILYTTYYESISI GYYFFNGLLMLLQLLHVFWSCLILKMLYSFMKKGQMEKI EESDSSEEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVI RHTTAT  AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRYLL PCSDPERKRFRPNSESESGEASSPDYFGPPAKNGVASI KEENPRA\SKAVEESDEERQRDLPAQRGEESSEBEE TRKKPVVKKQAPGKASVSRKQAREESEBEAEPVQRTA KGTKSLKESEQESEEILAQKKEQREESUEEERBEE PRTRSNGRRKSARERSCKQKSQAKRLLGDSDSEEGK DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDSG KGSRMMARLGSTSGEESDLEREVSDSEAGGGPQGERKN	AQCGL VGGLSV VLLELG KEQVIH MVNYMQ NRGPFF DIRSDV
WTELEDROGRVYPHPQDLLAALPLALVLLAMRLAFERFI RWLGVRDQTTRRQVKPNATLEKHFLTEGHRPKEPQLSLLA TLQQTQRWFRRRRNQDRPQLTKKFCEASWRFLFYLSSF\ LYHESWLWAPVMCWDRYPNQLTLSCPAADSEA\SLYWWY FYLSLLIRLPFDVKRKGGSPSSIKPRPHYDPPSTA\DFI HFVAVILMTESYSANLLRIGSLVLLLHDSSDYLLEACK YQQVCDALFLIFSFVFFYTRLVLFPTQILYTTYYESISN GYYFFNGLLMLLQLLHVFWSCLILRMLYSFMKKGQMEKI EESDSSEEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVI RHTTAT  AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLL PCSDPERKEFRPNSESEGSEASSPDYFGPPAKNGVASI KEENPRA\SKAVEESSDEERQRDLPAQRGEESSEBEE TRKKPVVKKQAPGKASVSRKQAREESEBSEAEPVQRTA KGTKSLKESEQESEEEILAQKKEQREEEVEEEEKEBDE PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEEQK DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDGS KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKN	AQCGL VGGLSV VLLELG KEQVIH MVNYMQ NRGPFF DIRSDV
RWLGVRDQTRRQVKPNATLEKHFLTEGHRPKEPQLSLLAT TLQQTQRWFRRRRNQDRPQLTKKFCEASWRFLFYLSSF\ LYHESWLWAPVMCWDRYPNQLTLSCPAADSEA\SLYWWY FYLSLLIRLPFDVKRKGGGPSSIKPRPHYDPPSTA\DFI HFVAVILMTFSYSANLLRIGSLVLLLHDSSDYLLEACK) YQQVCDALFLIFSFVFFTTRLVLFPTQILYTTYYESISI GYYFFNGLLMLLQLLHVFWSCLILRMLYSFMKKGQMEKI EESDSSEEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVI RHTTAT AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLL PCSDPERKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLL PCSDPERKERFRNSESESGEASSPDYFGPPAKNGVASI KEENPRRA\SKAVEESSDEERQRDLPAQRGEESSEBEE TRKKPVVKKQAPGKASVSRKQAREESEESEAEPVQRTA KGTKSLKESEQESEEILAQKKEQREEEVEEEEKEBDE PRTRSNGRRKSARERSCKQKSQAKRLLGDSDSEEQK DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDGS KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKN	AAQCGL VGGLSV VLLELG KEQVIH MVNYMQ NRGPFF DIRSDV
TLQQTQRWFRRRRNQDRPQLTKKFCEASWRFLFYLSSFY LYHESWLWAPVMCWDRYPNQLTLSCPAADSEA\SLYWW) FYLSLLIRLPFDVKRKGGGPSSIKPRPHYDPPSTA\DFF HFVAVILMTFSYSANLLRIGSLVLLLHDSSDVLLEACK YQQVCDALFLIFSFVFFTTRLVLFFTQILYTTYYESISI GYYFFNGLLMLLQLLHVFWSCLILRMLYSFMKKGQMEKI EESDSSEEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVI RHTTAT  AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRYLL PCSDPERKEMQEF\TRSFF\RGRPDLSTLTHSIVRRYLL PCSDPERKENTSESESGEASSPDYFGPPAKNGVASI KEENPRRA\SKAVEESSDEERQRDLPAQRGEESSEBEE TRKKPVVKKQAPGKASVSRKQAREESEESEAEPVQRTA KGTKSLKESEQESEEILAQKKEQREEEVEEEEKEBDE PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEGQK DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDSG KGSRMMARLGSTSGEESDLEREVSDSEAGGPQGERKN	GGLSV LLELG KEQVIH AVNYMQ NRGPFF DIRSDV
LYHESWLWAPVMCWDRYPNQLTLSCPAADSEA\SLYWY FYLSLLIRLPFDVKRKGGGPSSIKPRPHYDPPSTA\DFI HFVAVILMTFSYSANLLRIGSLVLLLHDSSDYLLBACKY YQQVCDALFLIFSFVFTTRLVLFPTQILYTTYYESIS GYYFFNGLLMLQLLHVFWSCLILRMLYSFMKKGQMEKI EESDSSEBAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVI RHTTAT  AKWAEKEMQEF\TRSFF\RGRPDLSTLTHSIVRRYLL PCSDPERKRFRPNSESESGEASSPDYGPPAKNGVASI PCSDPERKRFRPNSESESGEASSPDYGPPAKNGVASI KEENPRRA\SKAVEESSDEERQRDLPAQRGEESSEBEE TRKKPVVKKQAPGKASVSRKQAREESEBEAEPVQRTA KGTKSLKESEQESEEILAQKKEQREEEVEEEKEBDE PRTRSNGRRKSAREERSCKQKSQAKRLLGGSDSEEGQK DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDSG KGSRMMARLGSTSGEESDLEREVSDSEAGGGPQGERKN	CLLELG CEQVIH VNYMQ NRGPFF DIRSDV
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SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		residue of	la demine Temponine, VaValine,
	amino acid	amino acid	V=Tyrosine, X=Unknown, *=Stop
	residue of		Codon /=possible nucleotide deletion,
	amino acid	sequence	\ible nucleotide insertion)
	sequence		PFLFSLPQPLAGQQTQFVTVSQPGLSTFTAQLPAPQPLASSAGH
		1	PFLFSLPQPLAGQQIQFVIVSQFGBSTTYHMFVHTGEKPHQCSI STASGQGEKKPYECTLCNKTFTAKQNYVKHMFVHTGEKPHQCSI
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	l	7.70:	SGRPFFFFFSNTDVYFIKKVTNRWTAGSSYKMTRMKSIGKILLL
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0,000		}	SGSLGYNLPQNH\GLLGRNTLVBLGQPRRTSFT HCLLCCMFHDL
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			EHLKOALEGGIDTVENKEVE DIEGA ANTIKATAN ENERKINKE
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			NESRLRLKRELEQARQARVCDKGCEAGRLRAKYSAQIEDLQVK
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	1	1	CNNRLQQPAVLQPLASCPRLVLLNLQGNPLCQAVGILEQLAEI
1			
			PSVSSVLT

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
_	sequence		SFPPLLSSPSAVGEGKVAVAAPCPGRSECARAKMAYIQLEPLNE
6970	3	1528	GFLSRISGLLLCRWTCRHCCQKCYESSCCQSSEDEVEILGPFPA
			QTPPWLMASRSSDKDGDSVHTASEVPLTPRTNSPDGRRSSSDTS
			KSTYSLTRRISSLESRRPSSPLIDIKPIBFGVLSAKKEPIQPSV
	İ		LRRTYNPDDYFRKFEPHLYSLDSNSDDVDSLTDEEILSKYQLGM
	}	1	LHFSTQYDLLHNHLTVRVIEARDLPPPISHDGSRQDMAHSNPYV
		1	KICLLPDQKNSKQTGVKRKTQKPVFEERYTFEIPFLEAQRRTLL
	1		LTVVDFDKFSRHCVIGKVSVPLCEVDLVKGGHWWKALIPSSQNE
			VELGELLLSLNYLPSAGRLNVDVIRAKQLLQTDVSQGSDPFVKI
	}	1	QLVHGLKLVKTKKTSFLRGTIDPFYNESFSFKVPQEELENASLV
		1	QLVHGLKLVKTKKTSFIRGTIDFFIRESTSFXVFQBEIGHTGEF FTVFGHNMKSSNDFIGRIVIG\QYSSGP\SEPNHWRRMLNTHRT
			FTVFGHNMKSSNDFIGKIVIG\QISSGF\BETMIKKKIDAYTIKY AVEQWHSLRSRAECDRVSPASLEVT
			AVEQWHSLRSRAECDRYSPASIEVI ACFYVPGSRSFKLIPRHGLVNMGRSGKLPSGVSAKLKRWKKGHS
6971	37	3702	SDSNPAICRHRQAARSRFFSRPSGRSDLTVDAVKLHNELQSGSL
			RLGKSEAPETPMEEEAELVLTEKSSGTFLSGLSDCTNVTFSKVQ
			RFWESNSAAHKEICAVLAAVTEVIRSQGGKETETEYFAALIRKA
			AQHGVCSVLKGSEFMFEKAPAHHPAAISTAKFCIQEIEKSGGSK
		l l	EATTTLHMLTLLKDLLPCFPEGLVKSCSETLLRVMTLSHVLVTA
			CAMQAFHSLFHARPGLSTLSAELNAQIITALYDYVPSENDLQPL
}	1	}	LAWLKVMEKAHINLVRLQWDLGLGHLPRFFGTAVTCLLSPHSQV
ĺ	İ		LTAATQSLKEILKECVAPHMADIGSVTSSASGPAQSVAKMFRAV
1	İ		EEGLTYKFHAAWSSVLQLLCVFFEACGRQAHPVMRKCLQSLCDL
	1	1	RLSPHFPHTAALDQAVGAAVTSMGPEVVLQAVPLEIDGSEETLD
		1	FPRSWLLPVIRDHVQETRLGFFTTYFLPLANTLKSKAMDLAQAG
ł			STVESKIYDTLQWQMWTLLPGFCTRPTDVAISFKGLARTLGMAI
<b> </b>			SERPOLRVIVCQALRILITKGCQAEADRAEVSRFAKNFLPILFN
1			LYGQPVAAGDTPAPRRAVLETIRTYLTITDTQLVNSLLEKASEK
1			VLDPASSDFTRLSVLDLVVALAPCADEAAISKLYSTIRPYLESK
			AHGVQKKAYRVLEEVCASPQGPGALFVQSHLBDLKKTLLDSLRS
			TSSPAKRPRLKCLLHIVRKLSAEHKEFITALIPEVILCTKEVSV
1		Į.	GARKNAFALLVEMGHAFLRFGSNQBEALQCYLVLIYPGLVGAVT
	1		MVSCSILALTHLLFEFKGLMGTSTVEQLLENVCLLLASRTRDVV
			KSALGFIKVAVTVMDVAHLAKHVQLVMEAIGKLSDDMRRHFRMK
	}		LRNLFT\KFIPK\FGILTWGKKAVGPKEYHRVLVNIRKAEARAK
	- {		RHRALSQAAVBEEEEEEEEEPAQGKGDSIEEILADSEDEEDNE
į .		Ì	EEERSRGKEQRKLARQRSRAWLKEGGGDEPLNFLDPKVAQRVLA
			TOPGPGRGRKKDHSFKVSADGRLIIREEADGNKMEEEEGAKGED
1			EEMADPMEDVIIRNKKHQKLKHQKEAEEEELEIPPQYQAGGSGI
1			HRPVAKKAMPGAEYKAKKAKGDVKKKGRPDPYAYIPLNRSKLNR
			PKKMKLOGOFKGLVKAAORGSOVGHKNRRKDRRP
		099	PGGAILLPLWRRTRPREATVPRGAAQRGRARSAEGRIPSSQSPS
6972	2179	973	PAEAGGATRSPPPRPPRPARPPGPSAPPLLRSDAGPGATVSAAA
			PAEAGGATRSPPPRPPRPRPT OF CHILDREN AND ALASTERARRGATMGAQLSTLGHMVLPPVWFLYSLLMKLFQRSTP
		•	AITLESPDIKYPLRLIDREIISHDTRRFRFALPSPQHILGLPVG
1			QHIYLSARIDGNLVVRPYTPISSDDDKGFVDLVIKVYFKDTHPK
			FPAGGKMSQYLESMQIGDTIEFRGPSGLLVYQGKGKFAIRPDKK
			SNPIIRTVKSVGMIAGGTGITPMLQVIRAIMKDPDDHTVCHLLF
		1	ANOTEKDILLRPELEELRNKHSARFKLWYTLDRAPEAWDYGQG\
1			FVNEEMIRDHLPPPE\EEPLVLMCGPPPMIQYACLPNL\DHVGH
		1	PTERCFVF
			LQPRCAHRGLRAQKCGRPAPGVDAMVLCPVIGKLLHKRVVLASA
	1	1964	SPRRQEILSNAGLRFEVVPSKFKEKLDKASFATPYGYAMETAKQ
6973		ı	SEKKORIDSHARDKE DA LEGIK KRIMONOM
6973			VALEUANDI VOKDI DA PDVVTGADTIVTVGGLILEKPVDKODAY
6973			KALEVANRLYQKDLRAPDVVIGADTIVTVGGLILEKPVDKQDAY
6973			DMLSDEF/SGREHSVFTGVAIVHCSSKDHQLDTRVSEFYEETKV
6973			KALEVANRLYQKDLRAPDVVIGADTIVTVGGLILEKPVDKQDAY RMLSRFE/SGREHSVFTGVAIVHCSSKDHQLDTRVSEFYEETKV KFSELSEELLWEYVHSGEPMDKAGGYGIQALGGMLVESVHGDFL NVVGFPLNHFCKQLVKLYYPPRPEDLRRSVKHDSIPAADTFBDL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
.}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	Bequence	\=possible nucleotide insertion)
<b> </b>	bequeine		SDVEGGGSEPTORDAGSRDEKAEAGEAGQATAEAECHRTRETLP
1			PFPTRLLELIEGFMLSKGLLTACKLKVFDLLKDEAPOKAADIAS
1			KVDASACGMERLLDICAAMGLLEKTEQGYSNTETANVYLASDGE
			YSLHGFIMHNNDLTWNLFTYLEFAIREGTNQHHRALGKKAEDLF
			QDAYYQSPETRLRFMRAMHGMTKLTACQVATAFNLSRFSSACDV
1			GGCTGALARELAREYPRMQVTVFDLPDIIELAAHFQPPGPQAVQ
			IHFAAGDFFRDPLPSAELYVLCRILHDWPDDKVHKLLSRVAESC
			KPGAGLLLVETLLDEEKRVAQRALMQSLNMLVQTEGKERSLGEY
1	1		QCLLELHGFHQVQVVHLGGVLDAIL\PPKWPPEAQAACSL
6974	3082	2172	RSCAAFASFASRPPLELFAPPGSHRSPPGRGVATSAQCALSVRK
05/4	3002	41.5	LLAARPGLGTKYQATMVYKTLFALCILTAGWRVQSLPTSAPLSV
	1		SLPTNIVPPTTIWTSSPONTDADTASPSNGTHNNSVLPVTASAP
			TSLLPKNISIESREEEITSPGSNWEGTNTDPSPSGFSSTSGGVH
			LTTTLEEHSLGTPEAGVAATLSQSAAEPPTLISPQAPASSPSSL
ł			STSPPEVFSASVITNHSSTVTSTQPTGAPTAPESPTEESSSDHT
-		ļ	PTSHATAEPVPQEKTPPTTVSGKVMCELIDMET\PPPFPG
6975	2	500	RPRPTVHCCKWALKLETAMETLINVFHAHSGKEGDKYKLSKKEL
1 05.5			KELLOTELSGFLDVKELML*ATEALKTFEEA*KSPIIQCSSSRS
1			SLPPAPOPPPYL+LSAVPFPIHLPLPLLPPQAQKDVDAVDKVMK
1			BLDENGDGEVDFQBYVVLVAALTVACNNFFWENS
6976	1216	970	GCOL*VAYGTTENSPVTFAHPPEDTVEQKAESVGRIMPHTEARI
1			MNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKW
1			YWTGDVATMNEQGFCKIVGRSKDMIIRGGENIYPAELEDFFHTH
			PKVQEVQVVGVKDDRMGEEICACIRLKDGBETTVEEIKAFCKGK
			ISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL*IKQQ
1		j	ACPGRLA
6977	1298	588	SLFINTNLLSNQIRKTSFGMCSEPISDNTEDQKGKLKTPDFA*R
İ			ANKKSKHHVNGNRTVEPFPEGTQMAVFGMGCFWGAERKFWVLKG
1		Į	VYSTQVGFAGGYTSNPTYKEVCSEKTGHAEVVRVVYQPEHMSFE
1			ELLKVFWENHDPTQGMRQGNDHGTQYRSAIYPTSAKQMEAALSS
•			KENYQKVLSEHGFGPITTDIREGQTFYYAEDYHQQYLSKNPNGY
}		}	CGLGGTGVSCPVGIKK
6978	3	242	SFPFRDSRRCGCCKGSSLRHTAVAMVKLSKBAKQRLQQLFKGSQ
			FAIRWGFIPLVIYLGFKRGADPGMPEPTVLSLLWG
6979	3917	1146	DEARVRGEAVAAAILSRCRHWSGPPPPPPSPPDRKGLRGTEPWE
		!	AGPGSGATPGARAMDVRRLKVNBLREELQRRGLDTRGLKTELAE
1			RLQAALEAEEPDDERELDADDEPGRPGHINEEVETEGGSELEGT
			AQPPPPGLQPHAEPGGYSGPDGHYAMDNITRQNQFYDTQVIKQE
	1		NESGYERRPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASQLKP
			DRQQFQSRKRPYEENRGRGYFEHREDRRGRSPQPPAEEDEDDFD
1	1	1	DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG
	1	1	VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQL
	1		GEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN
1	1		DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF
1	1		GQRAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECEILMMV
			GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVMGLRRQR
	1		NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR
			RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL
			EMKANFTLPDVGDFLDBVLFIELQREEADKLVRQYNEEGRKAGP
1	1		PPEKRFDNRGGGGFRGRGGGGGFQRYENRGPPGGNRGGFQNRGG
1			GSGGGGNYRGGFNRSGGGGYSQNRWGNNNRDNNNSNNRGSYNRA
			PQQQPPPQQPPPQQPPPQQPPPPSYSPARNPPGASTYNKNSNI
			PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNQGGYSQ
			GYTAPPPPPPPPAYNYGSYGGYNPAPYTPPPPPTAQTYPQPSY
	<del> </del>	<u> </u>	NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTQGGTSTQ
6980	11	420	GTRGRKTGRVAAPSTRRRTGNMQKLQTRSPAMSLSDPGLGYHPT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location		Gradult Acid, rememylatanine, Gegrycine,
1	1	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
		amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
]	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
1			CWTLRWPPLCSLHALHVFHCLFSSRLGTPVSPRLAMDPNCSCEA
1			GGSCACAGSCKCKKCKCTSCKKSCCSCCPLGCAKCAQGCICKGA
	I		SEKCSCCA
6981	10	1054	PGRGFRRASLRPAFAARGVFQGGLGQAKQARTRACAALPTPHPS
{			APRLLEPQGVFSLFPPPPGPWPNMILTKAQYDEIAQCLVSVPPT
1			RQSLRKLKQRFFSQSQATLLSIFSQEYQKHIKRTHAKHHTSEAI
{			ESYYORYLNGVVKNGAAPVLLDLANEVDYAPSLMARLILERFLO
			EHEETPPSKSIINSMLRDPSQIPDGVLANQVYQCIVNDCCYGPL
			VDCIKHAIGHEHEVLLRDLLLEKNLSFLDEDQLRAKGYDKTPDF
1			ILQVPVAVEGHIIHWIESKASFGDECSHHAYLHDQFWSYWNRFG
ì	ŀ		PGLVIYWYGFIQELDCNRERGILLKACFPTNIVTLCHSIA
6982	153	1285	FPQQDCSAPAAPGLAGSEPRRLRAYRRRQRARGLKRVAWLAPP
	1	1	PSLLQGLQGWAQAPVDGTLGPEDSRASSPMIQNSRPSLLQPQDV
			GDTVETLMLHPVIKAFLCGSISGTCSTLLFQPLDLLKTRLQTLQ
1			PSDHGSRRVGMLAVLLKVVRTESLLGLWKGMSPSIVRCVPGVGI
	}	-	YFGTLYSLKQYFLRGHPPTALESVMLGVGSRSVAGVCMSPITVI
			KTRYESGKYGYESIYAALRSIYHSEGHRGLFSGLTATLLRDAPF
			SGIYLMFYNQTKNIVPHDQVDATLIPITNFSCGIFAGILASLVT
1			QPADVIKTHMQLYPLKFQWIGQAVTLIFKDYGLRGFFQGGIPRA
6983	ļ		LRRTLMAAMAWTVYEEMMAKMGLKS
6983	82	773	EMSFLQDPSFFTMGMWSIGAGALGAAALALLLANTDVFLSKPQK
1	{		AALEYLEDIDLKTLEKEPRTFKAKELWEKNGAVIMAVRRPGCFL
1	İ		CREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDFQPYFKGE
	1		IFLDEKKKFYGPQRRKMMFMGFIRLGVWYNFFRAWNGGFSGNLE
	i		GEGFILGGVFVVGSGKQGILLEHREKEFGDKVNLLSVLEAAKMI
			KPQTLASEKK
6984	1845	1282	GGRSAYSLPAGSLPRVPATAAAKMASGVQVADEVCRIFYDMKVR
1	Ì		KCSTPEEIKKRKKAVIFCLSADKKCIIVEEGKEILVGDVGVTIT
1			DPFKHFVGMLPEKDCRYALYDASFETKESRKEELMFFLWAPELA
	1		PLKSKMIYASSKDAIKKKFQGIKHECQANGPEDLNRACIAEKLG
			GSLIVAFEGCPV
6985	1887	1324	RRTAGIYPCFPKPGRTRHALCSVVLLLLTGQLAFDDFQESCAMM
1	1		WQKYAGSRRSMPLGARILFHGVFYAGGFAIVYYLIQKFHSRALY
			YKLAVEQLQSHPEAQEALGPPLNIHYLKLIDRENFVDIVDAKLK
			IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFK
1	1		LSGENGDEVKKE
6986	642	1350	YHLYFKMGDPNSRKKQALNRLRAQLRKKKESLADQFDFKMYIAF
1			VFKEKKKKSALFEVSEVIPVMTNNYEENILKGVRDSSYSLESSL
	1	}	ELLQKDVVQLHAPRYQSMRRDVIGCTQEMDFILWPRNDIEKIVC
	1		LLFSRWKESDEPFRPVQAKFEFHHGDYEKQFLHVLSRKDKTGIV
1	1		VNNPNQSVFLFIDRQHLQTPKNKATIFKLCSICLYLPQEQLTHW
1	1	]	AVGTIEDHLRPYMPE
6987	1623	341	LEAAEKASRAFKESQRQTDSKNYETENWSPOKSORRYDMYNTAC
330,	1023	341	
	]		FLGEIEVGLYTIQILQLTPFFHKENELSKKHMVQFLSGKWTIPP
1	į.		DPRNECYLALSKFTSHLKNLQSDLKRCFDFFIDYMVLLKMRYTQ
	1		KEIABIMLSKKVSRCFRKYTELFCHLDPCLLQSKESQLLQBENC
	1		RKKLBALRADRFAGLLEYLNPNYKDATTMESIVNEYAFLLQQNS
	1	1	KKPMTNEKQNSILANIILSCLKPNSKLIQPLTTLKKQLREVLQF
	1		VGLSHQYPGPYFLACLLFWPENQELDQDSKLIEKYVSSLNRSFR
	1		GQYKRMCRSKQASTLFYLGKRKGLNSIVHKAKIEQYFDKAQNTN
İ	1		SLWHSGDVWKKNEVKDLLRRLTGQAEGKLISVEYGTEEKIKIPV
			ISVYSGPLRSGRNIERVSFYLGFSIEGPPGL
6988	3	689	TQLLRRPAVFVGSAASGIRSGLWSASSGHWCAPAAGRAHAPVPR
1			LVRGLGAASTAAPQDAQTGPQPMPRADCIMRHLPYFCRGQVVRG
			FGRGSKQLGIPTANFPEQVVDNLPADISTGIYYGWASVGSGDVH
i			KMVVSIGWNPYYKNTKKSMETHIMHTFKEDFYGEILNVAIVGYL
	<del></del>		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	<del> </del>	\-possible nucleotide insertion)  RPEKNFDSLESLISAIQGDIBEAKKRLELPEHLKIKEDNFFQVS
			KSKIMNGH
6989	2	1118	LMPSDRPLSPSTHASAGSHCHAPPTTARRAFPIPFGSKSNMATL
6969	2	1110	KDQLIYNLLKEEQTPQNKITVVGVGAVGMACAISILMKDLADEL
			ALVDVIEDKLKGEMMDLQHGSLFLRTPKIVSGKDYNVTANSKLV
			IITAGARQQEGESRLNLVQRNVNIFKFIIPNVVKYSPNCKLLIV
	-		SNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGV
j	}		HPLSCHGWVLGEHGDSSVPVWSGMNVAGVSLKTLHPDLGTDKDK
			EQWKEVHKQVVESAYEVIKLKGYTSWAIGLSVADLAESIMKNLR
			RVHPVSTMIKGLYGIKDDVFLSVPCILGQNGISDLVKVTLTSEE
	1		EARLKKSADTLWGIQKELQF
6990	719	258	THASGMASVVLALRTRTAVTSLLSPTPATALAVRYASKKSGGSS
ļ			KNLGGKSSGRRQGIKKMEGHYVHAGNIIATQRHFRWHPGAHVGV
ĺ		ł	GKNKCLYALEEGIVRYTKEVYVPHPRNTEAVDLITRLPKGAVLY
		<u> </u>	KTFVHVVPAKPEGTFKLVAML
6991	169	451	RRSSDFHNPGFLSRPVSLRENIHHQVICSTKNKRRNPKKTAYLL
1	]		SSLLMTNLNPNESTENQPVDAYWAFTLDQEFLTYACVEGTGCLF CGRHVH
6992	944	510	ROAPGCSSLALROVROVYCGLVRAPOVOTRPLSSRFVERRGALY
0992	) 344	310	RSPMNOENPPPYPGPGPTAPYPPYPPOPMGPGPMGGPYPPPOGY
			PYQGYPQYGWQGGPQEPPKTTVYVVEDQRRDELGPSTCLTACWT
			ALCCCCLWDMLT
6993	1 1	374	QWCVTCPQHNARQGPAVPPGIQAYGAAPFEDLQVDFTEMSKCRG
			DRVWIKNWNVASLCPLWKGPQTVVLSPPTAVKVEGIPAWIHHSH
		1	VKPAARETWEARPSPDNPFRVTLKKTTSPAPVTPGS
6994	346	1100	QWPEKDPVMAASSISSPWGKHVFKAILMVLVALILLHSALAQSR
	}		RDFAPPGQQKREAPVDVLTQIGRSVRGTLDAWIGPETMHLVSES
			SSQVLWAISSAISVAFFALSGIAAQLLNALGLAGDYLAQGLKLS
			PGQVQTFLLWGAGALVVYWLLSLLLGLVLALLGRILWGLKLVIF
		İ	LAGFVALMRSVPDPSTRALLLLALLILYALLSRLTGSRASGAQL
6995	144	1346	EAKVRGLERQVEELRWRQRRAAKGARSVEEE GSVAVGLSGIMAAQKDLWDAIVIGAGIQGCFTAYHLAKHRKRIL
6995	144	1346	LLEOFFLPHSRGSSHGQSRIIRKAYLEDFYTRMMHECYQIWAQL
		1	EHEAGTQLHRQTGLLLLGMKENQELKTIQANLSRQRVEHQCLSS
}	•	)	EELKORFPNIRLPRGEVGLLDNSGGVIYAYKALRALQDAIROLG
		İ	GIVRDGEKVVEINPGLLVTVKTTSRSYOAKSLVITAGPWTNOLL
		1	RPLGIEMPLQTLRINVCYWREMVPGSYGVSQAFPCFLWLGLCPH
			HIYGLPTGEYPGLMKVSYHHGNHADPEERDCPTARTDIGDVQIL
			SSFVRDHLPDLKPEPAVIESCMYTNTPDEQFILDRHPKYDNIVI
}		1	GAGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG
		<u> </u>	KAHL
6996	543	1942	ETANAEAAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDEE
			MDLFTKYYSEWKGGRKNTNEFYKTIPRFYYRLPAENEVLLQKLR
1		1	EESRAVFLQRKSRELLDNEELQNLWFLLDKHQTPPMIGEEAMIN YENFLKVGEKAGAKCKQFFTAKVFAKLLHTDSYGRISIMQFFNY
			VMRKVWLHOTRIGLSLYDVAGQGYLRESDLENYILELIPTLPQL
1			DGLEKSFYSFYVCTAVRKFFFFLDPLRTGKIKIQDILACSFLDD
			LLELRDEELSKESOETNWFSAPSALRVYGQYLNLDKDHNGMLSK
			EELSRYGTATMTNVFLDRVFQECLTYDGEMDYKTYLDFVLALEN
J			RKEPAALQYIFKLLDIENKGYLNVFSLNYFFRAIQELMKIHGQD
	1		PVSFQDVKDEIFDMVKPKDPLKISLQDLINSNQGDTVTTILIDL
j			NGFWTYENREALVANDSENSADLDDT
6997	370	1104	AMBLTIFILRLAIYILTFPLYLLNFLGLWSWICKKWFPYFLVRF
			TVIYNEQMASKKRELFSNLQEFAGPSGKLSLLEVGCGTGANFKF
1			YPPGCRVTCIDPNPNFEKFLIKSIAENRHLQFERFVVAAGENMH

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			nontide
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=nossible nucleotide insertion)
	Bequence	<del> </del>	OVADGSVDVVVCTLVLCSVKNQERILREVCRVLRPGGAFYFMEH
l			VAAECSTWNYFWQQVLDPAWHLLFDGCNLTRESWKALERASFSK
			1.KI.OHIOAPLSWELVRPHIYGYAVK
		616	FVSRALLRVRSRRHPABERAAPGRPEDAPIECPGATNCPEPLWC
6998	2	816	SHLPVPYAPPTMESRGKSASSPKPDTKVPQVTTEAKVPPAADGK
			APLTKPSKKEAPAEKQQPPAAPTTAPAKKTSAKADPALLNNHSN
			LKPAPTVPSSPDATPEPKGPGDGAEEDEAASGGPGGRGPWSCEN
			FNPLLVAGGVAVAAIALILGVAFLVRKK
			GRAGACSRRDTAMSIEIESSDVIRLIMQYLKENSLHRALATLQE
6999	14	1591	GRAGACSRRDTAMSIEIESSDVIRGIMQIBAENSBRAHAIDQE
		l	ETTVSLNTVDSIESFVADINSGHWDTVLQAIQSLKLPDKTLIDL
		1	YEQVVLELIELRELGAARSLLRQTDPMIMLKQTQPERYIHLENL
1	1 .		LARSYFDPREAYPDGSSKEKRRAAIAQALAGEVSVVPPSRLMAL
	· ·		LGQALKWQQHQGLLPPGMTIDLFRGKAAVKDVEEEKFPTQLSRH
			IKFGQKSHVECARFSPDGQYLVTGSVDGFIEVWNFTTGKIRKDL
			KYQAQDNFMMMDDAVLCMCFSRDTEMLATGAQDGKIKVWKIQSG
			QCLRRFERAHSKGVTCLSFSKDSSQILSASFDQTIRIHGLKSGK
1			TLKEFRGHSSFVNEATFTQDGHYIISASSDGTVKIWNMKTTECS
1		<b>,</b>	NTFKSLGSTAGTDITVNSVILLPKNPEHFVVCNRSNTVVIMNMQ
[		1	GOIVESFSSGKREGGDFVCCALSPRGEWIYCVGEDFVLYCFSTV
1			TGKLERTLTVHEKDVIGIAHHPHQNLIATYSBDGLLKLWKP
7000	1 2	827	GPGVVFLELMESEGPPESERSEFFSQREEENBEEEAQEPEETGP
7000	2	027	KNPLLQPALTGDVEGLQKIFEDPENPHHEQAMQLLLEEDIVGRN
1			LLYAACMAGQSDVIRALAKYGVNLNEKTTRGYTLLHCAAAWGRL
1	Ì		ETLKALVELDVDIEALNFREERARDVAARYSQTECVEFLDWADA
	i		RLTLKKYIAKVSLAVTDTEKGSGKLLKEDKNTILSACRAKNEWL
-			ETHTEASINELFEQRQQLEDIVTPIFTKMTTPCQVKSAKSVTSH
			DOKRSODDISM
			RRCLIIAFLKGCFIFIYFIFIFETEFLSCCPGWSAVAQSRLIAN
7001	2056	844	FASQVQAIFILPKDSQVGPDVKSEAAPKRALYESVFGSGEICGP
	Į.		TSPKRLCIRPSEPVDAVVVVSVKHDPLPLANGHRSTNSPTI
1		1	VSPAIVSPTQDSRPNMSRPLITRSPASPLNNQGIPTPAQLTKSN
1			VSPAIVSPTQUSRPNMSRPLITRSPASPLMNQGIPTPAQLIRS
1			APVHIDVGGHMYTSSLATLTKYPESRIGRLFDGTEPIVLDSLKQ
1		}	HYFIDRDGQMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYFQL
		<b>!</b>	QPMLLEMERWKQDRETGRFSRPCECLVVRVAPDLGERITLSGDK
			SLIEEVFPEIGDVMCNSVNAGWNHDSTHVIRFPLNGYCHLNSVQ
ł	Ì		VLERLQQRGFEIVGSCGGGVDSSQFSEYVLRRELRRTPRVPSVI
Į			RIKQEPLD
7002	1043	498	PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP
1			TPCSRHOSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS
1	1		SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV
			PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA
1			RGAEVC
	818	61	OGRFRAFCWORDFLOPPGMRLSALLALASKVTLPPHYRYGMSPP
7003	970		GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILEGKDA
			GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP
Į.			LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE
1		1	FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM
			GIKETR\NTRRSIGIEPGAEQLLPNFCPSLEG
			FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK
7004	121	2285	G\PKRTLKTQLG/YYCRVRPLGFPDQBCCIEVINNTTVQLHTPE
		1	GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH
}			GIKLNKNGDIKETQISEKQVEGINITQKEDEDVVAKEDVNDDIN
			GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF
		1	QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ
			VDPEFADMITVQBFCKAEEVDEDSVYGVFVSYIBIYNNYIYDLL
	1		EEVPFDPINPNLHNLNCFVKIKNHNMYVAGCTEVEVKSTEEAFE
	1		VFWRGQKKRRIANTHLNRESSRSHSVFNIKLVQAPLDADGDNVL
	· · · · · · · · · · · · · · · · · · ·		

	1 2 2 2 2	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	Giutamic Acid, Fernenylatanine, George Inc.
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			OEKEQITISQLSLVDLAGSERTNRTRAEGNRLREAGNINQSLMT
İ	1		LRTCMDVLRENOMYGTNKMVPYRDSKLTHLFKNYFDGEGKVRMI
1	· ·		VCVNPKAEDYEENLOVMRFAEVTQEVEVARPVDKAICGLTPGRR
ĺ			YRNOPRGP\IGNEPLVTDVVLQSFPPLPSCEILDINDEQTLPRL
[			IEALEKRHNLROMMIDEFNKOSNAFKALLQEFDNAVLSKENHMO
			GKLNEKEKMISGQKLEIERLEKKNKTLEYKIEILEKTTTIYEED
			KRNLOOELETQNQKLQRQFSDKRRLEARLQGMVTETTMKWEKEC
	ì		
1			ERRVAAKQLEMONKLWVKDEKLKQLKAIVTEPKTEKPERPSRER
			DREKVTQRSVSPSPVPVSYL
7005	63	876	RNMALYQRWRCLRLQGLQACRLHTAVVSTPPRWLAERLGLFEEL
			WAAQVKRLASMAQKEPRTIKISLPGGQKIDAVAWNTTPYQLARQ
			ISSTLADTAVAAQVNGEPYDLERPLETDSDLRFLTFDSPEGKAV
	}		FWHSSTHVLGAAAEQFLGAVLCRGPSTEYGFYHDFFLGKERTIR
			GSELPVLERICQELTAAARPFRRLEASRDQLRQLFKDNPFKLHL
1			IEEKVTGPTATVYGCGTLVDLCQGPHLRHTGQIGGLKLLSNSSS
	1	1	LWRSSG
7006	22	898	NAFGRHSTAVKMAAAAWLQVLPVILLLLGAHPSPLSFFSAGPAT
/000	22	0,50	VAAADRSKWHIPIPSGKNYFSFGKILFRNTTIFLKFDGEPCDLS
1			LNITWYLKSADCYNEIYNFKAEEVELYLEKLKEKRGLSGKYQTS
			SKLFQNCSELFKTQTFSGDFMHRLPLLGBKQEAKENGTNLTFIG
			DKTAMHEPLQTWQDAPYIFIVHIGISSSKESSKENSLSNLFTMT
1			
			VEVKGPYEYLTLEDYPLMIFFMVMCIVYVLFGVLWLAWSACYWR
			DLLRIQFWIGAVIFLGMLEKAVFYAGFQ
7007	2	1001	AMTVSGPGTPEPRPATPGASSVEQLRKEGNELFKCGDYGGALAA
1		1	YTQALGLDATPQDQAVLHRNRAACHLKLEDYDKAETEASKAIEK
i			DGGDVKALYRRSQALEKLGRLDQAVLDLQRCVSLEPKNKVFQEA
		1	LRNIGGQIQEKVRYMSSTDAKVEQMFQILLDPEEKGTEKKQKAS
1	1	1	QNLVVLAREDAGAEKIFRSNGVQLLQRLLDMGETDLMLAALRTL
l		1	VGICSEHQSRTVATLSILGTRRVVSILGVESQAVSLAACHLLQV
j	1	1	MFDALKEGVKKGFRGKEGALIVGEWKQVWGLLDVTVMEGMGLSQ
İ		}	PGQFFGDQTCSCRLFGIRFGDIILL
7008	70	1478	CRSALGHERPPPAHLPAGGRRLQTCPRSCRWLGRPPSGLPPGPR
1 /000	1 "		SPPPLAGPGQKMVQKKPAELQGFHRSFKGQNPFELAFSLDQPDH
1			GDSDFGLQCSARPDMPASQPIDIPDAKKRGKKKKRGRATDSFSG
1	1	1	RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH
1	1	<b>\</b>	IRSRVFREVEMLYQCQGHRNVLELIEFFEEEDRFYLVFEKMRGG
			SILSHIHKRRHFNBLEASVVVQDVASALDFLHNKGIAHRDLKPE
	1		NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS
1			AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG
Ì			RCGSDCGWDRGEACPACQNMLFESIQEGKYEFPDKDWAHISCAA
			KOGODOGWUKGEMOPA ON A OUT OVERHOOOS DENTI DEDIMU OD
1			KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR
			WDSHFLLPPHPCRIHVRPGGLVRTVTVNE
· 7009	1	626	ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG
1			RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKQGFYVA
1			LRLVACAQSGHEVTLSNLNLSMPPPKFHDTSSPLMVTPPSAEAH
1	1	1	WAVRVEEKAKFDGIFESLLPINGLLSGDKVKPVLMNSKLPLDVL
			GRVWDLSDIDKDGHLVRDEFAVAMHLVYRALE
7010	79	571	SHTRRAVVPETLLSPLCPLLGGGTAMSGGEQKPERYYVGVDVGT
1 ,010	"	1	GSVRAALVDQSGVLLAFADQPIKNWEPQFNHHEQSSEDIWAACC
1	1		VVTKKVVQGIDLNQIRGLGFDATCSLVVLDKQFHPLPVNQEGDS
	1		HRNVIMWLDHRAVSQVNRINETKHSVLQYVGG
			RIOTLPHONOSOTOPLLKTPPAVLQPIAPOTTFGVQTQPQPQSL
7011	3	994	KIOIDENGNOSOIQENDALE ONO PORTE COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROCUE A COROC
			LQAQISAASITPLLQTQPQPLLQQPQQKAGLLQPPVRIVSQPQP
1		1	ARRLDPPSRFSGRNDRGDQVPNRKDDRSRERERERRRSRERSPQ
			RKRSRERSPRRERERSPRRVRRVVPRYTVQFSKFSLDCPSCDMM
		1	ELRRRYQNLYIPSDFFDAQFTWVDAFPLSRPFQLGNYCNFYVMH

Deginning   nuclectide   location   corresponding   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cotton   cot	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Notestion   corresponding to first anino acid residue of anino acid residue of anino acid residue of anino acid sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequenc				Amino acid segment containing signal peptide
corresponding to first anino acid residue of anino acid residue of anino acid residue of anino acid sequence   Percine, Guclutamine, RaArginine, Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequenc	1			(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
to first amino acid residue of amino acid residue of amino acid sequence  Seserine, T-Threonine, V-Valine, S-Serine, T-Threonine, V-Valine, W-Trytophan, Y-Trytophan, Y-Tubknown, *-stop Codon, /-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion	NO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen				H=Histidine, I=Isoleucine, K=Lysine,
to first amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen	1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
amino acid residue of amino acid sequence whypophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, typtophan, ty	1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
residue of amino acid sequence (	1	amino acid	residue of	
Sequence   Sequence   Codom, /-possible nucleotide deletion,    -possible nucleotide insertion	1	residue of		W=Truntophan Y=Turosine Y=Unknown t=Chom
REVESIENNALIDPRDAHLYSKYMIMASPREMDLYHKSCAL AEDPCELEDPROHLYSKYMIMASPREMDLYHKSCAL AEDPCELEDPROHLYSKYMIMASPREMDLYHKSCAL AEDPCELEDPROHLYSKYMIMASPREMDLYHKSCAL AEDPCELEDPROHLYSLARCKALDE DPKKPSVLIKTVALRCCKALDE DPKKPSVLIKTVALRCCKALDE REAGSVKRGERELFGPFERGSERPLEPSAARREPLIGSKKAAD, AAAAAATGERGERGUTGAGGEBRUSGPKEVADGALGSPREVDGA VGERTPRKKPPPSASPPGGLAEPPGSAGPGAGTTVYDGSATPUT TGLAETPGGNERFSKRIKAKVSTREMDSIALNISEDFYSEERE NAKAEKEKKLPPPPPOAPPGBAPPGGAGPGAGTTVYDGSATPUT DPMTSCEAACFPULISSPOOTOWYPLFIRNTLQHILDPKYGSEER NAKAEKEKKLPPPPPOAPPGBERDSSPERBPSGVCGAAFGSRLPH DPMTSCEAACFPULISSPOOTOWYPLFIRNTLQHILDPKYGN TFEATLGQUEAPPMSDTVLURRVHSYLERIGLINGTUKRUFL PTKKTCKVII IGSGVCSULAARGLGSFGMUVTLLEARDRYGGRU ACFRKGNYVADLGAMVVTGLGGBFRAVVSGVAHAELKIKKGCE LYBANGGAVFKEKDENVEGSFRIKLEATS 15HGUDFNYLINGN VSLGGALEVVILGERHVYDRGGIEHKKIKVTGELEKLLINGNY NLEKIKELIGQYKEASEVKPPRDITAFFLVKSKHRDLTALKK YDELAETGKLEELGHRAVDSGVAHAEVSGVAHAELKIKKUKCE LDIKKNTAVKGVATTASGCELIAVMTRSTGSTFITKCDAVLCTL PLAVUKGOYPAVGEVPPLEEMKTSANGGMGFGNLIKKVULCPDRV FMDPSVNICHGWGSTTASGGELIAVMTRSTGSTFITKCDAVLCTL PLAVUKGOYPAVGEVPPLEEMKTSANGGMGFGNLIKKVULCPDRV FMDPSVNICHGWGSTTASGGELIAPPNILYRSTLAVGBRAG IMBNISDDVIVGRCLAILEGTFGSSAVPOPKETVVSSIRADDHA RGSYSVAAGSGRANTDAMAGHTTHNITASTHAYPRATPPSIDAPGPCIPFLPAGE HTTRNYPATHGALLSGLERGGRIADOFLGAMYTLPROATPOV AQOSSBM  7013  2661 RRAGSVKKRGBRLFGPTEKGSERPLEPSAARPEMLSGKKAANA RGSYSVAAGNSGRANTDAMAGHTHNITASGELIAVMTRSTGSPTFIKFDAG VGERTPRKKEPPRASPPGBGRAGPGRAGPTVVSGSATPHGA VGERTPRKKEPPRASPPGBGRAGPGRAGPTVVGGSATPHGA VGERTPRKEPPRASPPGBGRAGPGAGPTVVGGSATPHGA VGERTPRKSPVANDITULVIRFUKSSEPBESPGSGVGGAAFGSRLPH TGLATTFGGVRTSFRRRAKVEVERDESLALLSEDFYSEERE NAARAKKEKKLPPPPPOAPPEENESSPAAPGAGSGPBVGGA VGERTPRKSBVVADLGSBRAVGGRAGPTUNGGATPHALA TGLATTFGGVRTSFRRRAKVERDESLALLSETSTLEHGLDTVALKKC VGLAEFGVRAKFBPRASPPGAGTAGFFRRAKVERDESLANGFRAGPAGA TRAGNIVADLGARPANTVAGGELERELINGMY NALKELKELHGQVYFRKFRAFFAGTHYFTKRTALLATTLEAGTTAFTVAGTHALACK YGLLAFFAGTHATHAGAGGAGFAGTAGFFRAGTHYFTKATAGTHAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG				Codon /-nossible muslestide 1.2.4
REVESLERNATLD PPDAPHLYSAXVMIMAS PSMEDLYHKEGAL AEDDEGERADGFHARILVKFLVGKKKEMAMALGHSPELDGY PEKDPSVLKT\AIRCCKALTG  RRAGSVKRGSRALFGPPERGSERPLEFSAARREHLSGKKAANA AAAANATCRAGUGTAGGSENGSVAAQPAGLSGPAEVUGGA VUGETPRKEPPBG\RTSRRKRAKVSYREMBSLANLSGDEYVGGA VUGETPRKEPPBG\RTSRRKRAKVSYREMBSLANLSGDEYVGGA VUGETPRKEPPBG\RTSRRKRAKVSYREMBSLANLSGDEYVGGA VUGETPRKEPPBG\RTSRRKRAKVSYREMBSLANLSGDEYVGGA VUGETPRKEPPBG\RTSRRKRAKVSYREMBSLANLSGDEYVGGA VUGETPRKEPPBG\RTSRRKRAKVSYREMBSLANLSGDEYVGGA RAGKEKKLPPPPPGAFERSESPEBERGVKGAAFGSKLIG DRYTSGGALGVVIGLGEAPVNSDTVLVARVVISYLERRIGLINGGIYRKIRG PTKAGVIIISSGVGGAGAVVIGLGSFGMVTLEABDRVGGRV ATFRKSNYVADLGAMVVTGLGGFMAVVSKQVMMELAKIKGGE LYEANGAVPKEKEDWYGGETHKAKIKVTGGELEELLINGKY VSLGQALBVVIGLGEKHVKDGGIEHKKKIKVTGELEELELLINGKY VSLGQALBVVIGLGEKHVKDGGIEHKKKIKVTGGELEELLINGKY VSLGQALBVVIGLGEKHVKDGGIEHKKKIKVTGELEELELLINGKY VSLGQALBVVIGLGEKHVKDGGIEHKKKIKVTGELEELELLINGKY VSLGQALBVVIGLGEKHVKDGGIEHKKKIKVTGELEELELLINGKY VSLGQALBVVIGLGEKHVKDGGIEHKKKIKVTGELEELELLINGKY VSLGQALBVVIGLGEKHVKDGGIEHKKRIKVTGELEELELLINGKY VSLGQALBVVIGLGEKHVKDGGIEHKKRIKVTGELEELELLINGKY VSLGQALBVVIGLGEKHVKDGGIEHKKRIKVTGELEELELINGKY VSLGQALBVVIGLGEKHVGGARGRANTLARGTFTGFSIFTYKCDAVLCTIL  PLAVLKGOPPAVGEVPPLEEMKTSAVOGMAGFGINKVULCPDRV FWDSVNILGHVGSTTASSGGLFLFKNIJKAFILLALUAGBAAA RGSYSVAAGSSGNIDIDHAQPTTGFSIFTGAAPGPTERGFER RGSYSVAAGSSGNIDHAAQPTTGFSIFTAGAPGPTERGFER RGSYSVAAGSSGNIDHAAQPTTGFSIFTAGAPGPTERGFER VGCSPSM  7013  1 2661 RRAGSVKKGKARLEGPTERGSERRLEFSAAREREEMLSGKKAAAA AAAAAATTERGPTVAGGSENGSEVAAQPGALLSGDATVGGA VGETPRKEPPBGARPPEGAAPGPAGLAGGAPTVLPFGATPGB TGTAETPGGURTSAPPGGARPGPTVAGATTAGA VGRTPRKEPPBGURTSARRCAKVEYREMBSLALUGGAPTVGGATPGGA VGETPRKEPPBGARPPFEGAAPGPBCAGPQAGTUPGGATPGF TGTAETGGGURTSAVAGATGATTAGATTAGATTAGATTAGATTAGATTAGA			sequence	Codon, / Possible indirectide deletion,
AEDPGELBOFOHRALIVIFLYGMKGKDEAMAIGGHMSPSLLGG DPEKDPSVLIKT/AIRCCKAITG  REAGSVKRGERALFGPTERGSERPLEFSAARREFULGGKKAADA AAAAAATGTERGGTTAGGSENGSVAAQPAALGGPAEVIGGA VGERTPRKKEPPBAS PPGGLAEPPGAARGTWYGGATPME TGIAETPEG\RTTSRKRAKWSTREMBSIAMISSDEYTGSERG RAKAEKKALPPPPPGAPPEERBESPERSGYGGAAFGKLIPH DRHTSGEAAGFPILISGKAADA TFEATIQUEAPYNSDTVLVKWSYSLERKGLINGTYKRIKPL PTKKTGKVILIGSGYSGLAARGOLGSFGMDYTLLEARDBYGGGA ATPRKGTVALIGGGKKWENGPGTAVSTLEHGHGINGTYKRIKPL PTKKTGKVILIGSGYSGLAARGOLGSFGMDYTLLEARDBYGGAC ATPRKGTVALIGGGKKWENGPGTHKKHKVTGELEGLEKLINGTY NIKEKIKBLIGQYKSASEWSPRDITAFFLYKSKKRDLTALECK VSLGGALEVVIGLGKKWENGPGTHKKHKVTGELEKLELINGTY NIKEKIKBLIGQYKSASEWSPRDITAFFLYKSKKRDLTALECK YDELAGTGKLEEKLOLERANPSDVILSKRRGOLIDMIFANLE FANATPLSTISIKHHODDDDEPTGSHLTVENGYSCYPVALAEG LDIKKNTAVROVYTASGGELJAWTRSTGCFTYLOAVLGTI. PLGYUKOOPPAVQPVPLEBKKTSAVQBMGGNLAKVULGPBAV FMDDSVALLGHUSTTASGGELJAWTRSTGCFTYLOAVLGTI. PLGYUKOOPPAVQPVPLEBKTSAVQBMGGNLAKVULGPBAV FMDDSVALLGHUSTTASGGELJAPNTLANTSTOTTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGATTYTAGA		sequence		\=possible nucleotide insertion)
7012  1 2661  RRÁGSVKRGSRLFGPFERGSERELEFSAARREENLSGKKAAAA AAAAAAATGTERGUGTAGGSEROSEVAAQPAGLSGPAEVGPGA VGERTPRKKEPPRASP PPGGJAEP PGGAGGFTVUPGGATFUR TGTASTFEGVRTSRKRRAKVEYERMDSLAMLSEDEYTSEERE RAAGEKEKKLPPPPPAGPEERESSPEBESGVEGAAFGSRLFU DRHTSGEAACFEJI ISOPQOTOKVFLFTRRRTLGJLMEGYTKRIKDE PTKRTSCHAACFEJI ISOPQOTOKVFLFTRRRTLGJLMEGYTKRIKDE PTKRTGKVI II ISOSVSGLAARQLG-SFGMDTLTLEABRUGGTV ATFRKGNYVADLGAMVVTGLGFMMAVVSKOVMBLAKTKOKCP LYEANGAVPREKEVSEVSLAARQLG-SFGMDTLTLEABRUGGTV ATFRKGNYVADLGAMVVTGLGFMMAVVSKOVMBLAKTKOKCP LYEANGAVPREKEVBROTEVLWREVESTERHUKSTST-SHSHOVLNIKEV VSLGQALBEVVIGLGEHRVEGETHENKSTVTGEELKELLINGE UNEKTRELIGOVRASE EWER PDTTASFLVVSKREDLTALCKEV YDELAETOGKLEEKLGELEANPERDVYLSSERDGTLDMHFANLE FANATELSTILSLKEHADDDDFBPTGSHLTVRNGYSCOVPALAGE UNEKTRELIGOVRASE EWER PDTVATSSERDGTLDMHFANLE FANATELSTILSLKEHADDDDFBPTGSHLTVRNGYSCOVPALAGE UNEKTRELIGOVRASE EWER PDTVATSSERDGTLDMHFANLE FANATELSTILSLKEHADDDFBPTGSHLTVRNGYSCOVPALAGE UNEKTRELIGOVRASE EWER PROSPECTIVESMRADDMA RGSYSVAAGSSGNOTDLINAGTTPROSPICTORPTERFFERGE HTTRNYPATVHGALLSGLERGGTADOFLGAMYTLPRQATPOVP AQQSTSM RGSYSVAAGSGNOTDLINAGTTPROSPICTORPTERFFERGE HTTRNYPATVHGALLSGLERGGTADOFLGAMYTLPRQATPOVP AQSTSM  7013  1 2661 RRAGSVKKGGARLFGPTERGSERPLRFSAARPEMLSGKKAAD RAAAAAAATGTERGPTTAGGSERDSEVAADGALGSGDBVOGGA VGERTPRKKEPRASPEGGERVADGALGSDBVOGGATPME GTASFTERGLAVIT STERRILGVUNDSVANGVANGTUNGTYSEER NAKAEKEKLPPPPQAPPEEROSERVADGAGLGGBAVOTGA VGERTPRKKEPRASPEGGERVADGALGSDBVOGGATPME GTASFTERGALVIT STERRILGVUNDSVANGVANGTUNGTYSEER NAKAEKEKLPPPPQAPPEEROSERVADGAGLGGBAVOTGA VGERTPRKKEPRASPEGGERVADGAGLGGBAVOTGA VGERTPRKKEPRASPEGGERVADGAGLGGBAVOTGA VGERTPRKKEPRASPEGGERVADGAGLGGBAVOTGA VGERTPRKKEPRASPEGTAGGSVADGAGGTAVTSEGGERVADGAG TGTAFTATUNGTYSTOTT VDGTATTATUNGTYSTOTT VDGTATTATUNGTYSTOTT VDGTATTATUNGTYSTOTT VDGTATTATUNGTYSTOTT VDGTATTATUNGTYSTOTT VDGTATTATUNGTYSTOTT VDGTATTATUNGTYSTOTT VDGTATTATUNGTYSTOTT VDGTATTATUNGTYSTOTT VDGTATTATUNGTYSTOTT VDGTATTATUNGTYSTOTT VDGTATTATUNGTYSTOTT VDGTATTATUNGTYSTOTT VDGTATTATUNGTYSTOTT VDGTATTATUNGT VDGTATTATUNGT VDGTATTATUNGT VDGTATTATUNGT VDGTATTATUNGT VDGTATTA	1			
7012  1 2661  RRAGSYKRGERLIFGPTERGSERLLEFSAJRREENLISGKKAADA AAAADAATGTERGOTTAGGSENDSEVAD,POALOFBEVURGDA VGERTPRKKEPPRAS PPOGLAB PROSAGPQAGPTVVPGSATPME TGIAETPEO\RTSRKRAKVEYREMDSSIAM\SEDEYTGSERE NAKAEKEKLIP PEPPQAPEESHESSERSERSGVEAAFOSKLEPH DRHTSGRAACFEIIISGPQTTQKYFIFIRRHTLQIMLDNKKJC TFEATIQUEAPYNSDVILVIKIVESYLERHGIINGTYKRIKPL PTKKTGKVIIIGSGVSGLAAROQUSFGMOVTLLEBADBYVGGKY ATFRKGNYVALIGAMVVTLIGGBRAVVSQVMRHALKIKOKCV LYEANGQAJVEKGEMVENDEGTENKUSTERGHIINGTYKRIKPL PTKKTGKVIIIGSGVSGLAAROQUSFGMOVTLLEBADBYVGKCV LYEANGQAJVEKGEMVENDEGTENKUSTGTELHKKIKVTGELELLINGTY NIKEKIKSLIGQYKEASEWSPRDITAFFLYKSKHRDLTALECK VSLGQALEVVIQLGEKKVENDEGTENKKIVTGELEKLLINGTY NIKEKIKSLIGQTKEASGEVIAVTRSTCFTTYLANGVSCVPVALAEG LDIKKNTAVROVYTASGCELIAVTRSTCFTTYLANGVAGAUCTI PLAVIKOOPPAVQPVPPLEBKTSAJQBMGFONLAKVULCTPU PLAVIKOOPPAVQPVPPLEBKTSAJQBMGFONLAKVULCTPU PLAVIKOOPPAVQPVPPLEBKTSAJQBMGFONLAKVULCTPU PLAVIKOOPPAVQPVPPLEBKTSAJQBMGFONLAKVULCTPU PLAVIKOOPPAVQPVPPLEBKTSAJQBMGFONLAKVULCTPU PLAVIKOOPPAVQPVPPLEBKTSAJQBMGFONLAKVULCTPU PLAVIKOOPPAVQPVPPLEBKTSAJQBMGFONLAKVULCTPU PLAVIKOOPPAVQPVPPLEBKTSAJQBMGFONLAKVULCTPU PLAVIKOOPPAVQPVPPLEBKTSAJQBMGFONLAKVULCTPU PLAVIKOOPPAVQPVPPLEBKTSAJQBMGFONLAKVULCTPU PROSENIL FONLOGTTASGGELIPHTNIXAYA LILAUVAGBAQ IMBNISDDVIVGRCLALLIGTPGSAVPOPETVVSRMRADÞMA RGSYSVAAGSSGNODLANGPTTSSGRAPGSGRAPGSKGAA AAAAAAATTERAFGTAGGSENGSAVAAOPAGLISGBABVGGA VGERTPRKKEPPRASPPGGLEEPPGSAGRQAPTVYGGSATPME TGIAETPGG RRTGRKRAKVEYKEMDESLANLSEDBYJSEER NALARKEKKLPPPOAAPPESAAGRAPGSKLEPH DRHTSGRAACFPDIISGPOTOKVFLFIRRTLQIMLDHYALGY TFEATLQQLEAPYNSTOVILLEATSTLANGLAFAGKKEKLPPPOAAPPSAAGRAPGSKLEPH DRHTSGRAACFPDIISGPOTOKVFLFIRRTLQIMLDHYALGY ATTRKTYNAVALGARAVVEKERBGLINGTYNTKICHTYNTKYTALDAL VSLGQALEVVILLGEKRYLKUNTOGRAFGYKAKAYAL VSLGQALEVVILLGEKRYLKUNTOGRAFGYKAKAYAL VSLGQALEVVILLGEKRYLKUNTOGRAFGYKAKAYAL VSLGQALEVVILLGEKRYLKOOPPAGATGYVALEGE LDIKMTAVQVYTASGEVLAVTRSTSGTTINGTULMIHALL FANATPISTISLKSMOODDFTGFTGSHITVKNICYCOTALEGE LDIKMTAVQVYTASGSEVLAVATRSTSGTTINGTULMIHALGY TKORANGAVATCAGATAGATAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	1			AEDPQELRDGFQHPARLVKFLVGMKGKDEAMAIGGHWSPSLDGP
AAAAAAATGTEAGGTTAGGSENGSEVAAQPAGLSGPAEVUGGA VGERTPRIKEPPBAS PROGLADE POSAGPAGATVOGSATTME TGIAETPBG\RTSERKRAKVEYERMGESLANLSEDELYSEERE NAKAEREKKLP PPPPOAP PEEREMSEE PEERSEVEGVAAAPGSRLPH DRMTSOEAACPPDI ISGPQCTQKYFLFIRNTLQLWLDNPKIQL TFEATLAQUEAPYNAGLOSFOMDYTLLEARDRIVGGRY ACTRIKGNIVADLGANVYTGLGGNPHAVVSKQVNNELAKIKKOKCP LYEANGAVVEKEDEMVEGEFRELLEATSYLSHEDIATINISH VSIGQALEVVIQUEKHKUEGTEINKIVTTQEELKELLIKMY NLKEKIKELRQOYKSASKVPRPDITAEFLYKEDLTALCKE YDELAETTGKLEEKLQELEANPPSDVILSKERDGILDHNISHANLE FANATPLSTISLKHHDODDDFEPTGSHLTVARKUTTQEELKELLIKMY NLKEKIKELRQOYKSASKVPRPDITAEFLYKEDLTALCKE YDELAETTGKLEEKLQELEANPPSDVILSKERDGILDHNIFANLE FANATPLSTISLKHHDODDDFEPTGSHLTVARKUTTQEELKELLIKMY NLKEKIKELRQOYKSASKVPRPDITAEFLYKEDLTALCKE YDELAETTGKLEEKLQELEANPPSDVILSKERDGILDHNIFANLE FANATPLSTISLKHHDODDDFEPTGSSHLTVARKERDLTALCKE YDELAETTGKLEEKLQELEANPPSDVILSKERDGILDHNIFANLE FANATPLSTISLKHHDODDFEPTGSSHTGSTOFTIYKCDAVLCTL PLGVILKQOPPAVQFVPLPERBFFTSSHLTVARKOVLCPTRV PWDSVNLFGHVOSTTASRGELPFTSSTGOTTYKCDAVLCTL PLGVILKQOPPAVQFVPLPERBFTSSHTORTAVVLCPTRV PWDSVNLFGHVOSTTASRGELPFTSSTGOTTYKCDAVLCTL PLGVILKQOPPAVQFVPLPERBFTSSHTORTAVVLLCPTRV PWDSVNLFGHVOSTTASRGELPTGSSARGPQFTFTUSPARAPPAN RGSYSYAAAGSSGNDYDLAGGTTTGSSTGAPQFTFTUSPARAPPAN RGSYSYAAAASSGNDYDLAGGTTTGSSTGAPQFTFTUSPARAPPAN RGSYSYAAAGSSGNDYDLAGGTTTGSSTGAAPQSTRUM TRATPFEGNATARTSKRKAAVEYREMDESLANLSEDETYSSEERE NAKAKEKULPPPPGPPBAPPBGGLAEPPGSAGPQAGGGAAPGSKLPH DRMTSQEAACPPDIISGPQTGVVFLFIRRTLQLLNDPKIQL TFEATLQQLEAPYNSDTVLVHRVHSYLERHGLINFGTYKRIKPL DRMTSQEAACPPDIISGPQTGVKYFLFIRRTLQLLNDPKIQL TFEATLQQLEAPYNSDTVLVHRVHSYLERHGLINFGTYKRIKPL PTHKTGKVIIIGSGKAAAA AAFAAATTGAGGTTAGGSENGSFRAAVGGSGRAAFGSARDH URMTSQEAACPPROTISGPGTGGSENGSFRAAVGGGRAAFGSALLAD TRATPGGARAFAGAAGAGGSGGAAFGSKLPDH DRMTSQEAACPPROTISGPGTGGSENGSFRAAVGGGRAAFGS AFFRKGNIVADLGARAVTGGGENAVVSKGULLADERKALK VSLOGALEVVIJOLGEKKINGEGENAVVSKGULLADERKALK VSLOGALEVVIJOLGEKKINGEGENAVVSKGURGTGLINKKVINCTGELKELLIKKWV NLLEKIKELRQOYKTAGGGCVALTHRICATSTISHGLDFTVINKE VSLOGALEVVIJOLGEKKINGEGTALDOFLGRANGTGHLINKVILCCPRV PHDPSVILGHGVGSTTAGGGGGGAATADOFLGRANVTLERGAGTTBAGGGGAAGG LDLKINTAV		•		DPEKDPSVLIKT\AIRCCKALTG
AAAAAAATGTEAGGTTAGGSENGSEVAAQPAGLSGPAEVUGGA VGERTPRIKEPPBAS PROGLADE POSAGPAGATVOGSATTME TGIAETPBG\RTSERKRAKVEYERMGESLANLSEDELYSEERE NAKAEREKKLP PPPPOAP PEEREMSEE PEERSEVEGVAAAPGSRLPH DRMTSOEAACPPDI ISGPQCTQKYFLFIRNTLQLWLDNPKIQL TFEATLAQUEAPYNAGLOSFOMDYTLLEARDRIVGGRY ACTRIKGNIVADLGANVYTGLGGNPHAVVSKQVNNELAKIKKOKCP LYEANGAVVEKEDEMVEGEFRELLEATSYLSHEDIATINISH VSIGQALEVVIQUEKHKUEGTEINKIVTTQEELKELLIKMY NLKEKIKELRQOYKSASKVPRPDITAEFLYKEDLTALCKE YDELAETTGKLEEKLQELEANPPSDVILSKERDGILDHNISHANLE FANATPLSTISLKHHDODDDFEPTGSHLTVARKUTTQEELKELLIKMY NLKEKIKELRQOYKSASKVPRPDITAEFLYKEDLTALCKE YDELAETTGKLEEKLQELEANPPSDVILSKERDGILDHNIFANLE FANATPLSTISLKHHDODDDFEPTGSHLTVARKUTTQEELKELLIKMY NLKEKIKELRQOYKSASKVPRPDITAEFLYKEDLTALCKE YDELAETTGKLEEKLQELEANPPSDVILSKERDGILDHNIFANLE FANATPLSTISLKHHDODDDFEPTGSSHLTVARKERDLTALCKE YDELAETTGKLEEKLQELEANPPSDVILSKERDGILDHNIFANLE FANATPLSTISLKHHDODDFEPTGSSHTGSTOFTIYKCDAVLCTL PLGVILKQOPPAVQFVPLPERBFFTSSHLTVARKOVLCPTRV PWDSVNLFGHVOSTTASRGELPFTSSTGOTTYKCDAVLCTL PLGVILKQOPPAVQFVPLPERBFTSSHTORTAVVLCPTRV PWDSVNLFGHVOSTTASRGELPFTSSTGOTTYKCDAVLCTL PLGVILKQOPPAVQFVPLPERBFTSSHTORTAVVLLCPTRV PWDSVNLFGHVOSTTASRGELPTGSSARGPQFTFTUSPARAPPAN RGSYSYAAAGSSGNDYDLAGGTTTGSSTGAPQFTFTUSPARAPPAN RGSYSYAAAASSGNDYDLAGGTTTGSSTGAPQFTFTUSPARAPPAN RGSYSYAAAGSSGNDYDLAGGTTTGSSTGAAPQSTRUM TRATPFEGNATARTSKRKAAVEYREMDESLANLSEDETYSSEERE NAKAKEKULPPPPGPPBAPPBGGLAEPPGSAGPQAGGGAAPGSKLPH DRMTSQEAACPPDIISGPQTGVVFLFIRRTLQLLNDPKIQL TFEATLQQLEAPYNSDTVLVHRVHSYLERHGLINFGTYKRIKPL DRMTSQEAACPPDIISGPQTGVKYFLFIRRTLQLLNDPKIQL TFEATLQQLEAPYNSDTVLVHRVHSYLERHGLINFGTYKRIKPL PTHKTGKVIIIGSGKAAAA AAFAAATTGAGGTTAGGSENGSFRAAVGGSGRAAFGSARDH URMTSQEAACPPROTISGPGTGGSENGSFRAAVGGGRAAFGSALLAD TRATPGGARAFAGAAGAGGSGGAAFGSKLPDH DRMTSQEAACPPROTISGPGTGGSENGSFRAAVGGGRAAFGS AFFRKGNIVADLGARAVTGGGENAVVSKGULLADERKALK VSLOGALEVVIJOLGEKKINGEGENAVVSKGULLADERKALK VSLOGALEVVIJOLGEKKINGEGENAVVSKGURGTGLINKKVINCTGELKELLIKKWV NLLEKIKELRQOYKTAGGGCVALTHRICATSTISHGLDFTVINKE VSLOGALEVVIJOLGEKKINGEGTALDOFLGRANGTGHLINKVILCCPRV PHDPSVILGHGVGSTTAGGGGGGAATADOFLGRANVTLERGAGTTBAGGGGAAGG LDLKINTAV	7012	1	2661	RRAGSVKRGEARLEGPTEROSERPLEPSAARRDEMI.SCKKAAAA
GERTFRKEPPRASPPGGLAEPPGSAGPQAGPTVVPGSATTME TGIAETPEG, RETSERKRAKUYSTREMBUSLANDEDYTSEERE NAKARKEKLPPPPOAPPEERNESEPBESGVEGAAFQSKLPH DRMTSCEAACFPDIISGPQCTGXVFLFIRNETLQLWLDNPKIQL TFEATLQQLEAPYNDDTVLUMEVHSYLERKGLINFGIYKRKPLI PTKKTGKVIIIGSGVGGAARROLGSFGMVTLLEARDKVGGRV ATFRKGNYVADLGAMVVTGLGGCMPMAVVSKGVNMELAKIKOKCP LYEANQAVPKENDEMVEGEFRIKLEATSYLSHQLDPRVILNKE VSLGQALEVVIQLGEKHKNEGLEINKRKYCHLAKUK VSLGQALEVVIQLGEKHKNEGLEINKRKYKTY NILKEKIKGLOYKEASBVKPPRDITAEFLVKSKHRDLTALCKE YDELAETGGKLEEKLGLELANPESDVYLISSPRGILDMEHANLE FANATELSTLSLKHHDQDDFBFTGSHLTVENGGSCVPVALAEC LDIKLMTAVROVEYTASGCEVILAVRTSTGYFFIYKCDAVLCTL PLGVIKQOPPAVGFVPELEBWKTSAVGRAGFROINKVVLCFDRY FWDPSVNLFGHVUSTTASRGELPIPWNLYKAPILLALVAGERAG IMBNISDDVIVGCLAILKGIEGSSAVPQPKETVVSRWRADPHA RGSYSYVAAGSSGNDYDHAQPITTGFSIPGAPQPIPRLFFAGE HTTRYPATVHGALLSGLREGGRIADOFIGAMYTLPROATFGVV AQQSPSM RGSYSYVAAGSSGNDYDHAQPITTGFSIPGAPQPIPRLFFAGE HTTRYPATVGALLSGLREGGRIADOFIGAMYTLPROATFGVV AQQSPSM TGIAETFEGVRETSRRRAKVSYKEMDESLANLSDEVYSSEER NAFAKKEPPPASPPGGLAEPPGSAGRQAGPTVVFGSALPM TGIAETFEGVRETSRRRAKVSYKEMDESLANLSDEVYSSEER NAFAKKEPPPISGPPGINGSPCSARPPEMLGGKKAAAA NAAAAAATGTEAGFGTTAGGSERGLEFSFSGARPSSALPM TGIAETFEGVRETSRRRAKVSYKEMDESLANLSDEVYSSEER NAFAKKEPPPISGPPGINGSPCSARPPEMLGKKKLAPPPRGVSCKYAAGPAGLAGRAGHTVVSKYAAGPAGLAGATPME TGIAETFEGVRETSRRRAKVSYKEMDESLANLSDEVYSSEER NAFAKKEPPPISGPGGTCKVFFFFIRTLLAMINDFICLL TFEATLQULEAPYNSDTVLVHRVISSYLERHGLINFGIVKRIKPL FFRKTGVKIIIGSGVGLAARAGLGSFGMDVTLLEARDRVGGRV ATFRKGNVALDLGANVTGLGGNPMAVVSKQVMNELAKIKKCC LYERNGAVVBEKEDEMVEGFBRILLEATSTLACHLOMPVLINKR VSLGQALEVVIQLOEKHYNDEGIEHMKKIVKTQEELKELLINKW NLKEKIKELHQQYKRASEVKPPRIITAFELVKSHRDLIALKS TFRKGNVALDLGANVTGLGGNPMAVVSKQVMELAKIKKCC LYERNGAVAURTSTSGTTIFLLVKSHRDLIALKS TORDATAGRAGGTGGAPTVFTAGARPPMA RGSYSVAAGSGNOTULANGPTTFFIVKTGAVLCTL PLGVIKAQCPBAVGVPPLPRGSTTARGREFFFFINIKKAPPPPP PLGVIKAQPPAVGVPPLPRGSTTARGREFFFFINIKKAPPPPP PLGVIKAQPPAVGTAFGSTTARGRUFTFFINIKARGPPPP PROSVNLEGHVGSTTARGRGENTADQFLGRMYTLPROATFGGF DRATTPRYPTVHGALLSGLERGRIADQFLGRMYTLPROATFGGF DRATTPRYPTVHGALLSGLERGRIADQFLGRMYTLPROATFGGF DRATTPRYPTVHGALLSGLERGRIADQFLGRMYTL	1	}		AAAAAAATGTEAGDGTAGGGENGGENAAODAGLGGDAENGDGA
TGIAETPEG\RTSRKRARVETERMESELALSEEDIYSEERE NAKAREKKINDEPPPOAPPEERESEEDESEVERAAPGSKLIPH DRMTSGEACPPDIISGGCTOKVFLEIRRRTLOLMLDHPKIQL TFEATLQQLEAPYNSDTVLVHRVHSYLERHGLINFGIYKRIKPI PTKKTGKVI IIGSGVSGLAAARQLGSGMDHAVVEKQVNHELAKIKGKCE LYREANGAVIPEKEDEMVEGEFRIKLEATSISLDENVILARROK VORGK ATFRKRNYADLGAMVYTGLGGENPAAVVEKQVNHELAKIKKOKCE LYREANGAVIPEKEDEMVEGEFRIKLEATSISLDENVILARIKE VSIGQALEVVIGLEKHVEGELERNKRIVKTGEELKELLINGW NLKEKIKELIGGYKSEASKVPREDITAEPIKAFDLTALCKE YDELATTOGKLEEKLGLERNPESDVILSSENBOILDMIFRANLE FANATPLSTLSLKHNDQDDDEBTGSHLTVRNGYSTVACALEE LDIKINTAVRQVRYTASGESVLAVWTESTSGTFIYKCDAVLCTI PLAVLKOOPPAVGFVPILEBENTSAVQRMGFGNINKVVLCPRV PUPDSVNLFGHVGSSTASRGELFJFNNLYKAFJLALVAGEAAG IMENISDDVIVGRCLAILKGIFGSSAVPQKESTVSRWARDDWA RGSYSVAXAGSSONDYDLMAGPLTFORSIPGAPQFIFRHPAARE HTTRYPATVHGALLSGLREAGRIADQFIGAMYTLPQATPGVP AQQSPSM  7013 1 2661 RRAGSVKRGEARLFGPTERGSERPLRPSAARRPEMLSGKKAAAA AAAAAAATTERGFGTAGGSENGSEVAAQPAGLISGRAEVGFGA VGERTRRKERPFRASPFGGLABPFGSAGNGLGSGRAVGFGA VGERTRRKERPFASPFGGLABPFGSAGNGLGSGRAVGFGA VGERTRRKERPFASPFGGLABPFGSAGNGLGSGRAVGFGA VGERTRRKERPFASPFGGLABPFGSAGNGLGSGRAVGFGA TGIATTPEGVRTARGFTAGGSENGSEVAGPAGLISGRAVSLEPH DRMTSGEAACPPDIISGPQCTCKVFLFIRRTLOLMLINDPLIQL TPEATLQOLLEAPINSTVALHWISYLERRILGIDINGTYKRIKPL PTKTTGKVIIGSGVSGLAARGOLSFGMDVTLLEARRVGGX ATFRKGNIVADLGAMVVTGLGSNEMAVVSKOVNNELAKIKKCC LYEARGAGAVEKEDEMVEGEFRRILLEATSTISTIGTYKKELKPL PTKTTGKVIIGSGVSGLAARGOLSFGMDVTLLEARRVGGX ATFRKGNIVADLGAMVVTGLGSNEMAVVSKOVNNELAKIKKCC YDELAFTOGKLEEKLGELEKLOFFTONITHERIUSDFNVLINKF VSLGQALEVVIOLOEKHVDEGIEHMKKIVTOGELKELLIKMV NLKEKIKELIGGYKRAGEVIPFFONITHERIUSDFNVLINKF VSLGQALEVVIOLOEKHVDEGIEHMKKIVTTOGELKELLIKMV NLKEKIKELIGGYKRAGSKOPTITABGT THALLAHALAGRAAG IMMISDDVIVGRCLAILKGIFGSSAVPOPKETVVLREBREB LDIKLNTAVROVRYTASGCEVIAVWTRSTSGTFIYKCDAVLCTL PLOVIKGOPPAVGFYPELFRHNIKKAFTILLALVAGRAAG IMMISDDVIVGRCLAILKGIFGSSAVPOPKETVVLREBREB DRATTSPTSDPTEVVNGISGNOPTHOGSGCYPPALPAG SVSASRVKVFROGSFOLHMLASTYTKHHTSSVYSISERLERREPD CTISAFPSGESSPLHTSSDTCHEFFFINIKARPPIPP PLATDSPTSDPTEVVNGISGOPPRFFOVELDFRKGE POAGCLWEARATHSGGGSTDLDSKLITGGLEPERKALRPPPP DRATATSPTSPTEVLTELEGE				VCFDTDDVYFDDDACDDCGI AFDDCGACDCACDCACDCACDCACDCACDCACDCACDCACDC
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TFEATLQQLEAPYNSDTYLVARVUSYLERHGLINFGIYKRIKEN PTKKTGKVI LIGSGVSGLAARAQLOSFGMOUTLLEARDRVGGRV ATFRKGNYVADLGAMVUTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEVEGETHNKLIBATSYLSHQLDFAVLINKW VSLGQALBRVIQLQEKHVKDEQIEHNKLYDEELKELLINKWV NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKS YDELAETIGGKLEKKLQELEARPPSDVYLSSBDRQILDMEFANLE FANATLSTLSLKHMDQDDDFBPTGSHLTVENGYSCUPVALABG LDIKLNTAVRQVRYTASGCEVLAWTRSTSQTPIYKCDAVLCTL PLGVLKQQPAVQFVPPLDEWKTSAVQRMGFGKLNKVVLCPDRV FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLAMGEBAG IMENISDDVIVGRCLALKGIFGSSAVPOPKETTVSRWRADPHA RGSYSTVAAGSSGNDVDLMAQFTTPOPSIPGAPQTPFLFFAGE HTTRNYPATVIGALLSGLREAGRIADQFLGAMYTLPRQATFGVP AQGSPM  7013  1 2661 RRAGSVKRGEARLFGPTERQSERPLRFSAARFPEMLSGKKAAAA AAAAAAATGTEAGPGTAGGSENGSEVAAQPAGLSGPAEVGPGA VGERTPRKEPPRASPPGGSAGPQAGFTVVYGGATPME TGTATTPEG (RRTSRKRAKVEYREMDESLANLSBEGYPSEVGPGA VGERTPRKEPPRASPPGGAGPQAGFTVVYGGATPME TGTATTPEG (RRTSRKRAKVEYREMDESLANLSBEGYSEERE NAKAKEKKUPPPPOAPPEEENESPPEGAGPQAGFTVVYGGATPME TGTATTPEG (RRTSRKRAKVEYREMDESLANLSBEGYSEERE NAKAKEKKUPPPPOAPPEEENESPPEGAGPGAGFTVVTGGATPME TFATTAQCHAPTNSDTVLVHRVHSYLERHGLINFGIYKRI KPL PTKKTGKVI II GSGVSGLAAARGLOS FGMDVTLLEARPRVGGRV ATTRKGNIVADLGAMVTGLGSPPAAVVGMELAKI KÇKCC LYBANGQAVPKEKDEMVEQFENKLLEATSYLSHQLDFNVINNKY VSLGQALEVVIQLOEKHVEDGIEHKKLYGEBLKSLIKMW NLKEKI KELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDMFANLE FANATLSTISLKHMDQDDDFETTGSHLTVKNOYSCVPVALAGE LDIKLNTAVRQVRYTASGCEVIAVNTRSTSGTFI IKCDAVLCTL PLGVIKQGPAVQFVEPLPBEWKTSAQGRAGFGRILNKVVLCFDRV FWDFSVNLFGHVGSTTASRGELFLPMNLYKAPILLALAGGAAG IMENISDDVIVGRCLAILKGI FGSSAVPOPKETVVSRWADDWA RGSYSTVAAGSSGNDYDLMAQFTTGGFS IFGAGPQFIPRFFAGE HTIRNYPATVHGALLISGLREARGLADQFLGAMYTLPRQATGVP AQQSSBM  7014 3 3950 DEFUGGKIRIATUEGGBLEGSLKGRTGIFPYFFKVERCHEPTFAGE HTIRNYPATVHGALLISGLKERGRIGPPTFP DKILKTPOTYTERGE BENAPPGGAGAATISGGGGSTALPPTFAGGRICHNCVVLCFDDFY FWDFSVNLFGHVGSLARIPTSOTICSCHTOLLEREFGERGPTPP DKILRHFSIMDPNSEKDIVRGSSKLITEGELPERRALRPPPPR PCTFVSTSPILLIVDONLKPAPPLVVPRSRRAPPLPVSVGGRITH PCTFVSTSPILLIVDONLKPAPPLVVVPRSRRAPPLPVPRGAGRTDPD PCTFVSTSPILLIVDONLKPAPPLVVPRSRRAPPLPPRAG		]		NAKAEKEKKLPPPPPQAPPEEENESEPEEPSGVEGAAFQSRLPH
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location corresponding to first amino acid residue of amino acid sequence	VIE QMV AIA IKP INE LKH RES CER CLK GY VLQ QSE
corresponding to first amino acid residue of sequence P=Proline, Q=Glutamine, R=Arginine, residue of amino acid sequence S=Serine, T=Threonine, V=Valine, Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)  MELQQLREMTLLSSQSSSLVAPSGSVSAENPEQRMLEKRAK ELLQTERDYIRDLEMCIERIMYPMQQAQVPNIDFEGLFGNM IKVSKQLLAALEISDAVGPVFLGHRDELBGTYKIYCQNHDE LLEIYEKDEKIQKHLQDSLADLKSLYNEWGCTNYINLGSFL VQRVMRYPLLLMELLMSTPESHPDKVPLTNAVLAVKEINVN YKRRKDLVLKYRKGDEDSLMEKISKLNIHSIIKKSNRVSSH LTGFAPQIKDEVPEETEKNFFMQERLIKSFIRDLSLYLQHI ACVKVVAAVSMWDVCMERGHRDLEQFERVHRYISDQLFTNF TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAE DKKTLEELQSARNNYEALNAQLLDELPKFHQYAQGLFTNCV AEAHCDFVHQALEQLKPLLSLLKVAGREGNLIAIFHEEHSR QLQVFTFFPESLPATKKPFERKTIDRQSARKPLLGLPSYML ELRASLLARYPPEKLFQAERNFNAAQDLDVSLLEGDLVGVI DPMGSQNRWLIDNGVTKGFFYSSFLKFYNPRRSHSDASVGSI	VIE QMV AIA IKP INE LKH RES CER KLK IGY /LQ SE KK
amino acid residue of amino acid residue of amino acid sequence  P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=St Codon, /=possible nucleotide deletion, \text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\	VIE QMV AIA IKP INE LKH RES CER KLK IGY /LQ SE KK
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=St Codon, /=possible nucleotide deletion, \possible nucleotide insertion)  MELQQLREMTLLSSQSSSLVAPSGSVSAENPEQRMLEKRAK ELLQTERDYIRDLEMCIERIMVPMQQAQVPNIDFEGLFGNM IKVSKQLLAALEISDAVGPVFLGHRDELBGTYKIYCQNHDE LLEIYEKDEKIQKHLQDSLADLKSLYNEWGCTNYINLGSFL VQRVMRYPLLLMELLNSTPESHPDKVPLTNAVLAVKEINVN YKRRKDLVLKYRKGDEDSLMEKISKLNIHSIIKKSNRVSSH LTGFAPQIKDEVEFTEKNFFMQERLIKSFIRDLSLYLQHI ACVKVVAAVSMWDVCMERGHRDLEQFERVHRYISDQLFTNF TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAE DKKTLEELQSARNNYEALNAQLLDELPKFHQYAQGLFTNCV AEAHCDFVHQALEQLKPLLSLLKVAGREGNLIAIFHEEHSR QLQVFTFFPESLPATKKPFERKTIDRQSARKPLLGLPSYML ELRASLLARYPPEKLFQAERNFNAAQDLDVSLLEGDLVGVI DPMGSQNRWLIDNGVTKGFFYSSFLKFYNPRRSHSDASVGSI	VIE QMV AIA IKP INE LKH RES CER KLK IGY /LQ SE KK
residue of amino acid sequence	VIE QMV AIA IKP INE LKH RES CER KLK IGY /LQ SE KK
amino acid sequence  Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)  MELQQLREMTLLSSQSSSLVAPSGSVSAENPEQRMLEKRAK  ELLQTERDYIRDLEMCIERIMVPMQQAQVPNIDFEGLFGNM IKVSKQLLAALEISDAVGPVFLGHRDELEGTYKIYCQNHDE LLEIYEKDEKIQKHLQDSLADLKSLYNEWGCTNYINLGSFL VQRVMRYPLLLMELLNSTPESHPDKVPLTNAVLAVKEINVN YKRRKDLVLKYRKGDEDSLMEKISKLNIHSIIKKSNRVSSH LTGFAPQIKDEVFEETEKNFFMQERLIKSFIRDLSLYLQHI ACVKVVAAVSMWDVCMERGHRDLEQFERVHRYISDQLFTNF TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAE DKKTLBELQSARNNYEALNAQLLDELPKFHQYAQGLFTNCV AEAHCDFVHQALGQLKPLLSLKVAGREGNLIAIFHBEHSR QLQVFFFPESLPATKKPFERKTIDRQSARKPLLGLPSYML ELRASLLARYPPEKLFQAERNFNAAQDLDVSLLEGDLVGVI: DPMGSQNRWLIDNGVTKGFVYSSFLKFYNPRRSHSDASVGSI	VIE QMV AIA IKP INE LKH RES CER KLK IGY /LQ SE KK
≥possible nucleotide insertion     MELQQLREMTLLSSQSSSLVAPSGSVSAENPEQRMLEKRAK    BLLQTERDYIRDLEMCIERIMYPMQQAQVPNIDFEGLEGNM     IKVSKQLLAALEISDAVGPVFLGHRDELBGTYKIYCQNHDE     LLEIYEKDEKIQKHLQDSLADLKSLYNEWGCTNYINLGSFL     VQRVWRYPLLLMELLINSTPESHPDKVPLTNAVLAVKEINVN     YKRRKDLVLKYRKGDEDSLMEKISKLNIHSIIKSNRVSSH     LTGFAPQIKDEVFEETEKNFRMQERLIKSFIRDLSLYLQHI     ACVKVVAAVSMWDVCMERGHRDLEQFERVHRYISDQLFTNF     TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAE     DKKTLEELQSARNYEALNAQLLDELPKFHQYAQGLFTNCV     AEAHCDFVHQALEQLKPLLSLLKVAGREGNLIAIFHEEHSR     QLQVFTFPESLPATKKPFERKTIDRQSARKPLLGLPSYML     ELRASLLARYPPEKLFQAERNFNAAQDLDVSLLEGDLVGVI     DPMGSQNRWLIDNGVTKGFVYSSFLKFYNPRRSHSDASVGSI	QMV AIA IKP INE LKH RES CER CLK HGY VLQ QSE CKK
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BLLQTERDYIRDLEMCIERIMVPMQQQQVPNIDFEGLFGNM IKVSKQLLAALEISDAVGPVFLGHRDELEGTYKIYCQNHDE LLEIYEKDEKIQKHLQDSLADLKSLYNEWGCTNYINLGSFL VQRVMRYPLLLMELLNSTPESHPDKVPLTNAVLAVKEINVN YKRRKDLVLKYRKGDEDSLMEKISKLNIHSIIKKSNRVSSH LTGFAPQIKDEVFEETEKNFFMQERLIKSFIRDLSLYLQHI ACVKVVAAVSMWDVCMERGHRDLEQFERVHRYISDQLFTNF TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAE DKKTLBELQSARNNYEALNAQLLDELPKFHQYAQGLFTNCV AEAHCDFVHQALEQLKPLLSLKVAGREGNLIAIFHBEHSR QLQVFTFPESLPATKKPFERKTIDRQSARKPLLGLPSYML ELRASLLARYPPEKLFQAERNFNAAQDLDVSLLEGDLVGVI: DPMGSQNRWLIDNGVTKGFVYSSFLKFYNPRRSHSDASVGSI	QMV AIA IKP INE LKH RES CER CLK HGY VLQ QSE CKK
BLLQTERDYIRDLEMCIERIMVPMQQQQVPNIDFEGLFGNM IKVSKQLLAALEISDAVGPVFLGHRDELEGTYKIYCQNHDE LLEIYEKDEKIQKHLQDSLADLKSLYNEWGCTNYINLGSFL VQRVMRYPLLLMELLNSTPESHPDKVPLTNAVLAVKEINVN YKRRKDLVLKYRKGDEDSLMEKISKLNIHSIIKKSNRVSSH LTGFAPQIKDEVFEETEKNFFMQERLIKSFIRDLSLYLQHI ACVKVVAAVSMWDVCMERGHRDLEQFERVHRYISDQLFTNF TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAE DKKTLBELQSARNNYEALNAQLLDELPKFHQYAQGLFTNCV AEAHCDFVHQALEQLKPLLSLKVAGREGNLIAIFHBEHSR QLQVFTFPESLPATKKPFERKTIDRQSARKPLLGLPSYML ELRASLLARYPPEKLFQAERNFNAAQDLDVSLLEGDLVGVI: DPMGSQNRWLIDNGVTKGFVYSSFLKFYNPRRSHSDASVGSI	QMV AIA IKP INE LKH RES CER CLK HGY VLQ QSE CKK
IKVSKQLLAALEISDAVGPVFLGHRDELEGTYKIYCQNHDE  LLEIYEKDEKIQKHLQDSLADLKSLYNEWGCTNYINLGSFL VQRVMRYPLLLMELLNSTPESHPDKVPLTNAVLAVKEINVN YKRRKDLVLKYRKGDEDSLMEKISKLNIHSIIKKSNRVSSH LTGFAPQIKDEVPEETEKNFFMQERLIKSFIRDLSLYLQHI ACVKVVAAVSMWDVCMERGHRDLEQFERVHRYISDQLFTNF TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAE DKKTLBELQSARNYEALNAQLLDELPKFHQYAQGLFTNCVI AEAHCDFVHQALEQLKPLLSLLKVAGREGNLIAIFHEEHSR QLQVFTFFPESLPATKKPFERKTIDRQSARKPLLGLPSYML ELRASLLARYPPEKLFQAERNFNAAQDLDVSLLEGDLVGVII DPMGSQNRWLIDNGVTKGFVYSSFLKFYNPRRSHSDASVGSI	AIA IKP INE INE ICKH ICER ICLK IGY ILQ ISE ICKK
LLEIYEKDEKIQKHLQDSLADLKSLYNEWGCTNYINLGSFL VQRVMRYPLLLMELLNSTPESHPDKVPLTNAVLAVKEINVN YKRRKDLVLKYRKGDEDSLMEKISKLNIHSIIKKSNRVSSH LTGFAPQIKDEVFEETEKNFFMQERLIKSFIRDLSLYLQHI ACVKVVAAVSMWDVCMERGHRDLEQFERVHRYISDQLFTNF TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAE DKKTLEELQSARNNYEALNAQLLDELPKFHQYAQGLFTNCVI AEAHCDFVHQALEQLKPLLSLLKVAGREGNLIAIFHEEHSR QLQVVFTFFPESLPATKKPFERKTIDRQSARKPLLGLPSYMLI ELRASLLARYPPEKLFQAERNFNAAQDLDVSLLEGDLVGVII DPMGSQNRWLIDNGVTKGFVYSSFLKPYNPRRSHBDASVGSI	IKP INE IKH RES CER CLK IGY /LQ SEE CKK
VQRVMRYPLLLMELLNSTPESHPDKVPLTNAVLAVKEINVN YKRRKDLVLKYRKGDEDSLMEKISKLNIHSIIKKSNRVSSH LTGFAPQIKDEVFEETEKNFFMQERLIKSFIRDLSLYLQHI ACVKVVAAVSMUDVCMERGHRDLEQFERVHRYISDQLFTNF TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAE DKKTLEELQSARNNYEALNAQLLDELPKFHQYAQGLFTNCV AEAHCDFVHQALEQLKPLLSLLKVAGREGNLIAIFHEEHSR QLQVFTFFPESLPATKKPFERKTIDRQSARKPLLGLPSYML ELRASLLARYPPEKLFQAERNFNAAQDLDVSLLEGDLVGVI: DPMGSQNRWLIDNGVTKGFVYSSFLKPYNPRRSHSDASVGSI	INE LKH RES CER CLK IGY /LQ SEE CKK
YKRRKDLVLKYRKGDEDSLMEKISKLNIHSIIKKSNRVSSH LTGFAPQIKDEVFEETEKNFRMQERLIKSFIRDLSLYLQHI ACVKVVAAVSMWDVCMERGHRDLEQFERVHRYISDQLFTNF TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAE DKKTLEELQSARNNYEALNAQLLDELPKFHQYAQGLFTNCV AEAHCDFVHQALEQLKPLLSLLKVAGREGNLIAIFHEEHSR QLQVFTFFPESLPATKKPFERKTIDRQSARKPLLGLPSYML ELRASLLARYPPEKLFQAERNFNAAQDLDVSLLEGDLVGVI: DPMGSQNRWLIDNGVTKGFVYSSFLKPYNPRRSHSDASVGSI	CER CER CLK IGY /LQ SEE CKK
LTGFAPQIKDEVFEETEKNFRMQERLIKSFIRDLSLYLQHI ACVKVVAAVSMWDVCMERGHRDLEQFERVHRYISDQLFTNF TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAE DKKTLEELQSARNNYEALNAQLLDELPKFHQYAQGLFTNCV AEAHCDFVHQALEQLKPLLSLLKVAGREGNLIAIFHEEHSR QLQVFTFFPESLPATKKPFERKTIDRQSARKPLLGLPSYML ELRASLLARYPPEKLFQAERNFNAAQDLDVSLLEGDLVGVI: DPMGSQNRWLIDNGVTKGFVYSSFLKPYNPRRSHSDASVGSI	RES CER CLK IGY ILQ SE CKK
ACVKVVAAVSMWDVCMERGHRDLEQFERVHRYISDQLFTNF TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAE DKKTLEELQSARNYEALNAQLLDELPKFHQYAQGLFTNCV AEAHCDFVHQALEQLKPLLSLLKVAGREGNLIAIFHEEHSR QLQVFTFPESLPATKKPFERKTIDRQSARKPLLGLPSYML ELRASLLARYPPEKLFQAERNFNAAQDLDVSLLEGDLVGVI: DPMGSQNRWLIDNGVTKGFVYSSFLKFYNPRRSHSDASVGSI	CER CLK IGY VLQ SE CKK
TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAE  DKKTLEELQSARNNYEALNAQLLDELPKFHQYAQGLFTNCV.  AEAHCDFVHQALEQLKPLLSLLKVAGREGNLIAIFHEEHSR  QLQVFFFPESLPATKKPFERKTIDRQSARKPLLGLPSYML  ELRASLLARYPPEKLFQAERNFNAAQDLDVSLLEGDLVGVI:  DPMGSQNRWLIDNGVTKGFVYSSFLKFYNPRRSHSDASVGSI	CKK CKK CKK
DKKTLEELQSARNNYEALNAQLLDELPKFHQYAQGLFTNCV AEAHCDFVHQALEQLKPLLSLLKVAGREGNLIAIFHEEHSR QLQVFTFFPESLPATKKPFERKTIDRQSARKPLLGLPSYML ELRASLLARYPPEKLFQAERNFNAAQDLDVSLLEGDLVGVI DPMGSQNRWLIDNGVTKGFVYSSFLKPYNPRRSHSDASVGSI	IGY /LQ (KK
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ELRASLLARYPPEKLFQAERNFNAAQDLDVSLLEGDLVGVI DPMGSQNRWLIDNGVTKGFVYSSFLKPYNPRRSHSDASVGSI	CKK
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DPMGSQNAWLIDNGVTKGFVYSSFLKPYNPRRSHSDASVGS	
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DASPPPKEWDQGTLSASLNPSNSESSPSRCPSDPDSTSQPR	GD
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NQKLKILEFKDVTGNTEWWLAEVNGKKGYVPSNYIRKTEYT	
7015 1842 513 RQAWHE\VAAPSWRGARLVQSVLRVWQVGPHVARERVIPFS	LL
GFQRRCVSCVAGSAFSGPRLASASRSNGQGSALDHFLGFSO	DS
SVTPCVPAVSMNRDEQDVLLVHHPDMPENSRVLRVVLLGAPI	AG
KSTLSNQLLGRKVFPVSRKVHTTRCQALGVITEKETQVILLI	TP
GIISPGKQKRHHLELSLLEDPWKSMESADLVVVLVDVSDKW	'RN
QLSPQLLRCLTKYSQIPSVLVMNKVDCLKQKSVLLELTAAL	'EG
VVNGKKLKMRQAFHSHPGTHCPSPAVKDPNTQSVGNPQRIG	DH
FKE1FMLSALSQEDVKTLKQYLLTQAQPGPWEYHSAVLTSQT	יספי
EICANIIREKLLEHLPQBVPYNVQQKTAVWEEGPGGELVIQQ	VI
LVPKESYVKLLIGPKGHVISQIAQEAGHDLMDIFLCDVDIRI	CU
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7016 167 2513 ILNAPKPPPPRDSVEAVAAKRDTGGGSWGTGMDVSGQETDWR	O.D.
AFRQKLVSQIEDAMRKAGVAHSKSSKDMESHVFLKAKTRDEY	5 I
LVARLIIHFRDIHNKKSQASVSDPMNALQSLTGGPAAGAAGI	LS
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LPPQSQTQPLVSQAQALPGQMLYTQPPLKFVRAPMVVQQPPV	ΣÞ
QVQQQQTAVQTAQAAQMVAPGVQVSQSSLPMLSSPSPGQQVQ	ΓP
QSMPPPPQPSPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQ	P <b>F</b>
\QSPVTARTPQNFSVPSPGPLNTPVNPSSVMSPAGSSQAEEQ	ĮΥ
LDKLKQLSKYIEPLRRMINKIDKNEDRKKDLSKMKSLLDILT	OP.
SKRCPLKTLQKCBIALEKLKNDMAVPTPPPPPPPPTKQQYLC	ĮΡ
LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTR	CR.
RLEDDERQSIPSVLQGEVARLDPKFLVNLDPSHCSNNGTVHL	ıc
KLDDKDLPSVPPLELSVPADYPAQSPLWIDRQWQYDANPFLQ	3V
HRCMTSRLLQLPDKHSVTALLNTWAQSVHQACLSAA	
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FAFLAHTQREAYAPRIFFEASRPPWFTPRSQQDCSEYLRFLL	OR
LHEEEKILKVQASHKPSEILECSETSLQEVASKAAVLTETPR	rs
DGEKTLIEKMFGGKLRTHIRCLNCRSTSQKAEAFTDLSLAFW	· [
YSLEYMSCPDCSQSPSIQDGGLMQASVPGPSEEPVVYNPTTA	
ICDSLVNEKTIGSPPNEFYCSENTSVPNESNKILVNKDVPQK	2
GETTPSVTDLLNYFLAPEILTGDNQYYCENCASLQNAEKTMQ	AF
	AF PG
EEPEYLILTLLRFSYDQKYHVRRKILDNVSLPLVLELPVKRI	AF PG

,			
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	L.		
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ſ	amino acid	sequence	Codon, /=possible nucleotide deletion,
ľ	sequence		\=possible nucleotide insertion)
ļ	<del>                                     </del>	<u> </u>	FSSLSESWSVDVDFTDLSENLAKKLKPSGTDEASCTKLVPYLLS
Į	ļ	1	SVVVHSGISSESGHYYSYARNITSTDSSYOMYHOSEALALASSO
ł		1	
1		1	SHLLGRDSPSAVFEQDLENKEMSKEWFLFNDSRVTFTSFQSVQK
		1	ITSRFPKDTAYVLLYKKQHSTNGLSGNNPTSGLWINGDPPLQKE
1		1	LMDAITKDNKLYLQEQELNARARALQAASASCSFRPNGFDDNDP
		}	PGSCGPTGGGGGGFNTVGRLVF
7018	484	1066	SLVFRGNTWSGEAGHHCSALFNLAAYHOLFVGTERIRAPEIIFO
			PSLIGEEQAGIAETLQYILDRYPKDVQEMLVQNVFLTGGNTMYP
i	ł	1	
}	1	1	GMKARMEKELLEMRPFRSSFQVQLASNPVLDAWYGARDWALNHL
Ì		1	DDNEVWITRKEYEEKGGEYLKEHCASNIYVPIRLPKQASRSSDA
ŀ	Į.	1	QASSKGSAAGGGGAGEQA
7019	1048	335	APGGFLVTMVFPAPSPPWMLGCCSHEVTAGPPTLCKDMSALVAA
ĺ		1	RMRHIPLAPGSDWRDLPNIEVRLSDGTMARKLRYTHHDRKNGRS
			SSGALRGVCSCVEAGKACDPAARQFNTLIPWCLPHTGNRHNHWA
			GLYGRLEWDGFFSTTVTNPEPMGKQGRVLHPEQHRVVSVRECAR
1	}	1	SOGFPDTYRLFGNILDKHROVGNAVPPPLAKAIGLRIKLCMLAK
l .		ì	
L			ARESASAKIKEEEAAKD
7020	1	2154	FADSKRKSVLLDKIKNLQVALTSKQQSLETAMSFVARNTFKRVR
ì	1	1	NGFLMRKVAVFFSNTPTRASPQLREAVLKLSDAGITPLFLTRQE
	1	<b>,</b>	DROLINALQINNTAVGHALVLPAGRDLTDFLENVLTCHVCLDIC
	1		NIDPSCGFGSWRPSFRDRRAAGSDVDIDMAFILDSAETTTLFOF
1	J.	1	
l	Ì	1	NEMKKYIAYLVRQLDMSPDPKASQHFARVAVVQHAPSESVDNAS
1	1		MPPVKVEFSLTDYGSKEKLVDFLSRGMTQLQGTRALGSAIEYTI
	1		ENVFESAPNPRDLKIVVLMLTGEVPEQQLEEAQRVILQAKCKGY
	ł.	·	FFVVLGIGRKVNIKEVYTFASBPNDVFFKLVDKSTELNEEPLMR
i	1	1	FGRLLPSFVSSENAFYLSPDIRKQCDWFQGDQPTKNLVKFGHKQ
	1		VNVPNNVTSSPTSNPVTTTKPVTTTKPVTTTTKPVTT
1			INQPSVKPAAAKPAPAKPVAAKPVATKTATVRPPVAVKPATAAK
			<u> </u>
J	1	j	PVAAKPAAVRPPAAAAAKPVATKPEVPRPQAAKPAATKPATTKP
1			MVKMSREVQVFEITENSAKLHWERPEPPGPYFYDLTVTSAHDQS
1	1	1	LVLKQNLTVTDRVIGGLLAGQTYHVAVVCYLRSQVRATYHGSFS
			TKKSQPPPPQPARSASSSTINLMVSTEPLALTETDICKLPKDEG
	1	ľ	TCRDFILKWYYDPNTKSCARFWYGGCGGNBNKFGSQKBCEKVCA
			PVLAKPGVISVMGT
7021	2	338	VNAVSFFPNGYAFATGSDDATCRLFDLRADQELLLYSHDNIICG
1 ,021	1 4	336	-
1			ITSVAFSKSGRLLLAGYDDFNCNVWDTLKGDRAGVLAGHDNRVS
L			CLGVTDDGMAVATGSWDSFLRIWN
7022	2	856	VYIGSFWSHPLLIPDNRKLFEAEEQDLFRDIQSLPRNAALRKLN
	1 .	1	DLIKRARLAKVHAYIISSLKKEMPSVFGKDNKKKELVNNLAEIY
1	1		GRIEREHQISPGDFPNLKRMQDQLQAQDFSKFQPLKSKLLEVVD
	1		DMLAHDIAQLMVLVRQEESQRPIQMVKGGAFEGTLHGPFGHGYG
1			EGAGEGIDDAEWVVARDKPMYDEIFYTLSPVDGKITGANAKKEM
			VRSKLPNSVLGKIWKLADIDKDGMLDDDEFALANHLIKVKLEGH
1			ELPNELPAHLLPPSKRKVAE
7023	2	748	AMVFGGVVPYVPQYRDIRRTQNADGFSTYVCLVLLVANILRILF
1	1		WFGRRFESPLLWQSAIMILTMLLMLKLCTEVRVANELNARRRSF
	į.		<u>-</u>
1			TAADSKDEEVKVAPRRSFLDFDPHHFWQWSSFSDYVQCVLAFTG
1			VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST
1			EGMSIKMVLMWTSGDAFKTAYFLLKGAPLQFSVCGLLQVLVDLA
			ILGQAYAFARHPQKPAPHAVHPTGTKAL
7024	1207	190	RTGVTGVVAOVWMFGGGGVLSSGEOLOMPVKPERGLGPSDGWLV
1			SSRRGSPGTVLGLPFWLLTPVLVSRSIRSMLLLTRSPTAWHRLS
1	1	1	
			QLKPPVLPGTLGGQALHLRSWLLSRQGPAETGGQGQPQGPGLRT
1			RLLITGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAAVGQGD
			FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV
1		1	VRQLEAEPGLPPVQPVFITVDPERDDVEAMARYVQDFHPRLLGL
L	<u></u>		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Begacinee	\=possible nucleotide insertion)
	sequence		TGSTKQVAQASHSYRVYYNAGPKDEDQDYIVDHSIAIYLLNPDG
Į.			LFTDYYGRSRSAEQISDSVRRHMAAFRSVLS
2005	232	832	ERNSPIGNNENL*K\HSLDCLCFRGDWEGNTQFQTLQDNQEECF
7025	232	032	KQVIRTCEKRPTFNQHTVFNLHQRLNTGDKLNEFKELGKAFISG
l			SDHTQHQLIHTSEKFCGDKECGNTFLPDSEVIQYQTVHTVKKTY
}			ECKECGKSFSLRSSLTGHKRIHTGEKPFKCKDCGKAFRFHSQLS
1			VHKRIHTGEKSYECKECGKAFSCG
		1246	NPNPSIGDIKDIKKAAKSMLDPAHKSHFHPVTPSLVFLCFIFDG
7026	328	1146	LHOALLSVGVSKRSNTVVGNENEERGTPYASRFKDMPNFIALEK
}		}	SSVLRHCCDLLIGVAAGSSDKICTSSLQVQRRFKAMMASIGRLS
		i	HGESADLLISCNAESAIGWISSRPWVGELMFTFLFGDFESPLHK
1			LRKSS*LPRKHR*QPINAVRMFLDQCMDGSIALRAIVSEIPVFE
1			EKKNNG*KGIGEIF*VWGCTLPPHYWGAVTTNVPKLSNSGKLLG
		İ	
			QDEQPHIPG GRRLQQQQRPEDAEDGAEGGGKRGEAGWEGGYPEIVKENKLFEH
7027	43	954	
ļ.	į.		YYQELKIVPEGEWGQFMDALREPLPATLRITGYKSHAKEILHCL
]	ì		KNKYFKELEDLEMDGQKVEVPQPLSWYPEBLAWHTNLSRKILRK
1			SPHLEKFHQFLVSETESGNISRQEAVSMIPPLLLNVRPHHKILD
	}		MCAAPGSKTTQLIEMLHADMNVPFPEGFVIANDVDNKRCYLLVH
İ			QAKRLSSPCIMVVNHDASSIPRLQIDVDGRKEILFYDRILCDVP
			CSGDGTMRKNIDVWKKWTTLNSLQLHGLQLRIATRGAEQL
7028	189	608	SRPPPEPEGTMVEKGSDSSSEKGGVPGTPSTQSLGSRNFIRNS
Į			KKMQSWYSMLSPTYKQRNEDFRKLFSKLPEAERLIVDYSCALQR
ì	i		EILLQGRLYLSENWICFYSNIFRWETTISIQLKEVTCLKKEKTA
			KLIPNAIQ
7029	1343	40	VLESNTEAKQATGTSSKLRHGTGQEKGREGPRCPSGLAQLRLWG
1	ļ		/PCPHAGRETGPRASAPIPGS*GHGWHW*RKDGRGERSEGPSAL
1			SPHSPSLLNMQQAPTHVGPGMGSQRPRSSVVPEQVGVGSQLSRE
}		ļ	RWRA*RSLPGAAASERTEMTKERSP/RPCQGYDSSNWFTQPGKK
ì			TRKRNSRRNTMVSRGGGCLLYPLQSIMPE*QLR*GAHASPPTQG
l		1	R*GKGGPRSPLTKASGTTHIPTPFFGSIP/RPTRDSGPGTDNS\
I	1		AAPGQKRGHREA*QGPEPV/WGRVTTHLQGPAG*TKPLGS\RNW
l l			VPGPAEGEQGEGAGLEGRP*PLKGCRSTLTFSPQLSIPMVGKKP
i	į		PEGTTASFFP\RSCHSE*RKPPPSCPHAPALSLPHPLPLPLPLPL
1	1	ì	PLPLPGAGT*HSARSGRPGQSETGSLCHNCHHCPPHCPKCSPGG
L			T
7030	2	521	FVCFSAPGSGQGGKRRVNMELSAVGERVFAAEALLKRRIRKGRM
1			EYLVKWKGWSQKYSTWEPEENILDARLLAAFEEREREMELYGPK
			KRGPKPKTFLLKAQAKAKAKTYEFRSDSARGIRIPYPGRSPQDL
1		l.	ASTSRAREGLRN\RVCPRQRAAPAPAAP\PRRGPSGPGPRPG*G
}	1.		PGLHFPGPGGPSKHGFVPASEQHQHQQHLPRRGPSGPGPRPG
7031	960	59	HCSVPGAEWPRKPPAQICPQLTSRPHLSSPRSLSPGCGHSPGPG
		}	/CKPS/RHCDELHEGPSRTAALPCGKPQPKHGVEECG/PCPCLA
	1		PRRLTEPPALTVSPVGRAAPSGAL*PSGRACSACSHRLAPEAAL
1			SAAAPRPSLGSGQNASGLPAASLPPQDSSQPHKTVPSPARSVPP
			LGAQARAAPPRLWCPRALVSG*EASPEAVSVAAGPPVPGPTPST
1 .			SGSTASHSRRGC*SPR*TPAPPRRDHGRSAAFEVLTAAASAQPC
1			ASQGGPRPTGAGRTPSPLGLPFSRGPPAASARPFCRHPSL
7032	1393	2104	RRPGRTEPVEPPPVPPPPRASNSKSRCR*RNLHLAPL*QSPLRK
			SRQIGTSSLPFGRSAGERPRPAATFCLSRGGSSPVFL*PSSSSL
			EPWMKRQFGRLHSLFWKSWQKMNSFLLTPKLDTSLMSGWRYRQR
1			LPRLHTFLKKSLQMASELAPPLPTPAPLASSLPPPPGPPPLLPV
1			PLA*LSRSGILVPPNSGFSLSC\PLGDH*GSSGEVRGSCGSPPP
			HHCWVLPPPP*LLLPPR
7033	689	815	RSRDCLSSSATSNRARRSKCSGPKRATPLDSGPGP*APPGPSSA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence	bequence	\=possible nucleotide insertion)
	sequence	<del> </del>	LMMPSSCPWRTGALGPSPAGSRALGRCTSSVGPGSRWLTRTSSP
			GCATRTWRTMRMEPRPLRSRMGESAPGIPAELPSAAPSGPSAPS
			AAAPSAPTTPAAAGPNTL*SRRTAEWCWPPSCSCCWGWC*SWSA
	ł	Ì	WDWRRPPLOVSPAPSSSCRASCCWCLESIT*SSSTARSRATGAS
ļ	ļ		
			SSSTCPTSRSDRGAAWTP\SPMGAPLLPCSVPLISREEALQDPR
		<u> </u>	NPSP*GVCSGSSGHAGLALGKPPVACSVP
7034	92	1942	EDTSSMPFRLLIPLGLLCALLPOHHGAPGPDGSAPDPAHYRERV
			KAMFYHAYDSYLENAFPFDELRPLTCDGHDTWGSFSLTLIDALD
			TLL\TLFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI
İ			RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA
l			FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL
1		1	TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG
ł		1	IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW
i			YLWVOMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY
1			TVWKQFGGLPEFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT
1			GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF
}	}		FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI
l			FNTEAHPIDPAALHCCORLKEEOWEVEDLMRBFYSLKRSRSKFO
			KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS
ļ			OPFTSKLALLGOVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK
			K
7035	92	1942	EDTSSMPFRILIPLGLLCALLPOHHGAPGPDGSAPDPAHYRERV
/035	92	1942	KAMFYHAYDSYLENAFPFDELRPLTCDGHDTWGSFSLTLIDALD
ł			TLL\TLFYFOILGNVSEFORVVEVLQDSVDFDIDVNASVFETNI
ļ	1 .		
			RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA
Į	1		FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL
			TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG
			IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW
ļ		,	YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY
			TVWKQFGGLPEFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT
}			GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF
1			FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI
1			FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQ
1			KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS
i			QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK
1		}	K
7036	442	761	CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT
		1	RNW*BRKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP
1	,		PPPPPPPPPRRPPRNRRPG
7037	442	761	CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT
''''	1		RNW+ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP
1			PPPPPPPPPRRPPRNRPG
7030	155	891	GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL
7038	155	031	OYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ
			LOEMAQLRIKHOBELTELHKKRGELAQ\RVIDLNNQMQRKDREM
			QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA
1		1	LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR
		<u> </u>	LQEAASPAAERACRSSKGTSTSRTG
7039	155	891	GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL
1			QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ
1	1	1	LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM
1	1		QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA
	1	i	LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR
			LQEAASPAAERACRSSKGTSTSRTG
7040	34	789	KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS
	1		GYESVMRDSEATGSASSAQDSTSENSSSVGGRCRSLKTPKKRSN
1			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
No.	location	corresponding	H=Histidine, I=Isoleucine, K=bysine,
1		to first	
	corresponding		L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Í	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			PGSQRRRLIPALSLDTSSPVRKPPNSTGVRWVDGPLRSSPRGLG
		}	EPFEIKVYEIDDVERLQRRRGGASKEAMCFNAKLKILEHRQQRI
			AEVRAKYEWLMKELEATKQYLMLDPNKWLSEFDLEQVWELDSLE
			YLEALECVTERLESRVNFCKAHLMMITCFDIT
7041	1	567	SGRVAMGRRAPAGGSLGRALMRHQTQRSRSHRHTDSWLHTSEL
	_		NDGYDWGRLNLQSVTEQSSLDDFLATAELAGTEFVAEKLNIKFV
1	1	1	PAEARTGLLSFEBSQRIKKLHEENKQFLCIPRRPNWNQNTTPEE
	Ļ		LKQAEKDNFLEWRRQL\VRLEEEQKLILTPFERNLDFWRQLWRV
			IERSDIVVQIVDA
7043		245	
7042	7	345	PIHMAAAALRADI\ISPLFPHIQGYLLLSASHG\ATSLHTKGAL
1	1		PLETVTMYTVIPKSKYVLVKPDTQYPYSENLDEFKRLAENSASN
			DDLLMAEVAISDYGDKLTLELREKY
7043	2	2170	ARGMAARDSDSEEDLVSYGTGLEPLEEGERPKKPIPLQDQTVRD
1	1		EKGRYKRFHGAFSGGFSAGYFNTVGSKEGWTPSTFVSSRQNRAD
			KSVLGPEDFMDEEDLSEFGIAPKAIVTTDDFASKTKDRIREKAR
			QLAAATAPIPGATLLDDLITPAKLSVGFELLRKMGWKEGQGVGP
1	i		RVKRRPRRQKPDPGVKIYGCALPPGSSEGSEGEDDDYLPDNVTF
			APKDVTPVDFTPKDNVHGLAYKGLDPHQALFGTSGEHFNLFSGG
1		ļ	SERAGDLGEIGLNKGRKLGISGQAFGVGALEEEDDDIYATETLS
			KYDTVLKDEEPGDGLYGWTAPRQYKNQKESEKDLRYVGKILDGF
			SLASKPLSSKKIYPPPELPRDYRPVHYFRPMVAATSENSHLLQV
	<u> </u>		LSESAGKATPDPGTHSKHQLNASKRAELLGETPIQGSATSVLEF
			LSQKDKERIKEMKQATDLKAAQLKARSLAQNAQSSRAQPSPAAA
			AGHCSWNMALGGGTATLKASNFKPFAKDPEKOKRYDEFLVHMKO
			GQKDALERCLDPSMTEWERGRERDEFARAALLYASSHSTLSSRF
			1 1
1	{	ĺ	THAKEEDDSDQVEVPRDQENDVGDKQSAVKMKMFGKLTRDTFEW
1			HPDKLLFQ/RLVGLPRVKRDKYSVFNFLTLPETASLPTTQASSE
1			KVSQHRGPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK
	ļ		QQSSPLVNKEEEHAPELSAN
7044	276	734	EVYLTDEFAKGRKVADLYELVQYAGNIIPRLYLLITVGVVYVKS
	1		FPQSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQCTRNILPDEG
ŀ	Ì		EPTDEETTGDISDSMDFVLLNFAEMNKLWVRMQHQGHSRDREKR
	1		ERERQELRILVGTNLVRLSQV
7045	3	513	LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP
	1		KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK
1	1	1	DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE
1			ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG
7046	3	513	LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP
1	_		KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK
	1	1	DLEFOLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE
			ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG
7047	103	486	
, , , ,	103	****	QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN
			IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPRDFKEKY
<u></u>		<u> </u>	NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER
7048	92	627	FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEEEEANY
1	1	ļ	WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN
	1	1	RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA
			IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI
			EKKW
7049	393	938	KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL
			VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL
			NNYBIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT
1	1		EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX
ì		l	ASSLWG
7050	393	938	KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKI PARRCYEDEL
,,,,,	T 333	1	INCLOSED TOUR F FOLOGRATAAS VAGRCSSVGRI PARKCIEUEL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W*Tryptophan, Y*Tyrosine, X*Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	2042000	\=possible nucleotide insertion)
<del></del>	<u> </u>		VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL
			NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT
ļ.			EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLTAWX
1			ASSLWG
7051	119	816	KKMNLABICDNAKKGREYALLGNYDSSMVYYOGVMOOIORHCOS
			VRDPAIKGKWQQVRQELLEEYEQVKSIVGTLESFKIDKPPDFPV
1			SCQDEPFRDPAVWPPPVPAEHRAPPQIRR/RQSRSKTSEERNGR
}	}		SRSPGTCRPST\PISKSEKPSTSRDKDYRARGRDDKGRKNMODG
i			ASDGEMPKFDGAGYDKDLVEALERDIVSRNPSIHWDDIADLEEA
!			KKLLREAGVLPMWM
7052	467	715	SCPGRGKMSKLLNPEEMTSRDYYFDSYAHFGIHEEMLKDEVRTL
		1	TYRNSMYHNKHVFKDKVVLDVGSGTGILSMFAARQGPRR
7053	467	715	SCPGRGKMSKLLNPEEMTSRDYYFDSYAHFGIHEEMLKDEVRTL
1			TYRNSMYHNKHVFKDKVVLDVGSGTGILSMFAAROGPRR
7054	1	1036	GTSQRSRETDARRRSAGAEPTARLPWPAALEEWPSCPCEPLGPG
ļ			RRCRWDAMEYDEKLARFRQAHLNPFNKQSGPRQHEQGPGEEVPD
}	}		VTPEEALPELPPGEPEFRCPERVMDLGLSEDHFSRPVGLFLASD
	ļ		VQQLRQAIBECKQVILELPEQSBKQKDAVVRLIHLRLKLOELKD
j	ļ		PNEDEPNIRVLLEHRFYKEKSKSVKQTCDKCNTIIWGLIQTWYT
			CTGCYYRCHSKCLNLISKPCVSSKVSHQAEYELNICPETGLDSQ
1			DYRCAECRAPI/CS/DGVVPSEARQCDYTGQYYCSHCHWNDLAV
ĺ			IPARVVHNWDFEPRKVSRCSMRYLALMVSRPVLRLREIN
7055	2	527	DSRRVSWRSWLANE/WGKHLCLFIWLSMNVLLFWKTFLLYNQGP
ĺ	İ		EYHYLHQMLG/ALCLSRASASVLNLNCSLILLPMCRTLLAYLRG
			SQKVPSRRTRRLLDKSRTFHITCGATICIFSGVHVAAHLVNALN
ì			FSVNYSEDFVELNAARYRDEDPRKLLFTTVPGLTGVCMEVVLFL
			M
7056	2	527	DSRRVSWRSWLANE/WGKHLCLFIWLSMNVLLFWKTFLLYNQGP
ļ			EYHYLHQMLG/ALCLSRASASVLNLNCSLILLPMCRTLLAYLRG
j			SQKVPSRRTRRLLDKSRTFHITCGATICIFSGVHVAAHLVNALN
			FSVNYSEDFVELNAARYRDEDPRKLLFTTVPGLTGVCMEVVLFL
L			M
7057	1368	431	GIYLHVNEKIPRPTCIGDRQENDKENLNLENHRDQELLHASCQA
].			SGEVPSQASLRGFFTEDEPGCFGEGENLPEALQNIQDEGTGEQL
	[		SPQERISEKQLGQHLPNPHSGEMSTMWLEEKRETSQKGQPRAPM
			AQKLPTCRECGKTFYRNSQLIFHQRTHTGETYFQCTICKKAFLR
1		1	SSDFVKHQRTHTGEKPCKCDYCGKGFSDFSGLRHHEKIHTGEKP
[		'	YKCPICEKSFIQRSNFNRHQRVHTGEKPYKCSHCGKSFSWSSSL
			DKHQRSHLGKKPFQ*PVTKLSFPISISQPSHKNTQLHQEELCLR
7058		460	GYPC
1058	1	469	FSGFGAVPDALGCRMSDLRITEAFLYMDYLCFRALCCKGPPPAR
	J		PEYDLVCIGLTGSGKTSLLSKLCSESPDNVVSTTGFSIKAVPFQ
1			NAILNVKELGGADNIRKYWSRYYQGSQGVIFVLDSASSEDDLEA
7050	<del> </del>	1270	ARN*SCTQLLQHPQLCTLPFLILA
7059	1	1178	WPAFPRQPAAAAMDALLGTGPRRARGCLGAAGPTSSGRAARTPA
1			APWARPSAWLECVCVVTFDLELGQALELVYPNDFRLTDKEKSSI
	1	]	CYLSFPDSHSGCLGDTQFSFRMRQCGGQRSPWHADDRHYNSRAP
	l		VALQREPAHYFGYVYFRQVKDSSVKRGYFQKSLVLVSRLPFVRL
	1	ļ	FQALLSLIAPEYFDKLAPCLEAVCSEIDQWPAPAPGQTLNLPVM
	1	1	GVVVQVRIPSRVDKSESSPPKQFDQENLLPAPVVLASVHELDLF
	I	]	RCFRPVLTHMQTLWELMLLGEPLLVLAPSPDVSSEMVLALTSCL
	1		QPLRFCCDFRPYFTIHDSEFKBFTTRTQAPPNVVLGVTNPFFIK
7060	90		TLQHWPHILRVGEPKMSGDLPKQVKLKKPFKV*RPWDTKP
/580	90	1670	SVNLPPSLWPWEEAMDSTKSEPLKGSPEAEDGNIEYKKLVNPSQ
L	L	L	YRFEHLVTQMKWRLQEGRGEAVYQIGVEDNGLLVGLAEEEMRAS

Deginning   location   cortesponding to first   contrasponding to first   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue of   anino acid   residue	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No:   nucleotide   corresponding   corresponding   corresponding   corresponding   corresponding   cofirst   maino acid   residue of   maino acid   residue of   maino acid   sequence   sequence   sequence   sequence   sequence   sequence   codon, /-possible nucleotide deletion,   sequence   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide deletion,   codon, /-possible nucleotide				
corresponding to first anino acid residue of anino acid anino acid residue of anino acid sequence   E-		_ ~		
to first amino acid residue of residue of amino acid residue of amino acid sequence  Seserine, T-Threonine, V-Valine, amino acid sequence  Codon, /-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible n	NO:			
to first amino acid residue of amino acid residue of amino acid amino acid sequence  #TYPYEOplan, Y=Tyrosine, X=Unknown, *=Stop amino acid sequence  #TYPYEOplan, Y=Tyrosine, X=Unknown, *=Stop Codon, Y=possible nucleotide deletion LYCTHERMERVSADTYUREREVYDEODAPPKITEVUYREVDM OPPLATIVEREREVYDEODAPPKITEVUYREVDM OPPLATIVEREREVYDEODAPPKITEVUYREVDM OPPLATIVEREVYDEODAPPKITEVUYREVDM OPPLATIVEREVYDEODAPPKITEVUYREVDM OPPLATIVEREVYDEODAPPKITEVUYREVDM OPPLATIVEREVYDEODAPPKITEVUYREVDM OPPLATIVEREVYDEODAPPKITEVUYREVDM OPPLATIVEREVYDEODAPPKITEVUYREVDM OPPLATIVEREVYDEODAPPKITEVUYREVDM OPPLATIVEREVYDEODAPPKITEVUYREVED OPPLATIVEREVYDEODAPPKITEVUYREVED OPPLATIVEREVYDEODAPPKITEVUYREVED OPPLATIVEREVYDEODAPPKITEVUYREVE OPPLATIVEREVYDEODAPPKITEVUYREVE OPPLATIVEREVYDEODAPPKITEVUYREVE OPPLATIVEREVYDEODAPPKITEVUYREVE OPPLATIVEREVYDEODAPPKITEVUYREVE OPPLATIVEREVYDEODAPPKITEVUYREVE OPPLATIVEREVYDEODAPPKITEVUYREVE OPPLATIVEREVYDEODAPPKITEVUYREVE OPPLATIVEREVYDEODAPPKITEVUYREVE OPPLATIVEREVYDEODAPPKITEVUYREVE OPPLATIVEREV OPPLATIVEREVYDEODAPPKITEVUYREVE OPPLATIVEREV OPPLATIVEREVYDEODAPPKITEVUYREVE OPPLATIVEREV OPPLATIVEREVYDEODAPPKITEVUYREVE OPPLATIVEREV OPPLATIVEREVYDEODAPPKITEVUYREVE OPPLATIVEREV OPPLATIVEREVYDEODAPPKITEVUYREVE OPPLATIVEREVE OPPLATIVEREVYDEODAPPKITEVUYREVE OPPLATIVEREVE OPPLATIVEREVYDEODAPPKITEVUREVE OPPLATIVEREVE OPPLATIVEREVYDEODAPPKITEVUREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEROPORE  TOGO OPPLATIVE OPPLATIVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEREVE OPPLATIVEROPORE OPPLATIVE OPPLATIVE OPPLATIVE OPPLATIVE OPPLATIVE OPPLATIVE OPPLATIVE OPPLATIVE OPPLATIVE OPPLATIVE OPPLATIVE OPPLATIVE OPPLATIVE OPPLATIVE OPPLATIVE OPPLATIVE OPPLATIVE OP	ļ			
amino acid residue of amino acid sequence    W=TryPcophan, Y=Tyrcosine, Y=Valine,   W=TryPcophan, Y=Tyrcosine, Y=Unknown, *-Stop   Codon, /=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=possible nucleotide deletion,   V=po	ļ.			
meind acid sequence    W-Tryptoplan, Y-Tyrosine, X-Unknown, *-Stop   Codon, /-possible nucleotide deletion,     V-possible nucleotide deletion,     V-possible nucleotide deletion,     V-possible nucleotide deletion,     V-possible nucleotide insertion,     V-possible nucleotide insertion,     V-possible nucleotide insertion,     V-possible nucleotide insertion,     V-possible nucleotide insertion,     V-possible nucleotide insertion,     V-possible nucleotide insertion,     V-possible nucleotide insertion,     V-possible nucleotide insertion,     V-possible nucleotide insertion,     V-possible nucleotide insertion,     V-possible nucleotide insertion,     V-possible nucleotide insertion,     V-possible nucleotide insertion,     V-possible nucleotide insertion,     V-possible nucleotide insertion,     V-possible nucleotide     V-possible nucleotide insertion,     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-possible nucleotide     V-		1		
amino acid sequence Codom, /-possible nucleotide deletion, V-possible nucleotide insertion)  LKTLERMERCVADITYLERRENTYDEDMERKITEVLYREVEDM OOFLDLRVAVLENDVERSTLEUTIGELDNERGRARLHERH LHEI QSGRYSISFEILGFISKGEVENINGTORGRARLHERH LHEI QSGRYSISFEILGFISKGEVENINGTORGARLHERH LHEI QSGRYSISFEILGFISKGEVENINGTORGARLHERH VKIKKGCHFGNISLOFORSEOVGRAGRIH GYBALGQVYNYSDSS TABELCESSSKNITFIDLAGHKKTLHTITIGLISYCEPOCALLLY OLERVLKOPGCHKVPHILTSEDDAVTAAQGPAGSFNYTPIFTLS SVSGRSEDLLKVFHILTBEDDAVTAAQGPAGSFNYTPIFTLS SVSGRSEDLLKVFHILTBEDDAVTAAQGPAGSFNYTPIFTLS SVSGRSEDLLKVFHILTBEDDAVTAAQGPAGSFNYTPIFTLS SVSGRSEDLLKVFHILTBEDHTNSKEGELMQCITEFPOVERTY PEWGTVVGGTISSR IDLLATLEPTOSSITYSKTSWEGGDEGI 7061 364 710 ARPSFLOPELGPRONDETTILEEPTERARERGFCYGEVAGERE ALARLRELCCOMLOPERISKEGUNGENIVATEQPOVERTY EEPETAALRERGCYCQEVAGFREALAGLELCCOMLOPEAHSKE GGROGSFEERAALVSGLGIDE)-ARMSFLOPPCLTYMDPETTL EEPETAALRERGCYCQEVAGFREALAGLELCCOMLOPEAHSKE GGROGSFEERAALVSGLGIDE)-ARMSFLOPPCLTYMDPETTL EEPETAALRERGCYCQEVAGFREALAGLEELCCOMLOPEAHSKE GGROGSFEERALDVATHERSGCHOPEAHARENGAVENAVAGGREG OMLEWLAUEGFLGTLEPSFLORGHEIGHEN SCHOPPCHATAGER FOOLG  7062 71 744 ALAGTMERLINGSYFEIDEMINISTSGCHOPAGTAGGER TAIYCLTQNEWRLDEATDSFPONDSLERGAALVEGLQHD PGOLLG VKIKKOPQDBKKICVORIGQCFDOLSLEPSLOPPCHATAKOR FYOPTTTTAROPCKOLDSHKIKANLHERSGCHOVAGCTAGGER TAIYCLTQNEWRLDEATDSFPONDSLEQAEDLAARERA TQCEFSEREPLDOWRICHOSHSKIKANLHERSGCHOVAGCHACTAGER VKIKKOPQDBKKICVORIGQCFDOLSLEPSLOPPCHATAGATAGATAGATAGATAGATAGATAGATAGATAGATA		l		
A-possible nucleotide insertion	ſ			
LKTLHRMAEKVGADITVLEREVDYDSDMPRITTRVLVRKVPDD  OQPLOLRVAVLGNUDSGKSTLIGUTGQELDMGRAELINEPH LHSIGGGRTSSISPELIGINSKGEVGGINGTOWGGTLRWGAN*++  RT*PGGRVWRLEFU*+WANLGGLT** TSSAPLEKSWGADIA** HAN VKIRQGHPGNGLGPONSGOVGRAGREH*GPWALGQVVWYSDSR TABEIGBSSSKWITFIDLAGHRKTLHTI** FGUTSYCPCCALLU* SANTGAGTRENLEFT** LOUIS GROWN THE FLOURY COLOR TO THE STAPLEKS SANTATE TO THE STAPLEKS SANTATE TO THE SANTATE SANTATE TO THE SANTATE SANTATE TO THE SANTATE TO THE SANTATE SANTATE TO THE SANTATE SANTATE SANTATE TO THE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SANTATE SA	ļ		sequence	•
OQPELDER VALCENVOSCHSTELLGYNEGGERGERICHT WER HE HER INGGERTSSTEPE LIGHNEGGERGINGTOWGOTHEWGM** RT*DGGRWRLFEIV*NNALRGI*TSSAPLEKSMGNQLM*ING VKIKRQGHPONGEOVORAGRRH*OPPALGQVVMYSDSR TABEIGESSSKMITT IDLAGHRYLETTITGITSTYCDECALLEV SANTGIAGTTREHLGIALALAKVFFIVVSKIDLCAKTIVEKTYV QLERVLKOPGCIKVPMINTSEDDAVTAAQOPAGSMVTPIFTILS SVSGSSLDLLKVFLINILPPLINSKRGEELMQGLTEFQVDEITYT PROGTVVUGTISER*IDLALATLPOPSPITYSKTSMFKOPCOPTAGE TOGAL  7061 364 710 ARMPSELDPCLPVMDPETTLESPETAGLERFROFCYGEVAGFRE ALARLBELCOGULOPEANSKE MEMULUSOPIGLIPPSICAKTY RGQROSSEEMAALVEGLOHDP*ARMPSPLGPCLPVMDPETT EEPETALRERGFCYOEVAGREEAHERULICOCHOPEANSKE OMLEMILUSOPIGLAGHRENGLOOPPEANSKE OMLEMILUSOPIGLAGHRENGLOOPPEANSKE OMLEMILUSOPIGLAGHRENGLOOPPEANSKE OMLEMILUSOPIGLAGHRENGLOOPPEANSKE OMLEMILUSOPIGLAGHRENGLOOPPEANSKE OMLEMILUSOPIGLAGHRENGLOOPPEANSKE OMLEMILUSOPIGLAGHRENGLOOPPEANSKE OMLEMILUSOPIGLAGHRENGLOOPPEANSKE OMLEMILUSOPIGLAGHRENGLOOPPEANSKE OMLEMILUSOPIGLAGHRENGLOOPPEANSKE OMLEMILUSOPIGLAGHRENGLOOPPEANSKE OMLEMILUSOPIGLAGHRENGLOOPPEANSKE OMLEMILUSOPIGLAGHRENGLOOPPEANSKE OMLEMILUSOPIGLAGHRENGLOOPPEANSKE OMLEMILUSOPIGLAGHRENGLOOPPEANSKE OMLEMILUSOPIGLAGHRENGLOOPPEANSKE OMLEMILUSOPIGLAGHRENGLOOPPEANSKE OMLEMILUSOPIGLAGHRENGLOOPPEANSKE OMLEMILUSOPIGLAGHRENGLOOPPEANSKE TORTOTOPPETTAANSGORGLOOPPEANSKENDLAGHRENGLOOPPEANSKE TORTOTOPPETTAANSGORGLOOPPEANSKENDLAGHRENGLOOPPEANSKE TORTOTOPPETTAANSGORGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENGLOOPPEANSKENDLAGHRENG		seducince	<del> </del>	<u> </u>
LHEIGSGRESISPELGENSKEUWGINGTOMGGTLRMGM** HING PT*DGGRWALEUF** WANLAGU** TSAP, PLRSWOLGM** HING VKI KRGGHPGNIGJGPONSGOVGRAGREH** GPWALGQVVWYSDSR TABEIGBSSSWITT IDLAGHKYLETTI* TIGLTSYCPDCALLU* SANTGIAGTTREHGLALALWYFTUVSKIDLOCARTIVEKTUV QLERVLKOPGCKKVPMLVTSEDDAVTAAQOPAQSSWNTFIFTLY SVSGSSEDLLKVFILIDIPLINSKEGELMQQLTERTUVETY PEVGIVVGGTLSR** IDLAATLPTQPSPIYSKTSMFKGGDPGI  7061 364 710 ARMPSELGPPCLYDMFTTTLEBEPTALEKREFCYQEVAGFRE ALARLBELCOGNLOPEAHSKEQMLEMIVLEQFLOTIJPSPIYAGK RGQROSPEENAALVEGLOHD** ARMPSPIGAPPCIPVMPBTTTL EEPETARLRFRGFCYQEVAGPREALARLBELCCONLQPEAHSKE QMLEMIVLEQFLGTI-PPEIQAWVRGQRFGSPEENAALVEGLOHD* FGOLLG  7062 71 744 AKAGTNLERLHMLSYFFCIPKHLKSSQKDKVRQFHACTQAGER AKAGTNLERLHMLSYFFCIPKHLKSSQKDKVRQFHACTQAGER PGOLLG  7063 71 744 AKAGTNLERLHMLSYFFCIPKHLKSSQKDKVRQFHACTQAGER TAIYLCTONNEMLDEATDSFFQNPDSILHRESMRNADVRKKLERL YGRYKDDPQDBNKIGVDGIQOFCDDLSLDPASISVLVIJAMKFRAN TQCFFSRKFELDGDTFELGCDMBKKLRALLPRLEGELDATAKFKN FYOPTFTAANDGQKGLDL**AGAYWKLVLSGRFKFLYLMNTPL MEH  7063 2 562 LETYPDLGBREFRANRTCORR**PELDPDMSLEQAEDLXAFFER FYOPTSTANNEDFTISCITLIGLEPAGHKKVVARSILARARCTVLAS EYMMSCDDTGKLILKRPRHVQ**QSSLIVMGLKAFERISDTAKS HKOFLIRLIM  7064 300 584 RDTGSDFSSTRLCSTCTGH**PAEPIASPHSRGTCPPASSAS HKOFLIRLIM SRTGCWTCPPESGHAQARSRRRASASKWGARGAVRAARGG SSRAGRMLETFGRRGPPACAAAAGRLEGFAP**AAPPTASVPAR CCPAARTGAPAATMURRISGIARPALGRRSGGPSKASAP PLITPLAGREAGGRANS CREARTGAPAATMURRISGIARPALGRRSGGPSKASAP CREARTGAPAATMURRISGIARPALGRRSGGPSKASAP PLITPLAGREAGGRANS CREARTGAPAATMURRISGIARPALGRRSGGPSKASAP PLITPLAGREAGGRANS CREARTGAPAATMURRISGIARPALGRRSGGRANASAVAARGG CREARTGAPAATMURRISGIARPALGRRSGGPSKASAP CREARTGAPAATMURRISGIARPALGRRSGGRANASAVAARGG CREARTGAPAATMURRISGIARPALGRRSGGPSKASAP CREARTGAPAATMURRISGIARPALGRRSGGPSKASAP CREARTGAPAATMURRISGIARPALGRRSGGPSKASAP CREARTGAPAATMURRISGIARPALGRRSGGRANASAVAARGG CREARTGAPAATMURRISGIARPALGRRSGGRANASAVAARGG CREARTGAPAATMURRISGIARPALGRRSGGRANASAVAARGG CREARTGAPAATMURRISGIARPALGRRSGGRANASAVAARGG CREARTGAPAATMURRISGIARPALGRRSGGRANASAVARGG CREARTGAPATMURRISGIARPALGRAPAATMURQTCTT TYNGKUSTATMURCHTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	Į.			
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SRRTGCWTCPPESGHAQARRSRRASASRWGARGAVRSAVAARGC SSRAGRWLEFTGRRRGPPACAAAAGRLRGPAP*AAPPTASVPAR CRCPAARTGAPAAATWARRLSGLRAPALGRRRSPGPSPKSAAP PLITPLGAGRAGGSRANS  7065 1 555 ATTTHSARRSGRGAAAEAASAAGGRQKGFDRKAWEGRRTTPGG RSQSEPKAPPPQKRSEAAFASMAHSPVAVQVVGMQNNIADPEEL FTKLERIGKGSFGEVFKGIDNRTQQVVAIKIIDLEEAEDEIEDI QQEITVLSQCDSSYVTKYYGSYLKGSKLWIIMEYLGGGSALDLL RAGPFDEFQ 7066 356 676 PGPQRGPWRAREGGHPLDPADHPRAPASLRSNVRAATMMQICDT YNQKHSLFNAMNRFIGAVNNMDQTVMVPSLLRDVPLADPGLDND VGVEVGGSGGLBERTPP  7067 152 973 KENITMATEIGSPPRFFHMPRFQHQAPRQLFYKRPDFAQQQAMQ QLTFDGKRMRKAVNRKTIDYNPSVIKYLENRIWQRDQRDMRAIQ PDAGYYNDLVPPIGMLNNPMAVTTKFVRTSTNKVKCPVFVVRW TPEGRRLVTGASSGEFTLWNGLTFNFETILQAHDSPVRAMTWSH NDMMMLTADHGGYVKYWQSNMNNVKHFQAHKEAIREARFTHNIP FSVVPIVMVKLFSKCILGAEMHGLCOFLGNFLHPINTIFFFVFT HSPFCWAPF  7068 222 816 DTMKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDDDDNSLFPTRERSHFFPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILINNKLITKIHPKAPLITTKKLRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKIQKDTPKKK  7069 1147 1765 FRDHRYPFYNNEGSGESQWEFPGGEBEEESQQQENRDETLAKQ TLKDKTGTDSNTESSETSTGSLCKESFSQQVSSSSLMPLTPFW	7064	300	884	I
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NDMWMLTADHGGYVKYWQSNMNNVKMFQAHKEAIREARFIHNIP FSVVPIVMVKLFSKCILGAEMHGLCQFLGNFLHPINTIFFFVFT HSPFCWAPF  7068 222 816 DTMKEYVLLLFLALCSAKPFFSPSHTALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDDLFPTREPRSHFFPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKIQKDTFKKK  7069 1147 1765 FRDHRRYFYVNEQSGESQWEFPDGEBEEEESQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKBSFSGQVSSSSLMPLTPFW		] .		PDAGYYNDLVPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRW
FSVVPIVMVKLFSKCILGAEMHGLCQFLGNFLHPINTIFFFVFT HSPFCWAPF  7068 222 816 DTMKEYVLLLFLALCSAXPFFSPSHTALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDNSLFPTREPRSHFFPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKIQKDTFKKK  7069 1147 1765 FRDHRRYFYVNEQSGESQWEFPDGEBEEEESQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKBSFSGQVSSSSLMPLTPFW		1		TPEGRRLVTGASSGEFTLWNGLTFNFETILQAHDSPVRAMTWSH
HSPFCWAPF  7068 222 816 DTMKEYVLLIFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDDDDDDFDRSLFPTRE PRSHFFPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNI PFDTRMLDLQNNKI KEI KENDFKGLTSLY GLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEI PLNLPKSL AELRIHENKVKKI QKDTFKKK  7069 1147 1765 FRDHRRYFYVNEQSGESQWEFPDGEBEEEESQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKBSFSGQVSSSSLMPLTPFW		1		NDMWMLTADHGGYVKYWQSNMNNVKMFQAHKEAIREARFIHNIP
7068 222 816 DTMKEYVLLFLALCSAKPFFSPSHTALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDDNSLFPTREPRSHFFPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKIQKDTPKKK 7069 1147 1765 FRDHRRYFYVNEQSGESQWEFPDGEBEEEESQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKBSFSGQVSSSSLMPLTPFW	1			FSVVPIVMVKLFSKCILGAEMHGLCQFLGNFLHPINTIFFFVFT
DDDDDDDDDDDDDDDDLFPTREPRSHFFPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKIQKDTPKKK 7069 1147 1765 FRDHRRYFYVNEQSGESQWEFPDGEBEEEESQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKBSFSGQVSSSSLMPLTPFW				HSPFCWAPF
VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKIQKDTPKKK 7069 1147 1765 FRDHRRYFYVNEQSGESQWEFPDGEBEEEESQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKBSFSGQVSSSSLMPLTPFW	7068	222	816	DTMKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD
GLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKIQKDTPKKK  7069 1147 1765 FRDHRRYFYVNEQSGESQWEFPDGEBEEEESQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKBSFSGQVSSSSLMPLTPFW				DDDDDDDDDDDDDDDDDDSLFPTREPRSHFFPFDLFPMCPFGCQCYSRV
AELRIHENKVKKIQKDTFKKK  7069 1147 1765 FRDHRRYFYVNEQSGESQWEFPDGEBEEEESQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKBSFSGQVSSSSLMPLTPFW		1		VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY
7069 1147 1765 FRDHRRYFYVNEQSGESQWEFPDGEBEEEESQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKBSFSGQVSSSSLMPLTPFW		1		GLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL
TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW				AELRIHENKVKKIQKDTFKKK
	7069	1147	1765	FRDHRRYFYVNEQSGESQWEFPDGEBEEEESQAQENRDETLAKQ
TI, I, CONVENT CONTROL TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE				TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW
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SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ľ	amino acid	sequence	Codon, /=possible nucleotide deletion,
Į.	sequence		\=possible nucleotide insertion)
			EKTKKGRKDKAKKSKTKMPSLVKKWQSIQRELDEEDNSSSSEED
Į.			RVSTAQKRIEEWKQQQLVSGMAERNANFEA
7070	1	547	DGTMEDSEAVQRATALIEQRLAQEEENEKLRGDARQKLPMDLLV
}			LEDEKHHGAQSAALQKVKGQERVRKTSLDLRREIIDVGGIQNLI
			ELRKKRKQKKRDALAASHEPPPEPEEITGPVDEETFLKAAVEGK
1			MKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNG
1			ATVDFQ
7071	2	921	ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP
1	_		VSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIQY
1			FODPRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNV
1		1	PESSLPPASMPYADHYSTFSPRDRMNSSPYQPPPPQPYGPVPPV
			PSGMYAPVYDSRRIWRPPMYORDDIIRSNSLPPMDVMHSSVYOT
1			SLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQ
	j		IRRKPDOWAQYHTQKAPLVSSTLPVATQSPTPPSTLNRGEGS
7072	2	921	ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP
7072	1 4	1 721	VSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIQY
į.		l	FQDPRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNV
		1	PESSLPPASMPYADHYSTFSPRDRMNSSPYQPPPPQPYGPVPPV
1			PSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQT
1	Į.		SLRERYNSLDGYYSVACOPPSEPRTTVPLPREPCGHLKTSCEEQ
1	i		1
			IRRKPDQWAQYHTQKAPLVSSTLPVATQSPTPPSTLNRGEGS
7073	50	504	LAHGSFGVSDFPAPAAAPAHTLTSFSGSLSPQFRKPLGRAPAMP
ļ			LVRYRKVVILGYRCVGKTSLAHQFVEGEFSEGYDPTVENTYSKI
			VTLGKDEFHLHLVDTAGQDEYSILPYSFIIGVHGYVLVYSVTSL
	<u> </u>		HSFQVIESLYQKLHEGHGK
7074	263	1003	VCPVLCSTRQEPGHSSLVTYFGKPTRRKEFLLGHCIAAGKMNIS
			VDLETNYAELVLDVGRVTLGENSRKKMKDCKLRKKQNERVSRAM
			CALLNSGGGVIKAEIENEDYSYTKDGIGLDLENSFSNILLFVPE
			YLDFMQNGNYFLIFVKSWSLNTSGLRITTLSSNLYKRDITSAKV
			MNATAALEFLKDMKKTRGRLYLRPELLAKRPRVDIQEENNMKAL
			AGVFFDRTELDRKEKLTFTESTHVEI
7075	598	1005	NYINFFFRKEYPPHVQKVEINPVRLSRLQGVERIMKKTEESESQ
1			VEPEIKRKVQQKRHCSTYQPTPPLSPASKKCLTHLEDLQRNCRQ
			AITLNESTGPLLRTSIHQNSGGQKSQNTGLTTKKFYGNNVEKVP
			IDII
7076	279	1049	LQSESSNAAEGNEQRHEDEQRSKRGGWSKGRKRKKPLRDSNAPK
			SPLTGYVRFMNERREQLRAKRPEVPFPEITRMLGNEWSKLPPEE
			KQRYLDEADRDKERYMKELEQYQKTEAYKVFSRKTQDRQKGKSH
			RODAARQATHDHEKETEVKERSVFDIPIFTEEFLNHSKAREAEL
			RQLRKSNMEFEERNAALQKHVESMRTAVEKLEVDVIQERSRNTV
			LQQHLETLRQVLTSSFASMPLPEXGETPTVDTIDSYM
7077	3	1119	SSMGSNSEINGLALRKTDKYGFLGGSQYSGSLKSSIPVDVARQR
1			ELKWLDMFSNWDKWLSRRFQKVKLRCRKGIPSSLRAKAWQYLSN
			SKELLEONPRKFEELERAPGDPKWLDVIEKDLHRQFPFHEMFAA
			RGGHGQQDLYRILKAYTIYRPDEGYCQAQAPVAAVLLMHMPAEQ
			AFWCLVQICDKYLPGYYSAGLBAIQLDGBIFFALLRRASPLAHR
			HLRRQRIDPVLYMTEWFMCIFARTLPWASVLRVWDMFFCEGVKI
1			IFRVALVLLRHTLGSVEKLRSCQGMYETMBQLRNLPQQCMQEDF
1	1		LVHEVTNLPVTEALIERENAAQLKKWRETRGELQYRPSRRLHGS
1			RAIHEERRRQQPPLGPSSS
7078	483	767	FOGORMAGEOKPSSNLLEOFILLAKGTSGSALTALISQVLEAPG
1	1	1	VYVFGELLELANVQBLAEGANAAYLQLLNLFAYGTYPDYIANKE
			SLPELY
7079	<del></del>	376	SVVEFKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ
10,3	1	]	MOARKKRRGIIEKRRRDRINSSLSELRRLVPTAFEKQGSSKLEK
L			

Deginning   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Corresponding   Cofficial   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Co	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No.   nucleotide   coattion   corresponding to first   smin acid   residue of   residue of   amino acid   residue of   amino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   sequence   smino acid   smino acid   smino acid   smino acid   smino acid   smino acid   smino acid   smino acid   smino acid   smino acid   smino acid   smino acid   smino acid   smin			i e	(A=Alanine, C=Cvsteine, D=Aspartic Acid, E=
Cocation   Corresponding   Corresponding   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   C				
L-Leucine, M-Methionine, N-Asparagine, brists amino acid residue of amino acid residue of amino acid sequence   S-Serine, T-Effreonine, V-Valine, manno acid sequence   S-Serine, T-Effreonine, V-Valine, manno acid sequence   S-Serine, T-Effreonine, V-Valine, w-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan, Y-Typophan	NO:			
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NLLLLHEALAKHEAFFIRCGIFLILEKLKIITYRNLFKKVYLLL KTHQLSLDAFLVALKFMQVEDVDIDEVQCILANLIYMGHVKGYI SHQHQKLVVSKQNPFPPLSTGC  7086 256 525 ILAARMGKQNSKLRPEVMQDLLESTDFTEHBIQEWYKGFLRDCP SGHLSMEEFKKIYGNFFPYGDASKFAEHVFRTFDANGDGTIDFR EF  7087 166 723 LSGSSAGKVAAPCVPPSNHELVPITTENAPKNVVDKGEGASRGG NTRKSLEDNGSTRVTPSVQPHLQPIRNMSVSRTMEDSCBLDLVY VTERIIAVSPPSTANEENFRSNLREVAQMLKSKHGGNYLLFNLS ERRPDITKLHAKVLEFGWPDLHTPALEKICSICKAMDTWLNAHP HRCRVLHNKG  7088 104 759 GTSAASPSSLLEMAGEITETGELYSSYVGLVYMFNLIVGTGALT MPKAFATAGWLVSLVLLVFLGFMSFMTTTFVIEAMAANAQLHW KRMENLKEEEDDDSSTASDSDVLIRDNYERABKRPILSVQRRGS PNPPEITDRVEMGQMASMFFNKVGVNLFYFCIIVYLYGDLAIYA AAVPFSLMQVTCSATGNDSCGVEADTKYNDTDRCWGPLRRVD  7089 33 1775 SVCWEDRYLKARMEESPLSRAPSRGGVWFLNVARTYIPNTKVEC HYTLPPGTMPSASDWIGIFKVEAACVRDYHTFVWSSVPESTTDG SPIHTSVQFQASYLPKPGAQLYQFRYVNRQGQVCGQSPPPQFRE PRPMDELVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLM QLKLQLEGQVTELRSRVQBLERALATARQEHTBLMEQYKGISRS HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELD	l		1	VNVPMTLTVI DVVMT.T.CUMPTVPT.T.KKVHI.MOFAKVTRAVSEG
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SHQHQKLVVSKQNPFPPLSTGC  7086 256 525 ILAARMGKQNSKLRPEVMQDLLESTDFTEHBIQEWYKGFLRDCP SGHLSMEEFKKIYGNFFPYGDASKFAEHVFRTFDANGDGTIDFR EF  7087 166 723 LSGSSAGKVAAPCVPPSNHELVPITTENAPKNVVDKGEGASRGG NTRKSLEDNGSTRVTPSVQPHLQPIRNMSVSRTMEDSCBLDLVY VTERIIAVSFPSTANEENFRSNLREVAQMLKSKHGGNYLLFNLS ERRPDITKLHAKVLEFGWPDLHTPALEKICSICKAMDTWLNAHP HRCRVLHNKG T088 104 759 GTSAASPSSLLEMAGEITETGELYSSYVGLVYMFNLIVGTGALT MPKAFATAGWLVSLVLLLVFLGFMSFMTTTFVIEAMAAANAQLHW KRMENLKEEBDDDSSTASDSDVLIRDNYERABKRPILSVQRRGS PNPFEITDRVEMGQMASMFFNKVGVNLFYFCIIVYLYGDLAIYA AAVPFSLMQVTCSATGNDSCGVEADTKYNDTDRCWGPLRRVD T089 33 1775 SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYIPNTKVEC HYTLPPGTMPSASDWIGIFKVEAACVRDYHTFFWSSVPESTTDG SPIHTSVQFQASYLPKPGAQLYQFRYVNRQGQVCGQSPFQFRE PRPMDELVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLM QLKLQLEGQVTELRSRVQBLERALATARQEHTBLMEQYKGISRS HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELD	1	1	1	
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7087 166 723 LSGSSAGKVAAPCVPPSNHELVPITTENAPKNVVDKGEGASRGG NTRKSLEDNGSTRVTPSVQPHLQPIRNMSVSRTMEDSCELDLVY VTERIIAVSPPSTANEENFRSNLREVAQMLKSKHGGNYLLFNLS ERRPDITKLHAKVLEFGWPDLHTPALEKICSICKAMDIWLNAHP HRCRVLHNKG TO88 104 759 GTSAASPSSLLEMAGEITETGELYSSYVGLVYMFNLIVGTGALT MPKAFATAGWLVSLVLLUFLGFMSPMTTTFVIEAMAANAQLHW KRMENLKEEEDDDSSTASDSDVLIRDNYERABKRPILSVQRRGS PNPPEITDRVEMGQMASMFFNKVGVNLFYFCIIVYLYGDLAIYA AAVPFSLMQVTCSATGNDSCGVEADTKYNDTDRCWGPLRRVD TO89 33 1775 SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYIPNTKVEC HYTLPPGTMPSADWIGIFKVEAACVRDYHTFVWSSVPESTTDG SPIHTSVQFQASYLPKGAQLYQFRYVNRQGQVCGQSPPPGFRE PRPMDELVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLM QLKLQLEGQVTELRSRVQELERALATARQEHTBLMEQYKGISRS HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELD	1	1	į	SGHLSMEEFKKIYGNFFPYGDASKFAEHVFRTFDANGDGTIDFR
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MPKAFATAGWLVSLVLLVFLGFMSFMTTTFVIEAMAAANAQLHW KRMENLKEEEDDDSSTASDSDVLIRDNYERABKRPILSVQRRGS PNPPEITDRVEMGQMASMFFNKVGVNLFYFCIIVYLYGDLAIYA AAVPFSLMQVTCSATGNDSCGVEADTKYNDTDRCWGPLRRVD SVCWEDRYLKARMEESPLSRAPSRGVNFLNVARTYIPNTKVEC HYTLPPGTMPSASDWIGIFKVEAACVRDYHTFVWSSVPESTTDG SPIHTSVQFPQASYLPKPGAQLYQFRYVNRQGQVCGQSPPFQFRE PRPMDELVTLERADGGSDILLVVPKATVLQNQLDESQQERNDLM QLKLQLEGQVTELRSRVQELERALATARQEHTBLMEQYKGISRS HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELD				
KRMENLKEEEDDDSSTASDSDVLIRDNYERABKRPILSVQRRGS PNPPEITDRVEMGQMASMFFNKVGVNLFYFCIIVYLYGDLAIYA AAVPFSLMQVTCSATGNDSCGVEADTKYNDTDRCWGPLRRVD  7089 33 1775 SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYIPNTKVEC HYTLPPGTMPSASDWIGIFKVEAACVRDYHTFWSSVPESTTDG SPIHTSVQFPQASYLPKPGAQLYQFRYVNRQGQVCGQSPPFQFRE PRPMDELVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLM QLKLQLEGQVTELRSRVQELERALATARQEHTELMEQYKGISRS HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELD	7088	104	759	
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SPIHTSVQFQASYLPKPGAQLYQFRYVNRQGQVCGQSPPFQFRE PRPMDELVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLM QLKLQLEGQVTELRSRVQELERALATARQEHTELMEQYKGISRS HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELD	1,	1		HYTLPPGTMPSASDWIGIFKVEAACVRDYHTFVWSSVPESTTDG
PRPMDELVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLM QLKLQLEGQVTELRSRVQELERALATARQEHTELMEQYKGISRS HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELD	1			SPIHTSVOFOASYLPKPGAOLYOFRYVNROGOVCGQSPPFQFRE
QLKLQLEGQVTELRSRVQELERALATARQEHTELMEQYKGISRS HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELD	ł			DEDMORTATERADGGSDILIAVVEKATVI ONOLDESOOERNDI.M
HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELD				OF AT OT ECONTEL PODODI ED AL ATABORETRI MEDVICISES
HGETTEEKDILSKQQGDHVAKILEDEDDIQTISEKVDIKEVEII				UTELEBERTI CEUCOCOUNTI EI EDDIOTICEVILTEVEURI.D
		}		HGETTEEKDILSKQQGDHVAKILEEDEDDIQIISBAVBIAEVEDD
RIRDTVKALTKEQEKLIGQIKEVQADKEQEBABIQVAQQEMHA		1		RLRDTVKALTREQEKLLGQLKEVQADKEQSEABLQVAQQENHHL
NLDLKEAKSWQEEQSAQAQRLKDKVAQMKDTIGQAQQRVABBBBP		1	<u> </u>	NLDLKEAKSWQEEQSAQAQRLKDKVAQMKDTLGQAQQRVABLEP

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
No.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
[	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	L .	residue of	S=Serine, T=Threonine, V=Valine,
1	amino acid	1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1 .	residue of	amino acid	
]	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1		]	LKEQLRGAQELAASSQQKATLLGEELASAAAARDRTIAELHRSR
			LEVAEVNGKLAELGLHLKEEKCQWSKERAGLLQSVEAEKDKILK
1		1	LSAEILRLEKAVQEERTQNQVFKTELAREKDSSLVQLSESKREB
ł			TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN
	ļ		EDATTEDERAAVGLSCPAALTDSEDESPEDMRLHPMAFVSVETQ
	Ì		ASLLLGLE
7090	33	1775	SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYIPNTKVEC
			HYTLPPGTMPSASDWIGIFKVEAACVRDYHTFVWSSVPESTTDG
			SPIHTSVQFQASYLPKPGAQLYQFRYVNRQGQVCGQSPPFQFRE
			PRPMDELVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLM
]			OLKLOLEGOVTELRSRVQELERALATARQEHTELMEQYKGISRS
			HGEITEERDILSROOGDHVARILELEDDIQTISEKVLTKEVELD
1			RLRDTVKALTREOEKLLGOLKEVQADKEQSEAELQVAQQENHHL
}	1	<b>[</b>	NLDLKEAKSWQEEQSAQAQRLKDKVAQMKDTLGQAQQRVAELEP
1	1	!	LKBOLRGAOELAASSOOKATLLGEELASAAAARDRTIAELHRSR
	1		LEVAEVNGKLAELGLHLKEEKCQWSKERAGLLQSVEAEKDKILK
	1	1	LSAEILRLEKAVQEERTQNQVFKTELAREKDSSLVQLSESKREL
	1		TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN
			EDATTEDERAAVGLSCPAALTDSEDESPEDMRLHPMAFVSVETQ
			ASLLLGLE
7091	186	1076	EGMLTREHRCGRSEEQELEPWPSPKKARSGRWLRNGFKRKMEEP
1			EEPADSGQSLVPVYIYSPEYVSMCDSLAKIPKRASMVHSLIEAY
		1	ALHKQMRIVKPKVASMEEMATFHTDAYLQHLQKVSQEGDDDHPD
			SIEYGLGYDCPATEGIFDYAAAIGGATITAAQCLIDGMCKVAIN
		ł	WSGGWHHAKKDEASGFCYLNDAVLGILRLRRKFERILYVDLDLH
İ			HGDGVEDAFSFTSKVMTVSLHKFSPGFFPGTGDVSDVGLGKGRY
ľ	Į.	l	YSVNVPIQDGIQDEKYYQICERYEPPAPNPGL
7092	522	809	KQGINEDQEESQKPRLGEGCEPISKRQMKKLIKQKQWEEQRELR
		1	KQKRKEKRKKKLERQCQMEPNSDGHDRKRVRRDVVHSTLRLII
			DCSFDXLM
7093	454	655	NFGVSGVELAQQASMVRMSFVIAACQLVLGLLMTSLTESSIQNS
			ECPQLCVCEIRPWFTPQSTYREA
7094	- 2	508	FVRSMHWGVGFASSRPCVVDLSWNQSISFFGWWAGSEEPFSFYG
"""	•		DIIAFPLODYGGIMAGLGSDPWWKKTLYLTGGALLAAAAYLLHE
			LLVIRKQQEIDSKDAIILHQFARPNNGVPSLSPFCLKMETYLRM
			ADLPYONYFGGKLSAQGKMPWIEYNHEKVSGTEFII
7095	<del> </del>	411	IASSLPKMASLLQSDRVLYLVQGEKKVRAPLSQLYFCRYCSELR
1095	1	411	SLECVSHEVDSHYCPSCLENMPSAEAKLKKNRCANCFDCPGCMH
			TLSTRATSISTQLPDDPAKTTMKKAYYLACGFCRWTSRDVGMAD
			KSVGE
7096	224	2067	ETRSLAVQEKPSQAGRRRSSRISFAGALFLTRFLLQELLLNNFC
			SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR
		7	APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE
			QREHYKLDWHRFNLKQRLKDKPLLSALDFEKQSSTGDLSSISGS
1			EDSDSASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQGQF
			LYAYRCVLGPHQDPPEEAELLLQNLQSKGPRDCVVLMAAAGHFA
		1	GAIFQGREVVTHKTFHRYTVRAKRGTAQGLRDARGGPSHSAGAN
			LRRYNEATLYKDVRDLLAGPSWAKALEEAGTILLRAPRSGRSLF
	1	}	FGGKGAPLQRGDPRLWDIPLATRRPTFQELQRVLHKLTTLHVYE
			EDPREAVRLHSPOTHWKTVREERKKPTEEEIRKICRDEKEALGO
			NEESPKQGSGSEGEDGFQVELELVELTVGTLDLCESEVLPKRRR
			RKRNKKEKSRDQEAGAHRTLLQQTQEEEPSTQSSQAVAAPLGPL
	1	1	LDEAKAPGQPELWNALLAACRAGDVGVLKLQLAPSPADPRVLSL
			LSAPLGSGGFTLLHAAAAAGRGSVVRLLLEAGADPTVQCQDH
7097	256	1228	IRTKSAATWEAWPQCGREGSRIITEPCEANAGSRQELQTERISS
,037	2.50	1440	FLAAQGDQAFHSGLETNNSNSELPLRVGLKVAQGSPLMGGQVSA
L	1	<u> L</u>	L HUNGODALL BODE TIMESMONDE BRICANDA ANGOS E BIOGA 24

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence	Jequence	\=possible nucleotide insertion)
<del></del>	1 - 1 - 1 - 1 - 1	··	SNSFSRLHCRNANEDWMSALCPRLWDVPLHHLSIPGSHDTMTYC
ļ			LNKKSPISHEESRLLQLLNKALPCITRPVVLKWSVTQALDVTEO
			LDAGVRYLDLRIAHMLEGSEKNLHFVHMVYTTALVEDTLTEISB
1		{	WLERHPREVVILACRNFEGLSEDLHEYLVACIKNIFGDMLCPRG
İ			EVPTLRQLWSRGQQVIVSYEDESSLRRHHELWPGVPYWWGNRVK
[			TEALIRYLETMKSCGR
7098	82	956	SSFLKRCRKVLGCWGIPSEQSLFSTLEEPRDKEIDNYCVMRLQT
[			EARSGFWAPNRFPVNICRMTAVDGDRGGSSRETCRCHFHPSLEA
1			LVLLLQDWQPGGVGICTSFLGISWALLDYHRALRTCLPSKPLLG
İ		1	LGSSVIYFLWNLLLLWPRVLAVALFSALFPSYVALHFLGLWLVL
1			LLWVWLQGTDFMPDPSSEWLYRVTVATILYFSWFNVAEGRTRGR
ĺ	1	1	AIIHFAFLLSDSILLVATWVTHSSWLPSGIPLQLWLPVGCGCFF
			LGLALRLVYYHWLHPSCCWKPDPDQVD
7099	992	210	LFRLAPGFLRSLARQGYHQIWAFPFLPSGATATWPAASRSRSLA
		1	ARSLPRSPARPGPNDALLGEHDFRGQGVRAQRFRFSEEPGPGAD
Ì			GAVLEVHVPQIGAGVSLPGILAAKCGAEVILSDSSELPHCLEVC
1			RQSCQMNNLPHLQVVGLTWGHISWDLLALPPQDIILASDVFFEP
İ			EDFEDILATIYFLMHKNPKVQLWSTYQVRSADWSLEALLYKWDM
L			KCVHIPLESFDADKEDIAESTLPGRHTVEMLVISFAKDSL
7100	205	671	ANGGFWEAAPGSEVSLPLWVPTASHSKTTALGIGSAPPPHLSVL
j		)	FLFSFPPQLGDPLEAFPVFKKYDRNGLNVSIECKRVSGLEPATV
			DWAFDLTKTNMQTMYEQSEWGWKDREKREEMTDDRAWYLIAWEN
			SSVPVAFSHFRFDVERGDEVLYW
7101	2	503	WRGGPRRAKRLAGGAVGWVLLVRGVHSVRAGGGRPPRAADMKKD
			VRILLVGEPRVGKTSLIMSLVSEEFPEEVPPRAEEITIPADVTP
Ì			ERVPTHIVDYSEAEQSDEQLHQEISQANVICIVYAVNNKHSIDK
7102	<del></del>	ļ	VTSRWIPLINERTDKDSRLPLILGGNKSDLVEYSR
/102	2	503	WRGGPRRAKRLAGGAVGWVLLVRGVHSVRAGGGRPPRAADMKKD
İ			VRILLVGEPRVGKTSLIMSLVSEEFPEEVPPRAEEITIPADVTP
			ERVPTHIVDYSEAEQSDEQLHQEISQANVICIVYAVNNKHSIDK
7103	119	438	VTSRWIPLINERTDKDSRLPLILGGNKSDLVEYSR
1103	119	438	GSQSSVAVNIRSGTDEESMDLMNGQASSVNIAATASEKSSSES
1			LSDKGSELKKSFDAVVFDVLKVTPBEYAGQITLMDVPVFKAIQP DBLSSCGWNKKEKYSSAP
7104	1670	795	RLWEHRSVSAGASGWGLSSPGCLLLHPSLPEEERVDILINNAGV
1.104	1370	, ,,,	MRCPHWTTEDGFEMQFGVNHLGEAWAGAAPWVQAILPRRPPKVL
			GF*V*VKSDLFIILNPGHFLLTNLLLDKLKASAPSRIINLSSLA
			HVAGHIDFDDLNWQTRKYNTKAAYCQS\KLAIVLFTKELSRRLO
]		ļ	GSGVTVNALHPGVARTELGRHTGIHGSTFLOHHN\WAHLLAAWS
			KSPRSWPAPAQHNTLAVAEELA\VISGKYFDGLKOKAPAPEAED
	}	ļ	EEVARRLWAESARLVGLEAPSVREQPLPR
7105	765	143	GOMCRRPSPKSTSCLSMTCDLP/RGLODPOCLALFRVAVDKHOA
		1	LLKAAMSGQGVDRHLFALYIVSRFLHLQSPFLTQVHSEQWQLST
			SQIPVQQMHLFDVHNYPDYVSSGGGFGPADDHGYGVSYIFMGDG
			MITFHISSKKSSTKTDSHRLGQHIEDALLDVASLFQAGQHFKRR
			FRGSGKENSRHRCGFLSRQTGASKASMTSTDF
7106	14	1064	GLQAGHPHPRSASRIPEADTH\YSKLQRAFDSIVNKDHKRMFGT
			YFRVGFFGSKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGQCF
			GAEFVEVIKDSTPVDKTKLDPNKAYIQITFVEPYFDEYEMKDRV
			TYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLTTMHAF
			PYIKTRISVIQKEEFVLTPIEVAIEDMKKKTLQLAVAINQEPPD
			AKMLQMVLQGSVGATVNQGPLEVAQVPLAEIPADPKLYRHHNKL
			RLCFKEFIMRCGEAVEKNKRLITADQREYQQELKKNYNKLKENL
			RPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGS
7107	1145	591	*I*WLQTGKKK
	<del></del>		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
7108	1	942	VKVALLLTNLEQPRTESEWENSFTLKMFLFQFVNLNSSTFYIAF
			FLGRFTGHPGAYLRLINRWRLEECHPSGCLIDLCMQMGIIMVLK
	)		QTWNNFMELGYPLIQNWWTRRKVRQEHGPERKISFPQWEKDYNL
			QPMNAYGLFDEYLEMILQFGFTTIFVAAFPLAPLLALLNNIIEI
	·		RLDAYKFVTQWRRPLASRAKDIGIWYGILEGIGILSVITNAFVI
1			AITSDFIPRLVYAYKYGPCAGQGEAGQKCMVGYVNASLSVFRIS
			DFENRSEPESDGSEFSGTPLKYCRYRDYRDPPHSLVPYGYTLQF
7100		100	WHYLAW
7109	964	102	WDQRKRNSLVPGPAHGPAQEEPWEKKESLGAAQEALSIQLQPKE TQPFPKSEQVYLHFLSVVTEDGPEPKDKGSLPQPPITEVESQVF
			SEKLATDTSTFEATSEGTLELQQRNPKAERLRWSPAQEESFRQM
	ļ		VVIHKEIPTGKKDHECSECGKTFIYNSHLVVHQRVHSGEKPYKC
1			SDCGKTFKQSSNLGQHQRIHTGEKPFECNECGKAFRWGAHLVQH
			QRIHSGEKPYECNECGKAFSQSSYLSQHRRIHSGEKPFICKECG
{			KAYGWCSELIRHRRVHARKEPSH
7110	96	697	RLDNFSGFLVEVTKEERHIVKPLYDRYRLVKQMLTRASITPVLG
/			SPSTKRRGOMLQPIIEGETAHFFEEIKEEEEDGVNLSSELGDML
ļ			KTAVQVQSSLKNSESDVEENQEKLALDLRLSSSRAASMPELLEQ
			LWKARAEKKKLRKTLREFEEAFYQQNGRNAQKEDRVPVLEEYRE
1			YKKIKAKLRLLEVLISKQDSSKSI
7111	2	414	GSGLYRGPTPGGQCIWKPNSMPPDHERNFGFTQFALELNELTAE
	İ		LKRSLPSTDTRLRPDQRYLEEGNIQAAEAQKRRIEQLQRDRRKV
ì			MEENNIVHQARFFRRQTDSSGKEWWVTNNTYWRLRAEPGYGNMD
1			GAVLW
7112	103	495	PRCFPVADRGRLIGGLPDVVTIMEGKTLNLTCTVFGNPDPEVIW
1	1		FKNDQDIQLSEHFSVKVEQAKYVSMTIKGVTSEDSGKYSINIKN
L			KYGGEKIDVTVSVYKHGEKIPDMAPPQQAKPKLIPASASAAGQ
7113	1	824	KCLRQAWHEAPSSLAFTRWCSREERAEGGGNLHRSITRDPKPPG
]	]	1	LRPSQRPMDDKKKKRSPKPCLAQPAQAPGTLRRVPVPTSHSGSL
	1		ALGLPHLPSPKQRAKFKRVGKEKCRPVLAGGGSGSAGTPLQHSF
			LTEVTDVYEMEGGLLNLLNDFHSGRLQAFGKECSFEQLEHVREM
1			QEKLARLHFSLDVCGEEEDDEEEEDGVTEGLPEEQKKTMADRNL
1	1	ļ	DQLLSNLGSCLGALVPGGMRGGEGTYSQSHSWALGEKVGVHGSK SSGPLNLPRR
7114	3	1492	VWEVDEQIDHYKESQDKFLWQAAFIGKETLKDBSGQECKICRKI
1114	1	1432	IYLNTDFVSVKORLPKYYSWERCSKHHLNFLGQNRSYVRKKDDG
			CKAYWKVCLHYNLHKAQPAERFFDPNQRGKALHQKQALRKSQRS
	1		OTGEKLYKCTECGKVFIQKANLVVHQRTHTGEKPYECCECAKAF
	1		SOKSTLIAHORTHTGEKPYECSECGKTFIQKSTLIKHQRTHTGE
		1	KPFVCDKCPKAFKSSYHLIRHEKTHIRQAFYKGIKCTTSSLIYQ
1 .		1	RIHTSEKPOCSEHGKASDEKPSPTKHWRTHTKENIYECSKCGKS
		1	FRGKSHLSVHORIHTGEKPYECSICGKTFSGKSHLSVHHRTHTG
		1	EKPYECRRCGKAFGEKSTLIVHQRMHTGEKPYKCNECGKAFSEK
	1		SPLIKHQRIHTGERPYECTDCKKAFSRKSTLIKHQRIHTGEKPY
			KCSECGKAFSVKSTLIVHHRTHTGEKPYECRDCGKAFSGKSTLI
		1	KHQRSHTGDKNL
7115	1	947	NAAHGYNWGLWCMYIIPPQDWLDRGDESAPIRTPAMIGCSFVVD
			REYFGDIGLLDPGMEVYGGENVKLGMRVWQCGGSMEVLPCSRVA
		1	HIERTRKPYNNDIDYYAKRNALRAAEVWMDDFKSHVYMAWNIPM
		1	SNPGVDFGDVSERLALRQRLKCRSFKWYLENVYPEMRVYNNTLT
			YGEVRNSKASAYCLDQGAEDGDRAILYPCHGMSSQLVRYSADGL
		}	LQLGPLGSTAFLPDSKCLVDDGTGRMPTLKKCEDVARPTQRLWD
		1	FTQSGPIVSRATGRCLEVEMSKDANFGLRLVVQRCSGQKWMIRN
			WIKHARH
7116	866	95	RVRMRRNAEVIEEKLSMKSWAKFRPGEPWKGYPNIDPETDPYVT
L	<u> </u>	L	PGSVINNLSINTVREVDHLRDRNSGSSSSLNTTLPSTSAWSSIR

Deginning   nucleotide   location   corresponding   to first   amino acid   residue of   amino acid   residue of   amino acid   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   se				
No:	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
corresponding				
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence solvent service of amino acid sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent sequence solvent seq	NO:			
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid acquence    Varipptophan, Varyrosine, Xauknown, *=Stop   Codon, /=possible nuclectide deletion	-			
amino acid residue of amino acid sequence S-serine, T-Threonine, V-Waline, W-rytcoshan, Y-Rytcoshan, X-Unknown, *-Stop Codon, /-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion,				
residue of amino acid sequence				
amino acid sequence   Codon, /-possible nucleotide deletion,	1			
Apossible mucleotide insertion	1			
ASMYNVELSTAGSTSANNSDSKLITHSPGSVYNTSLAHELIKKY LPPKNITAPSRAPPROLTGOKEP ISSTYMONSPLA IGGOKISDANY TOSSKGESSGRITHMULKUNITOLIOSTLETLCHOGGOLIT PHUNIPHORAL MYSSKEWUNGKSLITSDFLILT.  7117 695 1261 LLISTPGGCHPPPSSIEFTYTGAWGKALFAPHHPCAFGALPOKA FYSQAARAT PLLQPSQAAQAGCISQPARACOALCSLFMPLENNG SPILELRGGLERFTINDRIKTERSAAACKARAQHOTIJGPIKLISHR GKVCLRHPRITOVRGGPGAAGKGGMGTRRGTTFIGGARDPGA FYSQAARAT PLLQPSQAAQAGCGLSQPARACOALCSLFMPLENNG SPILELRGGLERFTINDRIKTERSAAACKARAQHOTIJGPIKLISHR GKVCLRHPRITOVRGGPGAAGKGGMGTRRGTTFIGGARDPGA FYSQAARAT PLLQPSQAAGKGGMGTRRGTTFIGGARDPGA FYSQAARAT PLLQPSQAAGKGGMGTRRGTTFIGGARDPGA FYSQAARAT PLLQPSQAAGKGGMGTRRGTTFIGGARDPGA FYSQAARAT PLLQPSQAAGKGGMGTRRGTTFIGGARDPGA FYSQAARAT PLLQPSQAAGKGGMGTRRGTTFIGGARDPGA FYSQAARAT PLLQPSQAAGKGGMGTRRGTTFIGGARDPGA FYSQAAAGTACAACKAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	Ĭ		sequence	
LPPNITIAPSRPPROLITOCK PLSTWONS PLRIGGSWONSDARY TROSSWORS SIGTINHULUKUIT POLDSTATINGOGGLIT PHINIPPHONALWYS SKEVYKAOKSLII SOLPILLT.  7117 695 1261 LLISTPGGCHPPSSIEFTYTGAWGKALFAPHMCAPGALPQCA FYSQAARAI PLLQREQAAQAEGLSQPARACQALCSLIPPLENNO SPILKLEVGLREPTYNOKTRIKSAAACWARAGWOTTIGPLIKIS GKYCLRIPPRTUKSGPGAAGAGGGGGGTRERGTT FISGARDEGGL RVEHRCOPTGHLP  7118 49 1863 PHEEPINGGAWVLEWUFBHAWGYALLALKEVEETSLLQPQVE ESVIALKKHIS VURLVAFOPFASSQVALKMARAVSECVHEDY NINIGSISLLOOLKOINTPSHAVREWGYGHPAGAGGG LKOVELHIPINILVKSLTDLSACKAQUSLISHYSRAKKREVININAT YCLAQPIGNRELINBUKEKLEELTMGGAKAKLILASSRSSWO MDISAIDLINI ESTSSRWVSLSSYROGLHTYLREVININAT YCHAQPIGNRELINBUKEKLEELTMGGAKAKLILASSRSSWO MDISAIDLINI ESTSSRWVSLSYROGLHTYLREVININAT RCHTCHKACLI FISTFICHARANKGRI SRYLLANKSIASRICHT RCHTCHKACLI FISTFICHARANKGRI SRYLLANKSIASRICHT RCHTCHKACLI FISTFICHARANKGRI SRYLLANKSIASRICHT RCHTCHKACLI FISTFICHARANKGRI SRYLLANKSIASRICHT RCHTCHKACLI FISTFICHARANKGRI SRYLLANKSIASRICHT RCHTCHKACLI FISTFICHARANKGRI SRYLLANKSIASRICHT RCHTCHKACLI FISTFICHARANKGRI SRYLLANKSIASRICHT RCHTCHKACLI FISTFICHARANKGRI SRYLLANKSIASRICHT RCHTCHKACLI FISTFICHARANKGRI SRYLLANKSIASRICHT RCHTCHKACLI FISTFICHARANKGRI SRYLLANKSIASRICHT RCHTCHKACLI FISTFICHARANKGRI SRYLLANKSIASRICHT RCHTCHKACLI FISTFICHARANKGRI SRYLLANKSIASRICHT RCHTCHKACLI FISTFICHARANKGRI SRYLANKSIASRICHT RCHTCHKACLI FISTFICHARANKGRI SRYLANKSIASRICHT RCHTCHKACLI FISTFICHARANKARGRI SRYLANKSIASRICHT RCHTCHKACLI FISTFICHARANKARGRI SRYLANKSIASRICHT RCHTCHKACLI FISTFICHARANKARGRI SRYLANKSIASRICHT RCHTCHKACLI FISTFICHARANKARGRI SRYLANKSIASRICHT RCHTCHKACLI FISTFICHARANKARGRI SRYLANKSIASRICHT RCHTCHKACLI FISTFICHARANKARGRI SRYLANKSIASRICHT RCHTCHKACLI FISTFICHARANKARGRI SRYLANKSIASRICHT RCHTCHKACLI FISTFICHARANKARGRI SRYLANKSIASRI CLOCH SCEPTSVPGEKLARGEVERLOFT FISTFICHARANSVYROV NMI 1051SLLOOLOKOINTSMRVENVOHDERSHARANKARI SRYLANKSIASRI CLOCH RCHAMMSSI IBERTORVAKKARGRI SRYLANKSIASRI CLOCH RCHAMMSSI IBERTORVAKKARGANGRI SRYLANKSIASRI CLOCH RCHAMMSSI IBERTORVAKKARGRI SRYLANKSIASRI CLOCH RCHAMMSSI BERTORVAKKARGRI SRYLANKSIASRI CLOCH RCHAMMSSI		sequence		1 · -
TPOSSMOESSSCRITMULIKNITPOIDSTLRTLCMORGELIT PHINIPHORAL WYS SKEEV WAG KSELH SIDLFLLIT.  7117 695 1261 LLISTPGGCHPPESIEFTYTOAWGKALFAPHMPCAFGALPOGA FYSQAARATIFLQYEGAAGAGCSLGYPARACGALCSLEPHIRM PENNOR SPILKLEGGIRFYTORKTERSHAMACKARAGHOTISPIKLISH GKVCLRHPRITOTWORGFGAAGAGGGMGTRRGTFTSGARDEGA GKVCLRHPRITOTWORGFGAAGAGGGMGTRRGTFTSGARDEGA GKVCLRHPRITOTWORGFGAAGAGGGMGTRRGTFTSGARDEGA GKVCLRHPRITOTWORGFGAAGAGGGMGTRRGTFTSGARDEGA GKVCLRHPRITOTWORGFGAAGAGGGMGTRRGTFTSGARDEGA GKVCLRHPRITOTWORGFGAAGAGGGMGTRRGTFTSGARDEGA GKVCLRHPRITOTWORGFGAAGAGGGMGTRRGTFTSGARDEGA GKVCLRHPRITOTWORGFGAAGAGGGAGHSTRAAVSGCVVHEDLR LLLETHLPSKKKKVLLGVGDRYGAAACGGAGHSTRAAVSGCVVHEDLR LLLETHLPSKKKKVLLGVGDRYGAAACGGAGHSTRAAVSGCVVHEDLR LLGETHLDSKKKKVLLGVGDRYGAAACGGAGHSTRAAVSGCVVHEDLR LLGETHLDSKKKKVLLGVGDRYGAAGAGGAGHSTAATLABASSSWA MDISAIDLINISSFSSRVVSLSBYRGSLHTYLRSKMSQVAPSLS ALIGBAVGARLILARAGSITNIARYPASTVQILGABRAAFALLDASSSWA MDISAIDLINISSFSSRVVSLSBYRGSLHTYLRSKMSQVAPSLS ALIGBAVGARLILARAGSSTNIARYPASTVQILGABRAAFAGAACA FSKEPPVSGPERAGKRSKKKKRHAAALAASSNSSSYTPBECE BYSERPKKKKKKGROEVPORGMGEDPSISFSFPKKKKSFFSEE EMSERPKKKKKKGROEVPORGMGEDPSISFSFPKKKKSFFSEE EMSERPKKKKKKGROEVPORGMGEDPSISFSFPKKKKSFFSEEL MSSDLETTAGSTSTPKKKSTFREETVUNDERAAMSSGCVVHEDLA LLLETHLPSFSKKKKKLLAGVODDRYGAAAACGAGGARSYSBAXVKKRNAMASSGCVVHEDLA LLETHLPSFSKKKKKLLAGVODDRYGAAAACGAGGARSYSBAXVKKRNAMASSGCVANEDLA LLGAVALHFRINLVGLIDLSACKAGGGAGARSYSBAXVKKRNAMASSGCVANEDLA LLGAVALHFRINLVGLIDLSACKAGGGAGAGSSKKKK KKPHKAGGDE  1063 PHOEPPINGAGANVLLHVLJEFBURGAAAACSAGAAAGAGAGAAAGAGAGAGAAAGAGAGAGAAAAAAAA				
PHINI.PRIGNALWYSSKEWYKAQKSLIFISDLFLITT.  7117 695 1261 LLISTEGGGIPPSSIEPTYTGAKGKALDAPIGAGALDQGA FVSQAARATIFLLQBSQAAQAGCISQBRAACGALCSLEPBLRNWG SPILRLPGGIRTPTINDRKTRTRSAAACGALCSLEPBLRNWG SPILRLPGGIRTPTINDRKTRTRSAAACGALCSLEPBLRNWG SPILRLPGGIRTPTINDRKTRTRSAAACGALCSLEPBLRNWG SPILRLPGGIRTPTINDRKTRTRSAAACGALCSLEPBLRNWG GKVCLRIPEPTTORKGPGAAAGGGGGGGGGRARGTFTEGGARDPGGL RVSHRCQPTGHLP  7118 49 1863 PHEEPINDRAKTRTSAAACGALGALGHSYSRAKVERVSKRW NEIGHTLAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG			ł	_
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YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLESYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAABITRKLEKQEKKRLKKEKKRLAALALASSENSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKSFSKEEL MSSDLEETAGSTSIPKRKSTPKEETVNDPEERGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKFHKASQED  7120 1991 64 QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGGGP RAEAMMRSSIBRGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFFLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLPHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY SSSAGSQGREEIVEDVTQNILLKVFEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY  7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	j	1		LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD
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EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREBIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLBLMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY  7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	1	1		1
DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREBIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLBLMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIRRGVALICALDY  7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	1			
LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFAKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIRRGVALICALDY 7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	.			
SSSAGSOGREEIVEDVTONILLKVPEPINLOWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLBLMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQMFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY  7121 2 546 RPLRPWVLSIGSMVGLMTYGRROFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF				
MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY  7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	ĺ			
ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALLDY 7121 2 546 RPLRPWULSLGSMVGLMTYGRRQFQSLDTTMRRLIPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	ł			
I PAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE  APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM  AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI  AVEIPTHQPQRHWIKRGVALICALDY  7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK  LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV  SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF				
APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY  7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	1			
AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY  7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	1			
AVEIPTHQPQRHWIKRGVALICALDY  7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF				
7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF		1		
LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	7.5.	<del> </del>	<del> </del>	
SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	7121	2	546	
1 1 = 1 = 1 = 1 = 1 = 1 = 1 = 1 = 1 = 1				-
GAYFNVLTNERFKDQTHHRVSSGLQEAKTQAALVLDCL		1		
		<u> </u>	L.,	GAIFNVLINGRUITUEAFAUQIHHRVSSGLQEAKTQAALVEDCE

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
}			1
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			ETRQE
7122	2	546	RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPPREASAK
			LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV
	ţ		SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF
İ	1		GAYFNVLINLRDITDEAFKDQIHHRVSSLLQEAKTQAALVLDCL
			ETRQE
7123	1	1092	KPAVPEARSAGTSEAGRSGAEEVSCGSVSGDGAAMRLTPRALCS
i		ľ	AAQAAWRENFPLCGRDVARWFPGHMAKGLKKMQSSLKLVDCIIE
1			VHDARIPLSGRNPLFQETLGLKPHLLVLNKMDLADLTEQQKIMQ
	,		HLEGEGLKNVIFTNCVKDENVKQIIPMVTELIGRSHRYHRKENL
	1		EYCIMVIGVPNVGKSSLINSLRRQHLRKGKATRVGGEPGITRAV
			MSKIQVSERPLMFLLDTPGVLAPRIESVETGLKLALCGTVLDHL
	1	ĺ	VGEETMADYLLYTLNKHQRFGYVQHYGLGSACDNVERVLKSVAV
			KLGKTOKVKVLTGTGNVNVIOPNYPAAARDFLOTFRRGLLGSVM
			LDLDVLRGHPRV
7124	2	382	LPLTLLLAAPFAHLLLPPGHDOSPCWHPGPALSPGTLGPLSWAM
/124	2	302	
İ			ANSGLQLLGYFLALGGWVGIIASTALPQWKQSSYAGDASIQLRS
			KVFVLESEWGGDSLGLPRDCGWSCLLHSAVRSEKGFWS
7125	166	1127	NCISEKRNYSFSMQKGKGRTSRIRRRKLCGSSESRGVNESHKSE
	1		FIELRKWLKARKFQDSNLAPACFPGTGRGLMSQTSLQEGQMIIS
ļ	1	j	LPESCLLT\RDTVIRSYLGAYITKWKPPPSPLLALCTFLVSEKH
1			AGHRSLLEA\YLEILPKAYTCPVCLEPEVVNLLPKSLKAKAEEQ
	1		RAHVQEFFASSRDFFSSLQPLFAEAVDSIFSYSALLWAWCTVNT
			RAVYL\SPGSGNAFLQSRTPVQLAPYLDLLNHSPHVQVKAAFNE
<b>(</b>			ETHSYEIRTTSRWRKHEEVFICYGPHDNQRLFLEYGFVSVHNPH
			ACVYVSRGWNQLCS
7126	1	733	CRDMAAFIVPSPARRCSQKGSLGHLPTQPWLWAAMSPRGQERGT
	1		SHSQAREPQRPGRWLLGSLQSSPGTLGQAGTASRRRGCMVQRWV
			QVATGRRAVQVPKGALGLALGETSPGASRGMSGGAGGCWALGWA
			PSPVLPSWLLEGPPPWLSIISDSGTQRPSPRRCPARPSPWGPQC
ł			WRGGRIASAEASST*TPGSGSRARSGRRSPGSRRRSASAPSPTP
			PTDACA*SCVARPAGSRSSRPAAA
7127	1311	277	GLPAMCST*KAGYYEETEGDCIPKDR*IEKRPFKEI*RRIPRIF
	1		AKQKQI*S*NSQKIGASEIDRGRKEADCSDAPAAARIGAVSVFR
		l	RSTQEARVSPRSNAKSANLRAVRAD*WEHFVLLFHTPEQFLAEC
1	1	,	ICRST**K*WHQLC*PLSSL*TGLKRKLLL*VLFRI*WLKDCDV
	1		*FCQKIFATNFCNWQNLIQ*EE*KPVEYSVEN*HIMNLLLPM*L
			CQSSLRDQTIVTWRM*RNYSMFRINMISSL*DGSIHIPLKLHFY
}	1	}	PALIFTLTVPINSCCQRPLPLFAHQSIKTLASSGSPMLACLRFL
			LVKKRAFIHTPRSPGCSV*CKHVLVKDNKNNCVGSEV
7128	1 2	5228	GRVDLWTILLGRSALRELSQIEAELNKHWRRLLEGLSYYKPPSP
, 120	1	3220	SSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCYLQE
1			1
			DYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHL
			LTYFQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTRAPT
1	1		WETHGNLMTERQVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSD
		1	LLVLTKMFKEQGFGSRQTNRHLVDETMDPFVDRIGYFSALILVE
			GMDIESLHKCALDDRRELHQFAQDGLICQDMDCLMLTFGDIPHH
			APVLLAWALLRHTLNPEETSSVVRKIGGTAIQLNVFQYLTRLLQ
			SLASGGNDCTTSTACMCVYGLLSFVLTSLELHTLGNQQDIIDTA
			CEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSPLLQLL
		{	RALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWR
		1	RQTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSW
			TLFTCEIEMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIA
			DCLLPITSRIYMLLQRLTTVISPPVDVIASCVNCLTVLAARNPA
1	1		KVWTDLRHTGFLPFVAHPVSSLSQMISAEGMNAGGYGNLLMNSE
			QPQGEYGVTIAFLRLITTLVKGQLGSTQSQGLVPCVMFVLKEML
	<del></del>		

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspaicic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
)	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l .	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
]	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
			PSYHKWRYNSHGVREQIGCLILELTHAILNLCHETDLHSSHTPS
			LQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQPRSDGAEG
ł			QGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQHGAH
			GNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLG
Ì	}	1	NDAAAIRDAFLTRLQSK\IE\DMRIK\VMIL\EFLTVA\VETQP
1	ļ		GLIELFLNLEVKDG\SDGSKEFSLGMW\SCLHAV/VWELIDSQQ
1			
1		]	QDRYWCPPLLHRAAIAFLHALWQDRRDSAMLVLRTKPKFWENLT
			SPLFGTLSPPSETSEPSILETCALIMKIICLEIYYVVKGSLDQP
•			LKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTSLLEYOM
		Ĭ	LVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV
			PASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEG
			VLQADQQLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNV
1		{	CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRHRDQ
			RDGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILPTLLTTLEV
ł			SLRMKQNLHFTEATLHLLLTLARTQQGATAVAGAGITQSICLPL
1			LSVYQLSTNGTAQTPSASRKSLDAPSWPGVYRLSMSLMEQLLKT
			LRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACLEEADHTVG
			FILOLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSFLHSRKML
ſ			OHYLONKNGDGLPSAV\AQRV\QRPPSAASAAPSSSKQPAADTE
ļ			ASEOOALHTVOYGLLKILSKTLAALRHFTPDVCQILLDQSLDLA
1			EYNFLFALSFTTPTFDSEVAPSFGTLLATVNVALNMLGELDKKK
			EPLTOAVGLSTOAEGTRTLKSLLMFTMENCFYLLISQAMRYLRD
1			PAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATGVLP
1			SPOGKSTSLSKASPESQEPLIQLVQAFVRHMQR
			FRRFRWRRRLH*AGPASSAGGSPGEASGTMSGELPPNINIKEPR
7129	1	1054	
			WDQSTFIGRANHFFTVTDPRNILLTNEQLESARKIVHDYRQGIV
Í			PPGLTENELWRAKYIYDSAFHPDTGEKMILIGRMSAQVPMNMTI
{		1	TGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTVNEL
	1		GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAANCI
	ĺ		NIPLMRQRELKVGIPVTDENGNRLGESANAAKQAITQVVVSRIL
1			MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGFCLVFA
1			TPLCCALFPQKSSMSVTSLEAELQAKIQESHPELRRVYFNKGL
7130	2	780	HEVPSLQTSDPLPGSVQRCSVVVSQPNKENWCQDHLYNSLGRKG
1		+	ISAKSQPYHRSQSSSSVLINKSMDSINYPSDVGKQQLLSLHRSS
1			RCESHQDLLPDIADSHQQGTEKLSDLTLQDSQKVVVVNRNLPLN
1			AOIATONYFSNFKETDGDEDDYVEIKSEEDESELELSHNRRRKS
1			DSKFVDADFSDNVCSGNTLHSLNSPRTPKKPVNSKLGLSPYLTP
]			YNDSDKLNDYLWRGPSPNQQNIVQSLREKFQCLSSSSFA
7131	805	573	AAAEGHIEVVKFLIEACKVNPFAKDRWGNIPLDDAVQFNHLEVV
/131	803	1 3/3	KLLQDYQDSYTLSETQAEAAAEALSKENLESMV
	1400	1002	IDMLLLSGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTVTA
7132	1420	1087	IIDGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLFLI
	1		
			RLIHKELSCPGSATGDQVPFKEQ
7133	2	3648	QQIPGLLPAHGESGDALRKPRLQKPITGHLDDLFFTLYPSLEKF
			EEELLELHVQDHFQEGCGPLDGGALEILERRLRVGVHNGLGFVQ
	1		RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVLRSRL
	1		RLPEMVGHPAFAVIFQLEYVFSSPAGVDGNAASVTSLSNLACMH
1 .		İ	MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSASMS
		1	SEEVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSRKP
	1		PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQHCL
i	1		The second of the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second secon
			ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLETS
			ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSQISLVLEIS IAEQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSGFP
			IAEQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSGFP
			IAEQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSGFP EILDANKQPAEAVSATEPVTFNPQKEESDCLQSNEMVLQFLAFS
			IAEQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSGFP EILDANKQPAEAVSATEPVTFNPQKEESDCLQSNEMVLQFLAFS RVAQDCRGTSWPKTVYFTFQFYRFPPATTPRLQLVQLDEAGQPS
			IAEQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSGFP EILDANKQPAEAVSATEPVTFNPQKEESDCLQSNEMVLQFLAFS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LEVVATEYEQDNMVVSGDMLGFGRVKPIGVHSVVKGRLHLTLAN
			VGHPCEQKVRGCSTLPPSRSRVISNDGASRFSGGSLLTTGSSRR
			KHVVQAQKLADVDSELAAMLLTHARQGKGPQDVSRESDATRRRK
			LERMRSVRLQEAGGDLGRRGTSVLAQQSVRTQHLRDLOVIAAYR
			ERTKAESIASLLSLAITTEHTLHATLGVABFFEFVLKNPHNTOH
	İ		TVTVEIDNPELSVIVDSQEWRDPKGAAGLHTPVEEDMFHLRGSL
			APQLYLRPHETAHVPFKFQSFSAGQLAMVQASPGLSNEKGMDAV
		:	SPWKSSAVPTKHAKVLFRASGGKPIAVLCLTVELQPHVVDQVFR
ļ			FYHPELSFLKKAIRLPPWHTFPGAPVGMLGEDPPVHVRCSDPNV
1			ICETQNVGPGEPRDIFLKVASGPSPEIKDFFVIIYSDRWLATPT
1		}	QTWQVYLHSLQRVDVSCVAGQLTRLSLVLRGTQTVRKVRAFTSH
			PQELKTDPKGVFVLPPRGVQDLHVGVRPLRAGSRFVHLNLVDVD
			CHQLVASWLVCLCCRQPLISKAFEIMLAAGEGKGVNKRITYTNP
			YPSRRTFHLHSDHPELLRFREDSFQVGGGETYTIGLQFAPSQRV
7174	<del> </del>		GEBEILIYINDHEDKNBEAFCVKVIYQ
7134	2115	1111	GGEGFSYPPHVGLSLGTPLDPHYVLLEVHYDNPTYEEGLIDNSG
}	i		LRLFYTMDIRKYDAGVIEAGLWVSLFHTIPPGMPEFQSEGHCTL
			ECLEEALEAEKPSGIHVFAVLLHAHLAGRGIRLRHFRKGKEMKL
l			LAYDDDFDFNFQEFQYLKEEQTILPGDNLITECRYNTKDRAEMT
			WGGLSTRSEMCLSYLLYYPRINLTRCASIPDIMEQLQFIGVKEI
l			YRPVTTWPFIIKSPKQYKNLSFMDAMNKFKWTKKEGLSFNKLVL
٠ .	1		SLPVNVRCSKTDNAEWSIQGMTALPPDIERPYKAEPLVCGTSSS SSLHRDFSINLLVCLLLLSCTLSTKSL
7135	2	2072	
, 133	_	2072	FVPRVTPRSLSLQGPKGESVGSITQPLPSSYL1FRAASESDGRC WLDALELALRCSSLLRLGTCKPGRDGEPGTSPDASPSSLCGLPA
			SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR
	İ		KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE
			ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH
			ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG
	1.		ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS
			GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG
			ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINOI
			SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR
	1		QRLRQHTVPLEEQTELESERLWQHVTRAISKGDQHRATQEKFAL
			EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP
			LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL
	1		RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC
			PRCRKEARRLQALHEAILSIREAQQBLHRHLSAMLSSTARAAQA
			PTPGLLQSPRSWFLLCVFLACQLFINHILK
7136	2	418	DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK
	1		SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM
	1		HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV
			IRVVET
7137	2	466	WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA
			GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI
			PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT
			RMEQLSDKESYKLSCQLEPENP
7138	2	466	WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA
	}		GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI
			PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT
			RMEQLSDKESYKLSCQLEPENP
7139	1	357	SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ
			LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ
			QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF
7140	1401	1957	RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF
	1		NMNVSLEKQLRPSQPWPRGKCRKTPGWBEARPKAQDLRGDLGKT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
I NO:	location	corresponding	Giutamic Acid, Farhenylaianine, Gaglycine,
1		to first	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding to first		L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			QAGPAEAHTRGPPRLPAATGCPPHLPGLLSGISVDIDPTGLQSQ
ļ	ļ	ĺ	WTPKGQDPPLMFSEDYQKSLLEQYHLGLDQKLRKYVVGELIWNF
			ADFMTNQCG
7141	124	1073	LDSRSCWLDMEDLEEDVRFIVDETLDFGGLSPSDSREEEDITVL
Į	[		VTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLEEILD
1			EANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFVLKDSP
1			VRDLLPTVNSLTRSTPS/LKQPDASTPE***EGVSQGSPGYIWK
			EALQHEEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA
1			AASEETRAAKLRGAAAKSSCQLPIPSAIPRPASRMPLTSRSVPP
			GRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQRLNLPVM
ļ			GATRSNLQPP
7142	658	839	LIFLMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL
1			KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT
			LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP
			ECFEFIEEAKRKDGVVLVHCNA
7143	3	773	SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGO
ł	i		GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGORGG
1			VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA
1	}		SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR
į			KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG
	]		HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI
7144	1	988	FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR
	]		RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD
			SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS
			DTTVKVWNAHKGFCMSTLRTHKDYVKALAYAKDKELVASAGLDR
1	1		QIFLWDVNTLTALTASNNTVTTSSLSGNKDSIYSLAMNOLGTII
			VSGSTEKVLRVWDPRTCAKLMKLKGHTDNVKALLLNRDGTOCLS
1			GSSDGTIRLWSLGQQRCIATYRVHDEGVWALQVNDAFTHVYSGG
			RDRKIYCTDLRNPDIRVLICE
L	L		

TRADOCS:1416260.1(%CSK01!.DOC)

#### WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, and complementary sequences thereof.

- 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
- 4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- 6. A vector comprising the polynucleotide of claim 1.
- 7. An expression vector comprising the polynucleotide of claim 1.
- 8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide encoded by any one of the polynucleotides of claim 1; and

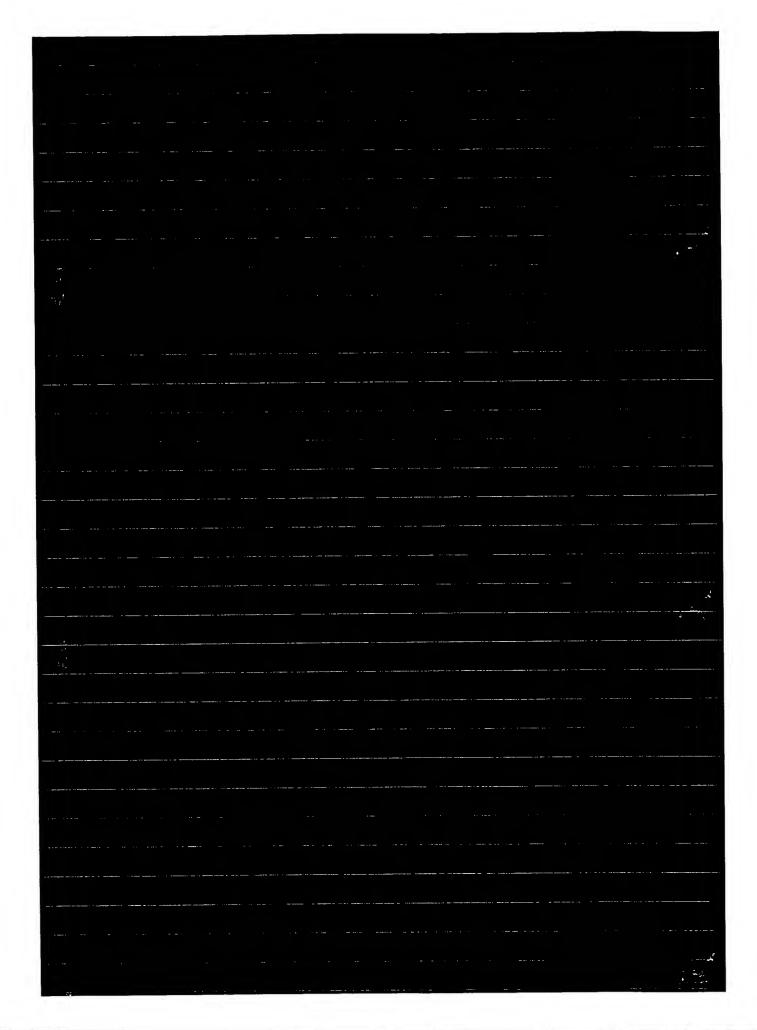
- (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1786 and 3573-5358.
- 11. A composition comprising the polypeptide of claim 10 and a carrier.
- 12. An antibody directed against the polypeptide of claim 10.
- 13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex;
   and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions:
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
- 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
- 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 19. A method of producing the polypeptide of claim 10, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO:1-1786 and 3573-5358, under conditions sufficient to express the polypeptide in said cell; and
  - b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO:1787 -3572 and 5359-7144, the mature protein portion thereof, or the active domain thereof.

- 21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
- 22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO:1-1786 and 3573-5358.
- 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
- 24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
- 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
- 26. The collection of claim 22, wherein the collection is provided in a computerreadable format.
- 27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
- 28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.



### INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

IPC(7)	A. CLASSIFICATION OF SUBJECT MATTER  IPC(7) : C07H 21/04; C12N 15/11, 15/63, 15/70, 15/82, 15/85; C07K 14/00					
US CL	US CL : 536/23.1; 435/320.1, 455, 468, 530/300, 350 According to International Patent Classification (IPC) or to both national classification and IPC					
		HOHAL CIASSIFICATION AND LEC				
	DS SEARCHED					
Minimum doo U.S.: 53	cumentation searched (classification system followed b 36/23.1; 435/320.1, 455, 468, 530/300, 350	y classification symbols)				
Documentation	on searched other than minimum documentation to the	extent that such documents are included in	n the fields searched			
Electronic da MEDLINE, I	ta base consulted during the international search (name	e of data base and, where practicable, sear	rch terms used)			
C. DOC	UMENTS CONSIDERED TO BE RELEVANT					
Category *	Citation of document, with indication, where a		Relevant to claim No.			
A	WAJIMA et al. The cDNA cloning and transient exp hydroxysteroid dehydrogenase of chickens. Gene. 19	oression of an ovary-specific 17beta- 199, Vol.233, pages 75-82	1-11, 13-16, and 19-26			
A	US 5,175,095 A (MARTINEAU et al) 29 December columns 3-18.	1992 (29.12.1992), see especially	1-11, 13-16, and 19-26			
A	Database PubMed, ID No. 2393392, FREUDENSTE inhibitor of metalloproteinase: sequence and expressi Biophys, Res. Commun. August 1990. Vol.171. No.	on in bovine ovarian tissue. Biochem.	I-11, 13-16, and 19-26			
A,P	Database PubMed, ID No. 10919256, HENNEBOL generation and characterization of an ovary-selective library. Endocrinology. August 2000. Vol.141. No.8	complementary deoxyribonucleic acid	1-11, 13-16, and 19-26			
A	Database PubMed, ID No. 2760883, BEIL et al. Syr the baboon (Papio anubis). J. Reprod. Fertil. July 19 Abstract.		1-11, 13-16, and 19-26			
A,P	A,P Database PubMed, ID No. 10830289, HINSHELWOOD et al. A 278 bp region just upstream of the human CYP19 (aromatase) gene mediates ovary-specific expression in transgenic mice. Endocrinology. June 2000. Vol.141. No.6. pages 2050-2053, see Abstract.					
	·					
	documents are listed in the continuation of Box C.	See patent family annex.				
• s	pecial categories of cited documents:	"T" later document published after the inte date and not in conflict with the applic				
	t defining the general state of the art which is not considered to be star relevance	principle or theory underlying the inventor of particular relevance; the	ention			
	plication or patent published on or after the international filing date	considered novel or cannot be conside when the document is taken alone				
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)  "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination						
"P" document published prior to the international filing date but later than the "&" document member of the same patent family priority date claimed						
Date of the actual completion of the international search  Date of mailing of the international search report  Date of mailing of the international search report						
Con Box	ailing address of the ISA/US nmissioner of Patents and Trademarks PCT	Authorizachofficer Michael Woodward	Allen for			
	shington, D.C. 20231 p. (703)305-3230	Telephone No. (703) 308-0196	<i>()</i>			

Form PCT/ISA/210 (second sheet) (July 1998)

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)
This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
1. Claim Nos.:  because they relate to subject matter not required to be searched by this Authority, namely:
Claim Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
Claim Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)
Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)
This International Searching Authority found multiple inventions in this international application, as follows: This includes 4 invention Groups and 3572 sequence species
1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.  2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.  3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:  Remark on Protest  The additional search fees were accompanied by the applicant's protest.  No protest accompanied the payment of additional search fees.

#### INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional serch fees must be paid. Group I, claims 1-11, 13-16, and 19-26, drawn to nucleic acid molecules, vector molecules and host cells containing said nucleic acids, polypeptides, methods of making said polypeptides and method of detection using said nucleic acids and polypeptides. Group II, claim 12 and 28, drawn to antibodies and method of treatment using composition comprising said antibodies. Group IV, claim 17-18, drawn to method of indentifying a binding partner to a polypeptides.

The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, udner PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I encompasses nucleic acids, polypeptides expressed thereby, vectors and host cells containg same, respectively, and methods of making as well as the first method of use of this jubject matter. Groups II-V all are directed to different special technical features as summarized as follows: Group II is directed to an antibody and method of treatment using same, which antibody undergoes recognition and binding reactions wherein what is bound is different from what is bound by the compositions of Group I. For example, the polypeptides of Group I do not bind the polypeptides of Group I as the antibody of Group II does. Identification of binding partner and treatment are clearly different special technical features from detection. Group III is directed to the identification of a binding partner of a polypeptide, which is not identified in any of the other Groups and thus clearly contains its own special technical feature. Group IV is directed to treatment, which is a clearly different methods than the methods in the other Groups. Thus, in summary, each of Groups I-IV are directed to different special technical features and thus support this lack of unity.

Additionally, each of the claims is directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows: The claims include a series of polynucleotides and the polypeptides encoded thereby as represented by the sequences of SEQ ID Nos: 1-1786, and 3573-5358. Each of these polynucleotide sequences encodes a separate polypeptide and thus represent a separate gene. Therefore, each of these genes defines its own special technical feature. In summary, one species is a gene represented by one polynucleotide sequence and one polypeptide sequence encoded thereby.

## **CORRECTED VERSION**

# (19) World Intellectual Property Organization International Bureau



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	C12N 15/11, 15/63, 15/70, 15/82, 15/85,	C07K 14/00

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09/598.042	9 July 2000 (09.07.2000)	US
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09/653,450	3 August 2000 (03.08.2000)	US
09/662,191	14 September 2000 (14.09.2000)	US
09/693,036	19 October 2000 (19.10.2000)	US
09/727.344	29 November 2000 (29.11.2000)	US
031721,011		

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

(CIP) to earlier applications.			
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25 April 2000 (25.04.2000)			
09/598,042 (CIP)			
9 July 2000 (09.07.2000)			
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19 July 2000 (19.07.2000)			
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3 August 2000 (03.08.2000)			
09/662,191 (CIP)			
14 September 2000 (14.09.2000)			
09/693,036 (CIP)			
19 October 2000 (19.10.2000)			
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#### Published:

with international search report

[Continued on next page]

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.



(48) Date of publication of this corrected version:

1 November 2001

(15) Information about Correction: see PCT Gazette No. 44/2001 of 1 November 2001, Section For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.